

**Table S5. InDel markers (17077) differentiating low pod number-containing parental accession (ILWC 46) and homozygous bulk (LPNB) of a mapping population (Pusa 256 x ILWC 46) from reference *kabuli* accession (CDC Frontier)**

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3') | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                               |                          |                         |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca1_P4_19084336  | Ca1                                     | 19084336                      | TGCAGG/TG                                                     | ACAACAAACCGTGCAATCAA     | ACCCTGGATGCTTGATGAA     | 60.0                             | 631                                           | CDS (FRAME SHIFT)                                 | Ca_17356                            | --                    | NF-X1  |
| Ca1_P4_2073961   | Ca1                                     | 2073961                       | CTTTT/CTTT                                                    | AGAGGCACGAGATTTCAGAA     | AAATATCCCCGCAATAAGGG    | 60.0                             | 336                                           | CDS (FRAME SHIFT)                                 | Ca_00263                            | T                     | M-type |
| Ca1_P4_33781062  | Ca1                                     | 33781062                      | CTTTTTTT/CTTTTTTTTT                                           | AATTTCCCAATCACCCCAAA     | TCCACAATGTCTCCCAAA      | 60.0                             | 517                                           | CDS (FRAME SHIFT)                                 | Ca_19460                            | --                    | --     |
| Ca1_P4_45244574  | Ca1                                     | 45244574                      | TC/TCATAAAGCTCAC                                              | TCGGGGTCTTGCAATAAAG      | GACAATGGGAATTCGCTAA     | 60.1                             | 532                                           | CDS (FRAME SHIFT)                                 | Ca_26020                            | --                    | --     |
| Ca2_P4_17551687  | Ca2                                     | 17551687                      | G/GC                                                          | ATGTGGTTGATAAGGCTCTCG    | AGCAAATGCAATGCTCTGAA    | 60.0                             | 398                                           | CDS (FRAME SHIFT)                                 | Ca_16000                            | OE                    | --     |
| Ca2_P4_3145520   | Ca2                                     | 3145520                       | GAAGTAAGT/GAAGT                                               | TCGAACTTCGCTTTGTGTG      | TCTTGAATCCCCGTAA        | 60.0                             | 385                                           | CDS (FRAME SHIFT)                                 | Ca_10533                            | --                    | AP2    |
| Ca2_P4_31960983  | Ca2                                     | 31960983                      | CA/C                                                          | TATCATCCTGCCAATGCAAA     | CCCCCTCCTCCTCTCACTAC    | 60.0                             | 322                                           | CDS (FRAME SHIFT)                                 | Ca_17822                            | E                     | --     |
| Ca2_P4_32424473  | Ca2                                     | 32424473                      | TGATGGAAGATA/T                                                | TTGCAATTGTATGCAAGTTTCTTT | CGGATTTTTTCAGTGTGAGGG   | 60.1                             | 775                                           | CDS (FRAME SHIFT)                                 | Ca_10276                            | --                    | SAP    |
| Ca2_P4_35715341  | Ca2                                     | 35715341                      | CCNNNNNNNNNC/CC                                               | TCTGCATCACTCTGCTTGCT     | GATCAATGGCACACAA        | 59.9                             | 100                                           | CDS (FRAME SHIFT)                                 | Ca_09742                            | O                     | --     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca3_P4_13185454  | Ca3                                     | 13185454                      | AT/ATTT                                                       | GCACACGACCTTCTCG<br>TACA | AATCTGGATCGGGAA<br>AATC  | 59.9                             | 302                                           | CDS (FRAME<br>SHIFT)                              | Ca_22687                            | --                    | Trihelix |
| Ca3_P4_33243720  | Ca3                                     | 33243720                      | CTT/CT                                                        | GATGTGGCTGCAACAG<br>CTTA | TGACAGACTCGTCGTT<br>CAGG | 60.0                             | 462                                           | CDS (FRAME<br>SHIFT)                              | Ca_12059                            | --                    | --       |
| Ca3_P4_35768993  | Ca3                                     | 35768993                      | TAAAAAAAAA/TAAAAAAAAA                                         | AAAAAGCAAGAGCCCC<br>CTAA | TTTCTCTCAACCCACTC<br>ACC | 60.2                             | 477                                           | CDS (FRAME<br>SHIFT)                              | Ca_00863                            | U                     | bZIP     |
| Ca4_P4_2032207   | Ca4                                     | 2032207                       | TC/T                                                          | TGCTGAGTTCGAGAA<br>AGGT  | CACATCTCTGTTCGCT<br>CCA  | 60.0                             | 517                                           | CDS (FRAME<br>SHIFT)                              | Ca_07822                            | D                     | --       |
| Ca4_P4_2035160   | Ca4                                     | 2035160                       | CAA/CA                                                        | TAATGCATGGCCTGAC<br>AAAC | TGGGCAGCTTAGACTG<br>GACT | 59.5                             | 692                                           | CDS (FRAME<br>SHIFT)                              | Ca_07822                            | D                     | --       |
| Ca4_P4_25975114  | Ca4                                     | 25975114                      | TGGGG/TGGGGG                                                  | ACACATGTTGGCCAAT<br>GAGA | GAGTCCGATTTCATG<br>AGGA  | 60.0                             | 621                                           | CDS (FRAME<br>SHIFT)                              | Ca_16608                            | --                    | --       |
| Ca4_P4_27855296  | Ca4                                     | 27855296                      | CAAAAAAAAA/CAAAAAAAAA                                         | ATCTTCACAAAGCCATT<br>GCC | CGTTCCATGGTGTCTT<br>TGTG | 60.1                             | 927                                           | CDS (FRAME<br>SHIFT)                              | Ca_21302                            | --                    | --       |
| Ca4_P4_39780105  | Ca4                                     | 39780105                      | GACA/GA                                                       | TGAAGCTAAGGCATCC<br>AACA | TTTCCATGTGTCGAGA<br>CCCT | 59.4                             | 295                                           | CDS (FRAME<br>SHIFT)                              | Ca_14927                            | --                    | --       |
| Ca4_P4_5960166   | Ca4                                     | 5960166                       | CTTGTGGTGATGTGT/CTTGTGGTG<br>ATGTGTTGTGGTGATGTGT              | GAATCAGCCACTGAGT<br>GCAA | AATGCCACCTACCTCA<br>ACG  | 60.0                             | 257                                           | CDS (FRAME<br>SHIFT)                              | Ca_03652                            | --                    | HD-ZIP   |
| Ca4_P4_8342865   | Ca4                                     | 8342865                       | T/TTAAG                                                       | GAGCTTCAACCACAAG<br>CACA | GCTTTTGTAGCAACTC<br>GTCC | 60.0                             | 691                                           | CDS (FRAME<br>SHIFT)                              | Ca_08321                            | --                    | --       |

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|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_11169613  | Ca5                                     | 11169613                      | C/CG                                                          | TGAAGCAGTTGTTGG<br>GTGA  | GAGCCCAATCCAAA<br>TTCA   | 60.3                             | 225                                           | CDS (FRAME<br>SHIFT)                              | Ca_23744                            | A                     | --  |
| Ca5_P4_23672060  | Ca5                                     | 23672060                      | TC/TCGCCC                                                     | TGAGTAAGGGGGCTGA<br>AATG | TGAGAGACGGTGGTTT<br>ACCC | 60.1                             | 822                                           | CDS (FRAME<br>SHIFT)                              | Ca_17683                            | --                    | --  |
| Ca5_P4_25856813  | Ca5                                     | 25856813                      | CTTTT/CTTTTT                                                  | GAACCCGCGTATGACT<br>TGTT | TTACTGACGCAAAC<br>ACCC   | 60.0                             | 312                                           | CDS (FRAME<br>SHIFT)                              | Ca_09017                            | S                     | --  |
| Ca5_P4_31824861  | Ca5                                     | 31824861                      | CAA/CAAA                                                      | GTGGCATCGAGGAGAT<br>AAGC | CGACGTTAGGGGTCTT<br>TTGA | 59.8                             | 596                                           | CDS (FRAME<br>SHIFT)                              | Ca_04889                            | --                    | SAP |
| Ca5_P4_38085194  | Ca5                                     | 38085194                      | ATT/AT                                                        | TTTACTTGTTTCGCACG<br>CAG | CAATTTACCGGCGTTT<br>CCTA | 60.1                             | 233                                           | CDS (FRAME<br>SHIFT)                              | Ca_01410                            | --                    | --  |
| Ca5_P4_41768893  | Ca5                                     | 41768893                      | TGG/TG                                                        | ATGGCGTATATTCTGG<br>TCCG | ACGCCCAAAATGATAC<br>AAGC | 59.8                             | 238                                           | CDS (FRAME<br>SHIFT)                              | Ca_19205                            | O                     | --  |
| Ca6_P4_12233101  | Ca6                                     | 12233101                      | TG/TGG                                                        | CCTCAACGTGAGTTGC<br>AGAA | TGCATGGCATTGGAT<br>AAGA  | 60.0                             | 344                                           | CDS (FRAME<br>SHIFT)                              | Ca_24847                            | --                    | --  |
| Ca6_P4_1349360   | Ca6                                     | 1349360                       | A/ACTCT                                                       | ATGCCTCATTCCCAA<br>CAAG  | TTCTGAGTGGCACCT<br>ATCC  | 59.9                             | 165                                           | CDS (FRAME<br>SHIFT)                              | Ca_27264                            | S                     | --  |
| Ca6_P4_13987966  | Ca6                                     | 13987966                      | CG/CGTG                                                       | CAAACCTGCAAGAGTG<br>ACGA | TCCCCTGAAAAATGAG<br>ATGC | 60.0                             | 863                                           | CDS (FRAME<br>SHIFT)                              | Ca_05163                            | --                    | --  |
| Ca6_P4_17183232  | Ca6                                     | 17183232                      | ATTTT/ATTT                                                    | AATGGTTGAGTTGGCG<br>AGTC | CCAGTTTGGTCACACC<br>CTCT | 60.1                             | 680                                           | CDS (FRAME<br>SHIFT)                              | Ca_06338                            | L                     | --  |

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|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                                             |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca6_P4_2379069   | Ca6                                     | 2379069                       | T/TCAAG                                                                     | GGTCTCAGTTGCAGCA<br>CAAA | CCGATTGGGTTAGCTG<br>TGTT | 60.0                             | 305                                           | CDS (FRAME<br>SHIFT)                              | Ca_10369                            | T                     | MYB    |
| Ca6_P4_32124189  | Ca6                                     | 32124189                      | CTT/CTTT                                                                    | TTTGCCAATGTTGCTA<br>GCTG | CGAGCTAAGAAAAACC<br>GTGC | 60.0                             | 662                                           | CDS (FRAME<br>SHIFT)                              | Ca_15213                            | --                    | --     |
| Ca7_P4_14452319  | Ca7                                     | 14452319                      | ACNNNNNNNNNC/AC                                                             | TTGAAGCTGCAACAAG<br>AGGA | GGGGAACCTGTAGTGG<br>ACAA | 59.7                             | 305                                           | CDS (FRAME<br>SHIFT)                              | Ca_09993                            | C                     | bHLH   |
| Ca7_P4_20149771  | Ca7                                     | 20149771                      | CTTTTT/CTTTT                                                                | GACGAAAGTCTCTTCC<br>CGTG | TTGGTTTGTTTTTCCTT<br>CGG | 59.8                             | 398                                           | CDS (FRAME<br>SHIFT)                              | Ca_12378                            | --                    | --     |
| Ca7_P4_20488727  | Ca7                                     | 20488727                      | TC/T                                                                        | CAACATGGTGCTCTT<br>GTGC  | ATTGCCCCATGTTTCAA<br>GAG | 60.0                             | 731                                           | CDS (FRAME<br>SHIFT)                              | Ca_12399                            | T                     | M-type |
| Ca7_P4_22886024  | Ca7                                     | 22886024                      | G/GCTAC                                                                     | GCCCTTCTATGCTTGT<br>CAGC | TTGGGAAGGTATGAAG<br>GCAG | 60.0                             | 728                                           | CDS (FRAME<br>SHIFT)                              | Ca_19525                            | S                     | ARF    |
| Ca7_P4_25563600  | Ca7                                     | 25563600                      | AAGAGAGAGAGAGAGAGAGAGA<br>GAGAGAGA/AAGAGAGAGAGAGAG<br>AGAGAGAGAGAGAGAGAGAGA | CACAACAAGAACGAC<br>GGTG  | GAGGCTACGTGTTGTA<br>CGCA | 60.2                             | 603                                           | CDS (FRAME<br>SHIFT)                              | Ca_23609                            | KT                    | --     |
| Ca7_P4_26694678  | Ca7                                     | 26694678                      | TCCCCC/TCCCCCCCCC                                                           | CTCGCCATCCGAGAT<br>ATAA  | GCTCACTAACTCTGCC<br>TGGG | 60.0                             | 881                                           | CDS (FRAME<br>SHIFT)                              | Ca_16250                            | --                    | --     |
| Ca7_P4_30966048  | Ca7                                     | 30966048                      | CT/C                                                                        | CTTGCCAATTCCAGT<br>CCAT  | TATTCAGATCCCTTGCC<br>CAG | 59.9                             | 136                                           | CDS (FRAME<br>SHIFT)                              | Ca_23312                            | --                    | --     |
| Ca7_P4_35480318  | Ca7                                     | 35480318                      | CAAAA/CAAA                                                                  | GCGTCCAGTCTGGTAT<br>TGGT | AGGGTTAGTGGTCGTT<br>GGTG | 60.0                             | 201                                           | CDS (FRAME<br>SHIFT)                              | Ca_17756                            | --                    | --     |

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|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|----------|
|                        |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca7_P4_39347364        | Ca7                                     | 39347364                      | AGGGG/AGGG                                                    | CGTGTCTGAACGCTT<br>ATGA  | TGTCGTCCAAGACACC<br>ACAT | 60.0                             | 674                                           | CDS (FRAME<br>SHIFT)                                 | Ca_19589                            | R                     | bHLH     |
| Ca7_P4_40430153        | Ca7                                     | 40430153                      | AAGTAAGTA/AAGTAAGTAGTAAGTA                                    | GTTGGTTCAAAAGCAA<br>CCGT | ACAAGGATACGTGCAG<br>GGAC | 60.0                             | 493                                           | CDS (FRAME<br>SHIFT)                                 | Ca_20258                            | --                    | Trihelix |
| Ca7_P4_43840665        | Ca7                                     | 43840665                      | GC/GCCC                                                       | GCGTTTTTATGGTTGC<br>TGGT | GAGTCACCCCAAGTGC<br>AAAT | 60.0                             | 304                                           | CDS (FRAME<br>SHIFT)                                 | Ca_21356                            | --                    | --       |
| Ca7_P4_5911086         | Ca7                                     | 5911086                       | TGGGG/TGGGGG                                                  | CGGTAAAGCTTCAAAA<br>CCCA | TATGCAGCAAAATGAA<br>CCCA | 60.1                             | 379                                           | CDS (FRAME<br>SHIFT)                                 | Ca_06767                            | --                    | bHLH     |
| Ca8_P4_14074282        | Ca8                                     | 14074282                      | CCGCG/CCG                                                     | AAACAAAATCCACGCG<br>ACTC | TAGGTTCCAAAGGTGC<br>CAAC | 60.0                             | 606                                           | CDS (FRAME<br>SHIFT)                                 | Ca_22744                            | U                     | --       |
| scaffold1202_P4_253511 | scaffold1202                            | 253511                        | GCGACTCACGA/GCGA                                              | ACTCACGAGTCACCAG<br>TCCC | GTGGTACGAAAATCTC<br>CCGA | 60.2                             | 699                                           | CDS (FRAME<br>SHIFT)                                 | Ca_24668                            | --                    | --       |
| scaffold1252_P4_66355  | scaffold1252                            | 66355                         | AGGGGGG/AGGGGGGG                                              | AGGTGGGTTGAGTTGT<br>CAGG | TTGACTCTTGGGAAGT<br>TGGG | 60.0                             | 808                                           | CDS (FRAME<br>SHIFT)                                 | Ca_27777                            | --                    | --       |
| scaffold1414_P4_190587 | scaffold1414                            | 190587                        | GAA/GAAA                                                      | TCGGATCACGGTCTGA<br>TACA | GAGGCAATGGGACAA<br>GGTA  | 60.1                             | 611                                           | CDS (FRAME<br>SHIFT)                                 | Ca_25542                            | R                     | --       |
| scaffold1418_P4_15609  | scaffold1418                            | 15609                         | G/GC                                                          | GAACACTTGAAGGGCA<br>TGGT | GGATTTGGTGGAGGGA<br>AAAT | 60.0                             | 590                                           | CDS (FRAME<br>SHIFT)                                 | Ca_25260                            | R                     | bHLH     |
| scaffold1521_P4_19418  | scaffold1521                            | 19418                         | CAAAA/CAAA                                                    | GAAGAATGGGAACAAT<br>GCGT | CAACGGGCAAAAATGA<br>AACT | 59.9                             | 748                                           | CDS (FRAME<br>SHIFT)                                 | Ca_26979                            | --                    | bHLH     |

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|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1548_P4_887    | scaffold1548                            | 887                           | TTT/TTTATACATT                                                | CGTTTTCTTCTCCATT<br>GGG   | CAGCCATAACCAAGCC<br>ATT       | 59.5                             | 600                                           | CDS (FRAME<br>SHIFT)                              | Ca_27706                            | QI                    | --  |
| scaffold1580_P4_251123 | scaffold1580                            | 251123                        | CNNNNNNNNNN/C                                                 | TGTTCTCTTAGGGGGT<br>GGTG  | GGCCATCTTTTAAACC<br>CCTT      | 60.0                             | 569                                           | CDS (FRAME<br>SHIFT)                              | Ca_20799                            | B                     | --  |
| scaffold167_P4_63349   | scaffold167                             | 63349                         | AA/AAAACCAATGA                                                | ATGGTCAAGACCTGGA<br>TTGC  | TCATGGCTCTTGTGC<br>TCAC       | 59.9                             | 709                                           | CDS (FRAME<br>SHIFT)                              | Ca_24147                            | R                     | MYB |
| scaffold1722_P4_66168  | scaffold1722                            | 66168                         | TG/TGG                                                        | CCAGAGACGATGGACA<br>AGGT  | CGAACGGGTAGTTGAC<br>GATT      | 60.1                             | 649                                           | CDS (FRAME<br>SHIFT)                              | Ca_26630                            | G                     | --  |
| scaffold1964_P4_11803  | scaffold1964                            | 11803                         | TAGAATTATGCAG/TAGAATTATGCA<br>GAATTATGCAG                     | GCACCATTCCTCTTT<br>GGAA   | GATGGACCACCTTCTC<br>TCCA      | 60.1                             | 553                                           | CDS (FRAME<br>SHIFT)                              | Ca_25209                            | G                     | --  |
| scaffold273_P4_189091  | scaffold273                             | 189091                        | C/CCTAAGATTAA                                                 | TTTTGGTGACAACACC<br>TGGA  | GCAACTATGGTAGGGC<br>GGTA      | 60.0                             | 415                                           | CDS (FRAME<br>SHIFT)                              | Ca_26225                            | --                    | --  |
| scaffold290_P4_675706  | scaffold290                             | 675706                        | AAGC/AAGCTGGCATAGTGCAGC                                       | AAATGATGGTCCAAC<br>GAGC   | GGGCTACATGGTGATG<br>GAAC      | 59.9                             | 251                                           | CDS (FRAME<br>SHIFT)                              | Ca_19845                            | --                    | --  |
| scaffold3837_P4_5910   | scaffold3837                            | 5910                          | ACCC/ACC                                                      | ACCTCGATCTGGAAAT<br>CACG  | ATTGAGGGTAGGGGAG<br>CAGT      | 60.1                             | 467                                           | CDS (FRAME<br>SHIFT)                              | Ca_27570                            | --                    | --  |
| scaffold543_P4_69059   | scaffold543                             | 69059                         | TGGGG/TGGGGG                                                  | TCGCTACTGAAGATGG<br>GCTT  | TTGATAACTTGAAAACG<br>AAATGAAA | 60.0                             | 363                                           | CDS (FRAME<br>SHIFT)                              | Ca_24780                            | --                    | --  |
| scaffold587_P4_17163   | scaffold587                             | 17163                         | AC/A                                                          | GGAAAAATCCATGAGGC<br>AAGA | AGGCCCAAAGAAGAG<br>TGAT       | 60.0                             | 496                                           | CDS (FRAME<br>SHIFT)                              | Ca_27621                            | --                    | --  |

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|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                       |                                         |                               |                                                                     |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| scaffold599_P4_234597 | scaffold599                             | 234597                        | TC/T                                                                | TTGCTCCCTTCAACAAT<br>TCC | ATTGCAGGAACATGGA<br>AAGC | 60.1                             | 352                                           | CDS (FRAME<br>SHIFT)                              | Ca_25342                            | O                     | --   |
| scaffold772_P4_152481 | scaffold772                             | 152481                        | GTT/GT                                                              | GGAGGATCTATGGTGC<br>TGA  | GTGTTCTGCCGCTTTTT<br>CTC | 60.0                             | 170                                           | CDS (FRAME<br>SHIFT)                              | Ca_26416                            | --                    | --   |
| scaffold772_P4_23600  | scaffold772                             | 23600                         | G/GAGAGACATGTGTT                                                    | GGAAACAATGCCTCCA<br>AGAA | GGAGGATGGTAACGAC<br>GAAA | 60.1                             | 191                                           | CDS (FRAME<br>SHIFT)                              | Ca_26413                            | --                    | --   |
| scaffold864_P4_247808 | scaffold864                             | 247808                        | TGGGG/TGGGGG                                                        | TTCTGCCCTCATGGAT<br>TTTC | CATGGCTCGAGTGAAA<br>CAGA | 60.0                             | 349                                           | CDS (FRAME<br>SHIFT)                              | Ca_24213                            | --                    | --   |
| scaffold949_P4_3822   | scaffold949                             | 3822                          | CAAAAA/CAAAAAA                                                      | AAGAGGGGCGTGAAC<br>TTTT  | GCTTCATACCTGTTTT<br>GGG  | 60.1                             | 646                                           | CDS (FRAME<br>SHIFT)                              | Ca_25481                            | --                    | --   |
| Ca1_P4_14441702       | Ca1                                     | 14441702                      | CNNNNNNNNN/CNNNNNNN                                                 | TTTCATTTTCTCTGC<br>CAC   | TTGGTGTGGAATTG<br>TTGA   | 60.1                             | 408                                           | CDS (large-effect<br>mutations)                   | Ca_07092                            | --                    | --   |
| Ca1_P4_5494812        | Ca1                                     | 5494812                       | TTCA/T                                                              | GTAAAGCAGTTGCAGG<br>GGAG | CAATTTTGGCCATGAC<br>CTCT | 59.9                             | 551                                           | CDS (large-effect<br>mutations)                   | Ca_00634                            | --                    | --   |
| Ca1_P4_6417631        | Ca1                                     | 6417631                       | AAGGAGGAG/AAGGAG                                                    | TGTGATTGAGCCAGAA<br>AAGC | CCATCCTTTGGCAGTG<br>AAAT | 59.0                             | 454                                           | CDS (large-effect<br>mutations)                   | Ca_07905                            | P                     | MIKC |
| Ca1_P4_6489856        | Ca1                                     | 6489856                       | AAAGAGCAAGAGCAAGAGCAAGAG<br>CAAGAGCA/AAAGAGCAAGAGCAAG<br>AGCAAGAGCA | CCTGGTTGGCTGATGA<br>AAGT | CTCCGTTTAGGTGCTG<br>GAAC | 60.1                             | 513                                           | CDS (large-effect<br>mutations)                   | Ca_07911                            | D                     | B3   |
| Ca2_P4_30867703       | Ca2                                     | 30867703                      | GCAACAACA/GCAACA                                                    | AAGACGAGACTGGCTG<br>CAAT | AGGTCGTCGAAGTTTG<br>TTGG | 60.0                             | 496                                           | CDS (large-effect<br>mutations)                   | Ca_12474                            | R                     | C3H  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)  | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|-----------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                       |                                         |                               |                                                                |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca2_P4_35944964       | Ca2                                     | 35944964                      | CAAAA/CA                                                       | TCCAACCATACCTGAA<br>AGGC  | CTCGTGCGAACTTGTG<br>TGTT  | 59.9                             | 313                                           | CDS (large-effect<br>mutations)                   | Ca_09769                            | --                    | --          |
| Ca4_P4_44625405       | Ca4                                     | 44625405                      | CATGATGATGATGATGATGA/CATG<br>ATGATGATGATGA                     | TTGAGGGAGTCCAATC<br>CAAG  | AGCTTTCAAGGGCTTC<br>TTCC  | 60.0                             | 744                                           | CDS (large-effect<br>mutations)                   | Ca_09133                            | --                    | WRKY        |
| Ca5_P4_24097297       | Ca5                                     | 24097297                      | AAGCTTTGGATAC/A                                                | CAGAGCCAACACTACA<br>GGCA  | ATTTGAAGGGCCATGT<br>GAAG  | 60.0                             | 329                                           | CDS (large-effect<br>mutations)                   | Ca_17656                            | S                     | --          |
| scaffold290_P4_848963 | scaffold290                             | 848963                        | AGCGCGCCCTGCGCGCC/AGCGCG<br>CC                                 | GCAAACATACATCCGAC<br>AGCA | CCGAGTTCCCAAGAGT<br>CAAA  | 59.9                             | 215                                           | CDS (large-effect<br>mutations)                   | Ca_19852                            | --                    | --          |
| Ca1_P4_1801730        | Ca1                                     | 1801730                       | ACACACAACGAGTC/ACACACAACG<br>AGTCACACAACGAGTC                  | CAGGGAAAATTCCAAG<br>CTGA  | TGGACAAGAGCATCTG<br>CAAC  | 60.2                             | 565                                           | CDS (large-effect<br>mutations)                   | Ca_00228                            | F                     | MYB_related |
| Ca1_P4_6345643        | Ca1                                     | 6345643                       | AATGATGATGATGATGATGATG/AAT<br>GATGATGATGATGATGATGATG<br>ATGATG | CACCTTGTCACACAC<br>ACCC   | TTTGTTGCCAATGTTGT<br>TTCA | 59.9                             | 450                                           | CDS (large-effect<br>mutations)                   | Ca_07895                            | --                    | --          |
| Ca1_P4_7630412        | Ca1                                     | 7630412                       | G/GACAAAA                                                      | TCGTTGCGAAGATAGT<br>GTGG  | AGCATGAGTTGCACAA<br>GTGG  | 59.9                             | 768                                           | CDS (large-effect<br>mutations)                   | Ca_08016                            | --                    | HD-ZIP      |
| Ca2_P4_25228216       | Ca2                                     | 25228216                      | T/TTGG                                                         | TGTCCTTTTCAAACCCC<br>ATC  | ACAAGCAAAACCTCAC<br>CACC  | 59.8                             | 351                                           | CDS (large-effect<br>mutations)                   | Ca_14254                            | R                     | --          |
| Ca3_P4_30899185       | Ca3                                     | 30899185                      | G/GACA                                                         | CTTTAGTGGGAGCCA<br>TGAA   | GAAATTCGCCATTTTCT<br>GGA  | 60.1                             | 520                                           | CDS (large-effect<br>mutations)                   | Ca_12186                            | O                     | --          |
| Ca4_P4_11311023       | Ca4                                     | 11311023                      | CATTATTATTATTATTAT/CATT<br>TTATTATTATTATTAT                    | ATGTTTATGTCCGTC<br>CCTC   | GGCCAACCATCAACCA<br>TATC  | 59.8                             | 434                                           | CDS (large-effect<br>mutations)                   | Ca_04364                            | D                     | WRKY        |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)          | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                        |                            |                           |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_14398669  | Ca4                                     | 14398669                      | GTCTTCTT/GTCTTCTTCTT                                                   | GGCAAGTACAAAGGGC<br>ATGT   | GTTGCTGGAAGGCAGA<br>GTTC  | 60.0                             | 426                                           | CDS (large-effect<br>mutations)                      | Ca_05664                            | --                    | --   |
| Ca4_P4_17663581  | Ca4                                     | 17663581                      | CGTGGTGGTGGTGGTGG/CGT<br>GGTGGTGGTGGTGGTGG                             | TGCCGTGTGGACATGA<br>GTAT   | CCAACTAGGCCAAAAGC<br>TTCG | 60.0                             | 338                                           | CDS (large-effect<br>mutations)                      | Ca_05362                            | O                     | --   |
| Ca4_P4_26900710  | Ca4                                     | 26900710                      | TTGGTCCTGGTC/TTGGTCCTGGTC<br>CTGGTC                                    | CCACATGAGTGTGTG<br>AGGG    | TCTGATCTTCAGGACC<br>ACCC  | 60.0                             | 241                                           | CDS (large-effect<br>mutations)                      | Ca_20442                            | --                    | SAP  |
| Ca4_P4_28516642  | Ca4                                     | 28516642                      | TTCTAA/TTCTAACTCTAA                                                    | TAATCTTCGGCGAAAC<br>TGCT   | TAACAACTCTGGTGCTG<br>CTCG | 60.0                             | 897                                           | CDS (large-effect<br>mutations)                      | Ca_26231                            | --                    | --   |
| Ca4_P4_30538166  | Ca4                                     | 30538166                      | AAAGAAG/AAAGAAGAAG                                                     | TTGTTCTTGCATTTCCA<br>TTTTG | CGCCATCTTCCTCTTCT<br>TTG  | 60.0                             | 380                                           | CDS (large-effect<br>mutations)                      | Ca_14204                            | --                    | NAC  |
| Ca4_P4_39183756  | Ca4                                     | 39183756                      | A/ATGAAGTGGG                                                           | AATTTGCAGGTGGAAT<br>CGTC   | GCAAGCGAACAACATT<br>GAGA  | 59.9                             | 348                                           | CDS (large-effect<br>mutations)                      | Ca_13064                            | T                     | bHLH |
| Ca4_P4_40578315  | Ca4                                     | 40578315                      | G/GGTC                                                                 | GCAGGTCTTTTTGGTG<br>GAAA   | AACCCCTTCATCTTTCGC<br>CTT | 60.1                             | 608                                           | CDS (large-effect<br>mutations)                      | Ca_14868                            | K                     | --   |
| Ca4_P4_44968440  | Ca4                                     | 44968440                      | GATAATAATAATAATAATAATAA<br>TAATAA/GATAATAATAATAATAA<br>TAATAATAATAATAA | TAGGCCCCACTTAAAC<br>ATGC   | TCACCATCATCATTTGC<br>ACC  | 60.0                             | 348                                           | CDS (large-effect<br>mutations)                      | Ca_09160                            | R                     | C2H2 |
| Ca4_P4_8712908   | Ca4                                     | 8712908                       | GCAACAACAACAACA/GCAACA<br>ACAACAACAACAACA                              | TGGTGGACACAGAGCA<br>AGTC   | CCCCTTTTGCCTCTCTT<br>TCT  | 59.9                             | 836                                           | CDS (large-effect<br>mutations)                      | Ca_08367                            | R                     | C2H2 |
| Ca5_P4_192213    | Ca5                                     | 192213                        | AGA/AGATGATGA                                                          | TCTTCAGGGATCCCAA<br>CAAC   | CAGTCGGAATCATCCT<br>TGGT  | 59.9                             | 394                                           | CDS (large-effect<br>mutations)                      | Ca_18174                            | L                     | --   |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                       |                                         |                               |                                                                                   |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca6_P4_10848271       | Ca6                                     | 10848271                      | TGGC/TGGCGGC                                                                      | GGCCTCTTTCAACAA<br>TGA    | ACAAATTTGGTGGTG<br>TGGT  | 60.1                             | 311                                           | CDS (large-effect<br>mutations)                   | Ca_08513                            | K                     | MIKC |
| Ca6_P4_1212419        | Ca6                                     | 1212419                       | TTCTG/TTCTGGATCTG                                                                 | GCGTGCCATAGTGGA<br>GATT   | CTCCACCTTTACTTGC<br>TGC  | 60.1                             | 576                                           | CDS (large-effect<br>mutations)                   | Ca_13328                            | R                     | bHLH |
| Ca6_P4_5033352        | Ca6                                     | 5033352                       | TGAAGAAGAAGAAGAAG/T<br>GAAGAAGAAGAAGAAGAA<br>G                                    | ACCACCACTGATGATG<br>ACGA  | GAGCGTTGGAGTGAGA<br>GGAG | 60.0                             | 343                                           | CDS (large-effect<br>mutations)                   | Ca_05790                            | --                    | --   |
| Ca7_P4_12415176       | Ca7                                     | 12415176                      | ACACAATCACAATCACAATCACAAT<br>CACAAATCAACACAATCACAATCACA<br>ATCACAATCACAATCACAATCA | TGAAATCTCATGGCAT<br>GCTT  | ACCCTTTGGAGGCCT<br>AAGA  | 59.2                             | 370                                           | CDS (large-effect<br>mutations)                   | Ca_09274                            | --                    | --   |
| Ca7_P4_28454949       | Ca7                                     | 28454949                      | CTCTTCTTCTTCTTCTTCTTCTT<br>CTTC/CTCTTCTTCTTCTTCTTCTTC<br>TTCTTCTTCTTCTTC          | CAAAATGGAATGGTT<br>TGGG   | TGGAAGAAGGTTTGA<br>TCCG  | 60.0                             | 688                                           | CDS (large-effect<br>mutations)                   | Ca_18933                            | S                     | --   |
| Ca7_P4_3750531        | Ca7                                     | 3750531                       | ATCATCTTCATCTTC/ATCATCTTCA<br>TCTTCATCTTC                                         | TTGCCTTTGCTTTTGCT<br>TTT  | TCAACCAATGTGGTCC<br>TCAA | 60.0                             | 474                                           | CDS (large-effect<br>mutations)                   | Ca_03093                            | --                    | ARF  |
| Ca7_P4_6089038        | Ca7                                     | 6089038                       | TAAAAAAAAA/TAAAAAAAAA<br>A                                                        | TGTCCTTCGTATATTG<br>GGGG  | TCGAGCACATTCAACT<br>CCTG | 59.6                             | 321                                           | CDS (large-effect<br>mutations)                   | Ca_06750                            | O                     | --   |
| scaffold174_P4_379532 | scaffold174                             | 379532                        | T/TTAC                                                                            | GCCGTTTCATGTTCTAC<br>CGTT | GGTGGTCCTCGTAACC<br>TTGA | 60.0                             | 503                                           | CDS (large-effect<br>mutations)                   | Ca_21720                            | --                    | --   |
| scaffold2161_P4_7991  | scaffold2161                            | 7991                          | CAAG/CAAGAAG                                                                      | CGGACATGTTGGAGAC<br>ACAC  | ACCACCTTGACAAAC<br>TTCC  | 60.0                             | 277                                           | CDS (large-effect<br>mutations)                   | Ca_26956                            | H                     | --   |
| scaffold3015_P4_68656 | scaffold3015                            | 68656                         | A/AACCGGCACAGCC                                                                   | TTCGCAGACAAAATC<br>ATGC   | AGCATTATGGGCCATC<br>TGAG | 60.0                             | 283                                           | CDS (large-effect<br>mutations)                   | Ca_27318                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                 | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                                               |                           |                          |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca1_P4_1849075   | Ca1                                     | 1849075                       | AATTATTATTATTATTATTAT/AA<br>TTATTATTATTATTATTAT                                               | GAATTC AACGGTGTGG<br>GACT | TGTTTGAGCCAAATGT<br>GGAA | 59.8                             | 271                                           | CDS (large-effect<br>mutations)                      | Ca_00232                            | K                     | MYB  |
| Ca1_P4_38561475  | Ca1                                     | 38561475                      | AGAAGTTGAAG/AGAAG                                                                             | TGGTGTGCAAGAGCTG<br>AAAC  | CCACTTGCAAAATG<br>GTG    | 60.0                             | 160                                           | CDS (large-effect<br>mutations)                      | Ca_13957                            | --                    | --   |
| Ca3_P4_21635884  | Ca3                                     | 21635884                      | CGAAGACAAAGAAGAAGA/CGAAGA                                                                     | TGTCATGTTGTGGAGG<br>AGGA  | GGAAGCAATAGAAAT<br>GGCG  | 60.1                             | 573                                           | CDS (large-effect<br>mutations)                      | Ca_09516                            | --                    | --   |
| Ca3_P4_39963962  | Ca3                                     | 39963962                      | AGATCAGGATC/AGATC                                                                             | TTGCAGCCAACACTGA<br>ACTC  | CGTTCTTCGCCTTTCTC<br>AAC | 60.0                             | 578                                           | CDS (large-effect<br>mutations)                      | Ca_01380                            | --                    | --   |
| Ca4_P4_17769895  | Ca4                                     | 17769895                      | GCATCATCATCATCATCA/GCAT<br>CATCATCATCATCA                                                     | AAAACTGGTCGAGGC<br>TGAA   | GCACTCACTTTGCCCT<br>TCTC | 59.9                             | 560                                           | CDS (large-effect<br>mutations)                      | Ca_05348                            | --                    | --   |
| Ca4_P4_8711997   | Ca4                                     | 8711997                       | GAACAACAACAACAACAACAAC<br>AA/GAACAACAACAACA                                                   | AAGGTTTGGTTGGCAA<br>AGTG  | CCCTTGATTGTCCTTGT<br>GCT | 60.0                             | 751                                           | CDS (large-effect<br>mutations)                      | Ca_08367                            | R                     | C2H2 |
| Ca5_P4_5284789   | Ca5                                     | 5284789                       | AGAGGAG/AGAG                                                                                  | CACTGTCACTTTCCTC<br>CGGT  | AAATGTGCTCCAACGT<br>TTCC | 60.2                             | 309                                           | CDS (large-effect<br>mutations)                      | Ca_22622                            | --                    | bHLH |
| Ca6_P4_31218413  | Ca6                                     | 31218413                      | CAATGATAATGATAATGATAATGAT<br>AATGATAATGATAATGAT/CAATGAT<br>AATGATAATGATAATGATAATGATAA<br>TGAT | GCATTTGATAGACGCC<br>CATT  | TTTCACATTCCTTCC<br>CAT   | 59.9                             | 301                                           | CDS (large-effect<br>mutations)                      | Ca_15160                            | --                    | NAC  |
| Ca6_P4_39049911  | Ca6                                     | 39049911                      | TTCCCTCTCCCTCT/TTCCCTCT                                                                       | ATCCAAACATCACCCC<br>AAAA  | AGCGCTGTTTATCGCA<br>TTCT | 60.0                             | 752                                           | CDS (large-effect<br>mutations)                      | Ca_15907                            | --                    | --   |
| Ca7_P4_20609902  | Ca7                                     | 20609902                      | AAACATCGAC/A                                                                                  | AAACCTGACCATGAAG<br>TCGG  | ACAGGCCTAGATGGAG<br>CAGA | 60.0                             | 248                                           | CDS (large-effect<br>mutations)                      | Ca_12413                            | --                    | --   |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |           |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----------|
|                        |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs       |
| Ca7_P4_21698571        | Ca7                                     | 21698571                      | ATCGTCGT/ATCGT                                                | AAGGTAGGGAATCAAT<br>GGGG | CCGACGATGTTGCTTT<br>CTCT | 60.0                             | 423                                           | CDS (large-effect<br>mutations)                      | Ca_14517                            | --                    | NAC       |
| Ca7_P4_33278396        | Ca7                                     | 33278396                      | TTATTATTAATATTATTA/TTATTATT<br>A                              | ATTTATGCGTGGAGGA<br>GGAA | CTCGTTGCGACGTGTA<br>CTGT | 59.5                             | 763                                           | CDS (large-effect<br>mutations)                      | Ca_16155                            | --                    | S1Fa-like |
| Ca7_P4_34237238        | Ca7                                     | 34237238                      | GGTTGTTGTTGTTGTTGTTGTT<br>GT/GGTTGTTGTTGTTGT                  | TTCCCAATTGCAACAAT<br>CAA | GGTCTCATCTCATCCT<br>CCCA | 59.9                             | 437                                           | CDS (large-effect<br>mutations)                      | Ca_20997                            | --                    | S1Fa-like |
| Ca8_P4_1185649         | Ca8                                     | 1185649                       | TAGAAGAAGAA/TAGAAGAA                                          | GACTCGCCAACCAAC<br>CATT  | ACACATGCTCCATACC<br>ACCA | 60.1                             | 282                                           | CDS (large-effect<br>mutations)                      | Ca_15061                            | --                    | --        |
| Ca8_P4_15436905        | Ca8                                     | 15436905                      | GAGAAGAAGAAGAAG/GAGAAG<br>AAGAAGAAG                           | TCTTCCTCACCCACAA<br>GTCC | CCATCTCCACAAGCTT<br>CTCC | 60.1                             | 561                                           | CDS (large-effect<br>mutations)                      | Ca_17897                            | --                    | bHLH      |
| scaffold1006_P4_553062 | scaffold1006                            | 553062                        | GTGCTGCTGCTGCTGCTGCT/GTGC<br>TGCTGCTGCTGCT                    | CTTGCAACAGTATGGG<br>AGGT | AGATTTTCACCCGTTGT<br>TGC | 60.0                             | 376                                           | CDS (large-effect<br>mutations)                      | Ca_18040                            | --                    | --        |
| scaffold240_P4_7668    | scaffold240                             | 7668                          | GATCAT/GAT                                                    | CTGGAAGGCAGAGTTT<br>GGAG | GAAAAGCAACTTGGAT<br>GGGA | 60.0                             | 773                                           | CDS (large-effect<br>mutations)                      | Ca_25652                            | --                    | --        |
| Ca1_P4_3149193         | Ca1                                     | 3149193                       | GA/GATTA                                                      | GATTCGAACAGCAAG<br>AGCC  | ATTCCCGAATATGGTG<br>GACA | 60.0                             | 512                                           | CDS (large-effect<br>mutations)                      | Ca_00385                            | --                    | --        |
| Ca1_P4_6809796         | Ca1                                     | 6809796                       | CAGAAGAAGAAGAAG/CAGAAGAAG<br>AAGAAGAAG                        | CCTCTTGCTGCAACAC<br>AAAA | CCGAACAGAAAAAGCT<br>CGAC | 60.0                             | 528                                           | CDS (large-effect<br>mutations)                      | Ca_07947                            | S                     | --        |
| Ca1_P4_7992079         | Ca1                                     | 7992079                       | ACTCCTCCTCCTCCT/ACTCCTCCTC<br>CTCCTCCT                        | TGATTCTCTCCCATGC<br>CATT | TTCTTCAGCTGGTGTT<br>GCAC | 60.4                             | 450                                           | CDS (large-effect<br>mutations)                      | Ca_08049                            | --                    | WRKY      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                 | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                                                                               |                          |                          |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca1_P4_7992471   | Ca1                                     | 7992471                       | TGTAGTA/TGTAGTAGTA                                                                                            | GTGCAACACCAGCTGA<br>AGAA | CAACATCATGATCAATG<br>GCA | 60.0                             | 310                                           | CDS (large-effect<br>mutations)                      | Ca_08049                            | --                    | WRKY   |
| Ca2_P4_29314373  | Ca2                                     | 29314373                      | GATC/GATCATC                                                                                                  | CCAAAGCAAATCACAG<br>AGCA | AGGTGACATTCATGGG<br>CAGT | 60.0                             | 433                                           | CDS (large-effect<br>mutations)                      | Ca_25184                            | TR                    | FAR1   |
| Ca2_P4_29962574  | Ca2                                     | 29962574                      | TCCGCCGCCG/TCCGCCGCCGCCG                                                                                      | CGGACTCCATAACCTC<br>CTCA | CCTCCTAATCATGGCTT<br>CCA | 60.1                             | 266                                           | CDS (large-effect<br>mutations)                      | Ca_16094                            | A                     | --     |
| Ca2_P4_32243132  | Ca2                                     | 32243132                      | TCAA/TCAACAA                                                                                                  | TCTGAGGGGATTGTT<br>ATGC  | TCCATAACTCTTGCCAA<br>CCC | 60.0                             | 524                                           | CDS (large-effect<br>mutations)                      | Ca_10292                            | --                    | bHLH   |
| Ca2_P4_36372982  | Ca2                                     | 36372982                      | GATTATTATTATTATTAATATTATTAT<br>TA/GATTATTATTATTATTATTATTAT<br>TAATATTATTATTA                                  | TGAGCTGAAATTGTTC<br>GTGC | CCAATCCTCGTTGTCA<br>AGGT | 60.0                             | 274                                           | CDS (large-effect<br>mutations)                      | Ca_09826                            | --                    | HD-ZIP |
| Ca3_P4_22099014  | Ca3                                     | 22099014                      | CAGAAGAAGAAGAAGAAGAAGAAG<br>AAGAAGAAGAAGAAG/CAGAAGAAG<br>AAGAAGAAGAAGAAGAAGAAGAAG<br>AAGAAGAAGAAGAAGAAGAAGAAG | GGAACGAACGTGGAAG<br>TGAT | TCGCGTTAGTTGTTGT<br>GAGG | 60.0                             | 356                                           | CDS (large-effect<br>mutations)                      | Ca_20416                            | O                     | FAR1   |
| Ca3_P4_24304854  | Ca3                                     | 24304854                      | CAGCCT/CAGCCTTAGCCT                                                                                           | CCATAGGCGTCAAAGG<br>AAAA | CCCGTCTCATATCTAC<br>CCGA | 60.1                             | 523                                           | CDS (large-effect<br>mutations)                      | Ca_06090                            | --                    | --     |
| Ca3_P4_36119763  | Ca3                                     | 36119763                      | ACTT/ACTTCTT                                                                                                  | GCATATTCATCACCCC<br>CATC | TCCTTCTTGCAAGTGC<br>TTTT | 60.0                             | 376                                           | CDS (large-effect<br>mutations)                      | Ca_00911                            | D                     | --     |
| Ca3_P4_36426774  | Ca3                                     | 36426774                      | TAGATGAAGATGAAGATGAAGATGA<br>/TAGATGAAGATGAAGATGAAGATG<br>AAGATGA                                             | TCAAAGGAAGCTTAGC<br>CCAA | GCAAACGCTTCTCTGG<br>TTTC | 60.0                             | 861                                           | CDS (large-effect<br>mutations)                      | Ca_00956                            | GM                    | WRKY   |
| Ca3_P4_36429933  | Ca3                                     | 36429933                      | TTCTTCTTCTTCTTCTTCT/TTCTTCT<br>TCTTCTTCTTCTTCTTCTTCT                                                          | AGGGATGCACCAGCTG<br>TAAC | AGAGAAGAAACCTGGT<br>GCGA | 60.1                             | 593                                           | CDS (large-effect<br>mutations)                      | Ca_00957                            | H                     | --     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca3_P4_37211475  | Ca3                                     | 37211475                      | GAACAACAACA/GAACAACAACAAC<br>AACAACA                          | TGGTCAAATTCCTTGA<br>GCAA | TGATCACACCCCAAGT<br>TTTG | 59.2                             | 336                                           | CDS (large-effect<br>mutations)                      | Ca_01053                            | --                    | bHLH   |
| Ca3_P4_6838667   | Ca3                                     | 6838667                       | AGCA/AGCAGGATCCAATGCAATGG<br>CA                               | GGAACCCCAATCAT<br>CATC   | GCAGCCAATTTTGTG<br>CATA  | 60.0                             | 547                                           | CDS (large-effect<br>mutations)                      | Ca_16550                            | R                     | bHLH   |
| Ca4_P4_19228202  | Ca4                                     | 19228202                      | TATG/TATGATCGTGATG                                            | GCAATCTGGAAAGATG<br>GGAA | AAATTCGCCCTGTGTT<br>TTG  | 60.0                             | 288                                           | CDS (large-effect<br>mutations)                      | Ca_14021                            | T                     | WRKY   |
| Ca4_P4_4029055   | Ca4                                     | 4029055                       | GATCATCATCATCAT/GATCATCATC<br>ATCATCATCAT                     | ACATTCTGTGTGGTGG<br>TGGT | ACATTCCAGTCCAAAC<br>CCA  | 60.1                             | 612                                           | CDS (large-effect<br>mutations)                      | Ca_03849                            | --                    | Dof    |
| Ca5_P4_31241305  | Ca5                                     | 31241305                      | GAATTCCAATTCCAATTC/GAATTC<br>CAATTCCAATTCCAATTC               | CGATGAACGCAAACTC<br>AAGA | TAATATTACGCGGAAA<br>CCC  | 60.0                             | 325                                           | CDS (large-effect<br>mutations)                      | Ca_04830                            | R                     | --     |
| Ca5_P4_38030247  | Ca5                                     | 38030247                      | TTCTTG/TTCTTGTTTCATCTTG                                       | TCAAAAACGGACATGA<br>GCAA | TTATGGACAGCTCCC<br>GAAC  | 60.2                             | 614                                           | CDS (large-effect<br>mutations)                      | Ca_01418                            | R                     | DBB    |
| Ca6_P4_26884697  | Ca6                                     | 26884697                      | CT/CTGTGCTTTCCCTACTAAT                                        | TCCTCCAATGATGGCA<br>ATTT | TCAATGCTCAAGTCGC<br>ATTC | 60.3                             | 446                                           | CDS (large-effect<br>mutations)                      | Ca_16720                            | --                    | --     |
| Ca6_P4_7586339   | Ca6                                     | 7586339                       | GTGATGATGATGA/GTGATGATGAT<br>GATGA                            | GCACCTCTTGGACCAT<br>CAAT | ACAGTGTCAAGTCCTA<br>CCCC | 59.9                             | 454                                           | CDS (large-effect<br>mutations)                      | Ca_09626                            | C                     | --     |
| Ca7_P4_20562920  | Ca7                                     | 20562920                      | CTCTTCTTCTT/CTCTTCTTCTT                                       | CATTCTCGCCAATCA<br>GGTT  | TCGATAGCCTCTCGGA<br>GAAA | 60.1                             | 443                                           | CDS (large-effect<br>mutations)                      | Ca_12406                            | --                    | M-type |
| Ca7_P4_30207547  | Ca7                                     | 30207547                      | CCTTCTTCTTCT/CCTTCTTCTTCT<br>CTTCTTCT                         | TTTTGCAAGGAAATGG<br>GTTC | TTTCAATCCACATCGTC<br>CAA | 59.9                             | 380                                           | CDS (large-effect<br>mutations)                      | Ca_11706                            | --                    | --     |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                           | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |      |
|------------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|------|
|                        |                                         |                               |                                                                                         |                          |                          |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_31246533        | Ca7                                     | 31246533                      | CTCAACATCATCA/CTCAACATCATC<br>AACATCATCA                                                | ATCTGGGTTGTTGATC<br>CTGC | AGATGGAGGAGGATG<br>CCCT  | 59.9                             | 108                                           | CDS (large-effect<br>mutations)                      | Ca_10133                            | --                    | --   |
| Ca7_P4_33344144        | Ca7                                     | 33344144                      | CTCTTCGTCCTC/CTCTTCGTCCTCG<br>TCTTC                                                     | TAAATGATTTGCGGTG<br>GTGA | CGTCGATTTCAAGCAC<br>TCAA | 59.9                             | 277                                           | CDS (large-effect<br>mutations)                      | Ca_16160                            | --                    | --   |
| Ca7_P4_6148021         | Ca7                                     | 6148021                       | ATGTT/ATGTTGTT                                                                          | CTAAAGATCGCGGCAG<br>AAAG | GGGATACGTTTGGGGA<br>AAGT | 60.1                             | 471                                           | CDS (large-effect<br>mutations)                      | Ca_06742                            | --                    | --   |
| Ca8_P4_1155325         | Ca8                                     | 1155325                       | CTATTATTATTATTATTATTATTA<br>TTATTAT/CTATTATTATTATTAT<br>TATTATTATTATTAT                 | GCAAAGGAGACAGAAT<br>GGGA | CGCTAGGCTCAATTTT<br>CCTG | 60.2                             | 608                                           | CDS (large-effect<br>mutations)                      | Ca_15064                            | --                    | ERF  |
| Ca8_P4_15577896        | Ca8                                     | 15577896                      | CCA/CCATCA                                                                              | TTTTCAGCAAACCCCA<br>AAAG | TAGAGGCTTGTCATTC<br>GGCT | 60.1                             | 665                                           | CDS (large-effect<br>mutations)                      | Ca_17886                            | T                     | EIL  |
| Ca8_P4_4628017         | Ca8                                     | 4628017                       | GGCAGCAGCAGC/GGCAGCAGCAG<br>CAGC                                                        | CACCACCAACACTGCA<br>AAAC | CAAGAACTTGCTCGTC<br>CTCC | 60.0                             | 787                                           | CDS (large-effect<br>mutations)                      | Ca_02095                            | K                     | TALE |
| Ca8_P4_470107          | Ca8                                     | 470107                        | TTTCTTCTTCTTCTTCTTCTTCT<br>TCTTCTTCTTCTTCTTCTTCTTCT<br>CTTCTTCTTCTTCTTCTTCTTCT<br>TCTTC | AAGTATTCCGTCCGTT<br>GGTG | TCATGGCTTCAACTTAG<br>CCC | 59.9                             | 922                                           | CDS (large-effect<br>mutations)                      | Ca_11888                            | --                    | --   |
| scaffold1045_P4_35689  | scaffold1045                            | 35689                         | CCGATGTCT/CCGATGTCTGCGATG<br>TCT                                                        | AACGAGGCTGGTCCTC<br>ACTA | AGCTGGACTTGATTG<br>TGCT  | 59.9                             | 518                                           | CDS (large-effect<br>mutations)                      | Ca_27889                            | --                    | --   |
| scaffold1067_P4_213896 | scaffold1067                            | 213896                        | ACA/ACAGCA                                                                              | TTTCTTTTCGAGGTGC<br>TGAC | TTCCACCGAATGCTCC<br>TATC | 60.4                             | 370                                           | CDS (large-effect<br>mutations)                      | Ca_24426                            | --                    | --   |
| scaffold174_P4_192046  | scaffold174                             | 192046                        | GGGTGGTGGTGGTGGTGGTGG<br>TG                                                             | AGCAGCACTAGGGCTT<br>GGTA | ATCCCTCACACCATCA<br>CCAT | 60.0                             | 356                                           | CDS (large-effect<br>mutations)                      | Ca_21713                            | R                     | C2H2 |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |          |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|----------|
|                       |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| scaffold2763_P4_9760  | scaffold2763                            | 9760                          | C/CCTCACG                                                     | ATGCCAGTCGTTATTC<br>CCAG | GAGATGCCATTGAAGC<br>CATT | 60.0                             | 400                                           | CDS (large-effect<br>mutations)                      | Ca_24393                            | R                     | --       |
| scaffold584_P4_12275  | scaffold584                             | 12275                         | A/AAAT                                                        | GCAACGTCGGTTTGAA<br>AAGT | TCGTCGTTGTTGTCCA<br>TGTT | 60.2                             | 619                                           | CDS (large-effect<br>mutations)                      | Ca_25249                            | --                    | Trihelix |
| scaffold845_P4_66947  | scaffold845                             | 66947                         | GAACAACAACAACAACAACAA/GAA<br>CAACAACAACAACAACAACAA            | CACCCTAACCTCAACC<br>TCCA | TTGACGACGCATTGGT<br>ACAT | 60.0                             | 547                                           | CDS (large-effect<br>mutations)                      | Ca_22413                            | --                    | --       |
| scaffold847_P4_232160 | scaffold847                             | 232160                        | T/TCCCTCTTTTCTA                                               | TCCAGTCTCATCCGA<br>AATC  | AAGAGTCAACGTCAAT<br>GGGG | 60.0                             | 450                                           | CDS (large-effect<br>mutations)                      | Ca_25695                            | --                    | --       |
| C11140974_P4_511      | C11140974                               | 511                           | ATTTTTTTTTTT/ATTTTTTTTTT                                      | TTCATCACCAAAGTGA<br>GGG  | CATGATTGGTGTTGGC<br>AGTC | 59.3                             | 424                                           | DRR                                                  | Ca_27911                            | --                    | --       |
| C11154966_P4_887      | C11154966                               | 887                           | GAAAAAAAAA/GAAAAAAAAA                                         | TTCAAGAGTCTCCTAG<br>GGCG | TTGCTTGTGTCGTTAG<br>CTGC | 59.6                             | 669                                           | DRR                                                  | Ca_28249                            | E                     | MYB      |
| C11178328_P4_12753    | C11178328                               | 12753                         | CAT/CATTAT                                                    | CCATCTTTTAGGCCTC<br>CTCC | GAAGGCAACCATTCTA<br>GGCA | 60.0                             | 925                                           | DRR                                                  | Ca_28266                            | T                     | M-type   |
| Ca1_P4_10070211       | Ca1                                     | 10070211                      | GAATAATAATAATAATAATAATA<br>A/GAATAATAATAATAATAATAAT<br>AATAA  | TGCTGATGCGTCTGTC<br>CTAC | TTATATGGGAAACCGG<br>AGGG | 60.0                             | 410                                           | DRR                                                  | Ca_02782                            | --                    | --       |
| Ca1_P4_10733080       | Ca1                                     | 10733080                      | T/TG                                                          | CCGTAACGAGTTGTG<br>TTCA  | AAAATGGCACGTTTTTC<br>TGG | 59.6                             | 428                                           | DRR                                                  | Ca_02689                            | --                    | DBB      |
| Ca1_P4_11161524       | Ca1                                     | 11161524                      | ATATATATATTT/AT                                               | TGGAACAATCCGATAC<br>CGTT | AAAAACATGATTCCAAC<br>GCC | 60.2                             | 676                                           | DRR                                                  | Ca_02643                            | R                     | --       |





| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca1_P4_13676036  | Ca1                                     | 13676036                      | CTTTTTTT/CTTTTTT                                              | CCGCTACAAGGCGATA<br>GAAG | TTCTGATGAACGGGGG<br>ATTA   | 60.0                             | 248                                           | DRR                                               | Ca_14132                            | --                    | --   |
| Ca1_P4_13676235  | Ca1                                     | 13676235                      | T/TC                                                          | CCGCTACAAGGCGATA<br>GAAG | GGGTGTCATCATAGGT<br>GGCT   | 60.0                             | 856                                           | DRR                                               | Ca_14132                            | --                    | --   |
| Ca1_P4_13676261  | Ca1                                     | 13676261                      | ACT/ACTCT                                                     | CCGCTACAAGGCGATA<br>GAAG | GGGTGTCATCATAGGT<br>GGCT   | 60.0                             | 856                                           | DRR                                               | Ca_14132                            | --                    | --   |
| Ca1_P4_13676496  | Ca1                                     | 13676496                      | AT/A                                                          | TAATCCCCCGTTCATC<br>AGAA | GGGTGTCATCATAGGT<br>GGCT   | 60.3                             | 628                                           | DRR                                               | Ca_14132                            | --                    | --   |
| Ca1_P4_13676564  | Ca1                                     | 13676564                      | AG/A                                                          | TAATCCCCCGTTCATC<br>AGAA | CAAAATCCCCTGCCTC<br>TACA   | 60.3                             | 933                                           | DRR                                               | Ca_14132                            | --                    | --   |
| Ca1_P4_13677888  | Ca1                                     | 13677888                      | ATTTTTTTTT/ATTTTTTTTT                                         | CGGAATACCCTCTCAA<br>CCAA | GATTTTCCGAAAGGGA<br>ACAA   | 59.9                             | 314                                           | DRR                                               | Ca_14133                            | --                    | ERF  |
| Ca1_P4_13678173  | Ca1                                     | 13678173                      | CTATATATATATATATAT/CTATAT<br>ATATATATATAT                     | CGGAATACCCTCTCAA<br>CCAA | CAAACTCATTAGGAAA<br>AGGGA  | 59.9                             | 463                                           | DRR                                               | Ca_14133                            | --                    | ERF  |
| Ca1_P4_13678320  | Ca1                                     | 13678320                      | CATA/CATAAACGAGCCTATA                                         | TTGTTCCCTTTCGGAA<br>AATC | TCCAAAGTATTTCTGCA<br>TTGAA | 59.0                             | 675                                           | DRR                                               | Ca_14133                            | --                    | ERF  |
| Ca1_P4_13679372  | Ca1                                     | 13679372                      | CTTTT/CTTT                                                    | AGGTGCTCTCCTCTCC<br>ACAG | TTTGGCATGGATAGGG<br>GTTA   | 59.6                             | 429                                           | DRR                                               | Ca_14133                            | --                    | ERF  |
| Ca1_P4_13697453  | Ca1                                     | 13697453                      | TAAAAAAA/TAAAAAAA                                             | TCTGAAACAATTTCCC<br>CTTG | CTAGACCATGGCCGTT<br>CAAT   | 59.1                             | 865                                           | DRR                                               | Ca_14135                            | --                    | bHLH |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                  | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                                                                                                |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca1_P4_13939746  | Ca1                                     | 13939746                      | TATTA/TACTTTATTAATAAATTA                                                                                                                       | TCAGGTGTCTCATCCA<br>CTGC   | TGGATTTCAATGCCA<br>GACA     | 59.8                             | 755                                           | DRR                                               | Ca_07137                            | --                    | --   |
| Ca1_P4_14385063  | Ca1                                     | 14385063                      | CAA/CAAA                                                                                                                                       | AATCGTCTCCGTCACA<br>CACA   | GCGAATTGCAGACTGA<br>AACA    | 60.2                             | 662                                           | DRR                                               | Ca_07096                            | --                    | SAP  |
| Ca1_P4_14591320  | Ca1                                     | 14591320                      | AATATATATATATATATAT/AATATAT<br>ATATATATATATAT                                                                                                  | TTACCTCCGGTGGATG<br>TAGC   | TTGCATGATCAGTGGA<br>AGGT    | 60.0                             | 470                                           | DRR                                               | Ca_07075                            | --                    | --   |
| Ca1_P4_14800179  | Ca1                                     | 14800179                      | AATATATATATATATATA/AATATA<br>TATATATATATATA                                                                                                    | TTGGATGTTGATAAAT<br>GAAGCA | GAGGAATTGTTATTGG<br>TTGTTGG | 59.5                             | 284                                           | DRR                                               | Ca_07050                            | R                     | MYB  |
| Ca1_P4_16215217  | Ca1                                     | 16215217                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATT/TTTATTATTATTATT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>T | GGAAAAAGAGAGAGTG<br>GGGG   | TGAGAGTTTGTGGTCC<br>CCTC    | 60.0                             | 787                                           | DRR                                               | Ca_06936                            | --                    | bHLH |
| Ca1_P4_16866662  | Ca1                                     | 16866662                      | AATATATATATATAT/AATATATATAT<br>ATATAT                                                                                                          | CAATTTGGGTCGTCCA<br>TCTC   | TTAAGACCAACCCGAA<br>CCTG    | 60.3                             | 614                                           | DRR                                               | Ca_06887                            | --                    | --   |
| Ca1_P4_16943629  | Ca1                                     | 16943629                      | TTTTAAATTTA/TTTTAAATTTAAATT<br>TA                                                                                                              | TTTTCTTAAGACGGGC<br>ATGA   | TGAAGGGTATACGGCA<br>CCTC    | 58.4                             | 776                                           | DRR                                               | Ca_06876                            | O                     | --   |
| Ca1_P4_1716073   | Ca1                                     | 1716073                       | TTATATATATATATATATA/TTATATA<br>TATATATATA                                                                                                      | GCCTGAATTTAGCAGA<br>TGGG   | GATTATTGCACAAATC<br>CAAAAA  | 59.7                             | 466                                           | DRR                                               | Ca_00214                            | --                    | bHLH |
| Ca1_P4_1785166   | Ca1                                     | 1785166                       | AG/A                                                                                                                                           | TCTACTTGCGGCAACT<br>TGTG   | CATCATTCCAATCAAGC<br>ACG    | 60.1                             | 319                                           | DRR                                               | Ca_00224                            | S                     | --   |
| Ca1_P4_1785215   | Ca1                                     | 1785215                       | A/AAATG                                                                                                                                        | TCTACTTGCGGCAACT<br>TGTG   | CATCATTCCAATCAAGC<br>ACG    | 60.1                             | 319                                           | DRR                                               | Ca_00224                            | S                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca1_P4_1804269   | Ca1                                     | 1804269                       | CTCAGAA/C                                                     | TCACTTCGAAAGCATG<br>CAAC   | TTGTGGCGTTTGCTAA<br>CTTG    | 60.0                             | 281                                           | DRR                                               | Ca_00228                            | F                     | MYB_related |
| Ca1_P4_1805050   | Ca1                                     | 1805050                       | TAAA/TAAAA                                                    | TTCAGTTGACCTTTCTG<br>CATTT | GGTTGGGATTTTTC<br>ATCA      | 58.9                             | 727                                           | DRR                                               | Ca_00228                            | F                     | MYB_related |
| Ca1_P4_1848130   | Ca1                                     | 1848130                       | AC/A                                                          | ATCTTGGACTCACTGT<br>CGGG   | ACATGCCGTATTCAATC<br>CAT    | 60.1                             | 969                                           | DRR                                               | Ca_00232                            | K                     | MYB         |
| Ca1_P4_1856274   | Ca1                                     | 1856274                       | ACAT/A                                                        | TGTTGGCCACGATCTA<br>ATGA   | TGCCTCGCTATTTTCT<br>AACG    | 60.1                             | 390                                           | DRR                                               | Ca_00233                            | FP                    | bHLH        |
| Ca1_P4_186939    | Ca1                                     | 186939                        | TAA/TAAA                                                      | CTCTTGGGGATCTTC<br>ATCA    | GCATGCCATGTAGTGC<br>ATTT    | 60.0                             | 329                                           | DRR                                               | Ca_00014                            | --                    | --          |
| Ca1_P4_1907609   | Ca1                                     | 1907609                       | ATTTCTTTT/ATTTCTTTCTTTT                                       | TGCAATGATGTCAATT<br>GCTCT  | AAATCAATTTTGGTCCG<br>CTC    | 59.3                             | 926                                           | DRR                                               | Ca_00239                            | --                    | --          |
| Ca1_P4_1907983   | Ca1                                     | 1907983                       | CTT/C                                                         | TTCCCGTGAATTCATC<br>CAT    | GCATGGGAGGATAAAA<br>GCAA    | 60.1                             | 721                                           | DRR                                               | Ca_00239                            | --                    | --          |
| Ca1_P4_1908061   | Ca1                                     | 1908061                       | TTATATA/TTATA                                                 | TTCCCGTGAATTCATC<br>CAT    | GCATGGGAGGATAAAA<br>GCAA    | 60.1                             | 721                                           | DRR                                               | Ca_00239                            | --                    | --          |
| Ca1_P4_1964395   | Ca1                                     | 1964395                       | GTTTTTTT/GTTTTTT                                              | TCCCGCTATGCACATT<br>GTAA   | TGTTTTTCTTCTGGGG<br>TGG     | 60.1                             | 672                                           | DRR                                               | Ca_00244                            | --                    | B3          |
| Ca1_P4_1966252   | Ca1                                     | 1966252                       | TTCTCT/TTCTCTCT                                               | GGCAAGAGAGCATCAA<br>AAGG   | CAAGTGAAGTTTGTATT<br>CAAGGG | 60.0                             | 703                                           | DRR                                               | Ca_00245                            | U                     | bZIP        |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca1_P4_1966518   | Ca1                                     | 1966518                       | CTTTT/CTTT                                                    | CATGCATGTTTACTGA<br>CAATGG | TTTCGAGTTGATTGATT<br>TCGG    | 59.0                             | 540                                           | DRR                                               | Ca_00245                            | U                     | bZIP   |
| Ca1_P4_1986222   | Ca1                                     | 1986222                       | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                 | TATTTTGTCTGTTTGCA<br>CCG   | GAGAAAAAGTTGAAACC<br>ATGACCA | 59.7                             | 394                                           | DRR                                               | Ca_00248                            | T                     | --     |
| Ca1_P4_1987558   | Ca1                                     | 1987558                       | ATAGTAG/ATAG                                                  | GTGGCATAGGCTCCAA<br>TCAT   | GGAATGGTGCTGGACA<br>TTTT     | 59.9                             | 922                                           | DRR                                               | Ca_00248                            | T                     | --     |
| Ca1_P4_2001586   | Ca1                                     | 2001586                       | TAAG/TAAGAAG                                                  | AGCACTGGGCAGAAAG<br>AAAA   | TATCCCTGGCTGATGT<br>AGCA     | 60.0                             | 538                                           | DRR                                               | Ca_00251                            | J                     | --     |
| Ca1_P4_2001789   | Ca1                                     | 2001789                       | ATGT/AT                                                       | AGCACTGGGCAGAAAG<br>AAAA   | CACACGTCATGATCCC<br>CATA     | 60.0                             | 751                                           | DRR                                               | Ca_00251                            | J                     | --     |
| Ca1_P4_2006799   | Ca1                                     | 2006799                       | CTTT/CTTTT                                                    | ATAGACCTCTTGTGGT<br>GCGG   | TGTGTTTGGGTGTGA<br>GAGA      | 60.1                             | 400                                           | DRR                                               | Ca_00252                            | --                    | TCP    |
| Ca1_P4_2015582   | Ca1                                     | 2015582                       | TTGT/TT                                                       | CTCTAGAACCCCAAC<br>TCCC    | CTCCAATGTTGGGAGA<br>CTACG    | 59.9                             | 499                                           | DRR                                               | Ca_00253                            | E                     | --     |
| Ca1_P4_2023148   | Ca1                                     | 2023148                       | A/AC                                                          | TGCAGTTTCGGTAGGG<br>AAGT   | CGACGAGATTTACTTT<br>GACCG    | 59.7                             | 541                                           | DRR                                               | Ca_00254                            | FP                    | bHLH   |
| Ca1_P4_2023898   | Ca1                                     | 2023898                       | TAA/TAAA                                                      | TAATGAGGGCTTGAAT<br>TCGC   | TCCGTTTGTGAGGATG<br>ATGA     | 60.2                             | 386                                           | DRR                                               | Ca_00255                            | --                    | --     |
| Ca1_P4_2055811   | Ca1                                     | 2055811                       | ATTTTTT/ATTTTTTT                                              | TCGTTTCCCTGTAATT<br>CTTGG  | CAACAACCTCTCATGCT<br>CGC     | 60.3                             | 573                                           | DRR                                               | Ca_00260                            | T                     | M-type |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca1_P4_2058722   | Ca1                                     | 2058722                       | CAGAGAGA/CAGAGA                                               | CGGTTCTACCGTCCTA<br>ACCA   | CAATCCTCCTCCCCTT<br>CTC     | 60.0                             | 204                                           | DRR                                               | Ca_00261                            | --                    | --          |
| Ca1_P4_2058843   | Ca1                                     | 2058843                       | CAAAA/CAA                                                     | GAGAAAGGGGAGGAG<br>GATTG   | AGACTCTGCAGCCACC<br>TCAT    | 60.0                             | 357                                           | DRR                                               | Ca_00261                            | --                    | --          |
| Ca1_P4_2091338   | Ca1                                     | 2091338                       | T/TA                                                          | GTGTGGAAAGTAGCCC<br>CAAA   | TCGAACTGTTGTTCTG<br>GCTG    | 60.0                             | 164                                           | DRR                                               | Ca_00266                            | --                    | MYB_related |
| Ca1_P4_2213930   | Ca1                                     | 2213930                       | GATAATAATAATAATAATAATA<br>TA/GATAATAATAATAATAATA              | TGTGCAACAGCAATG<br>AATG    | TACGTTGCTGAATTC<br>GTG      | 59.3                             | 341                                           | DRR                                               | Ca_00276                            | --                    | --          |
| Ca1_P4_22204858  | Ca1                                     | 22204858                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATAT                   | TGACATTTGAACTTGA<br>GTTTCC | CACAAGTCGCCATTTG<br>GAAT    | 60.5                             | 532                                           | DRR                                               | Ca_20635                            | --                    | TALE        |
| Ca1_P4_2248466   | Ca1                                     | 2248466                       | AT/AATT                                                       | GCCGGATTCACGTGAT<br>AGAT   | CGATGTCTGTTGACGG<br>AGTG    | 59.9                             | 593                                           | DRR                                               | Ca_00281                            | O                     | --          |
| Ca1_P4_2299200   | Ca1                                     | 2299200                       | TAAA/TAAAA                                                    | CAGCAACTGCGATGAG<br>ATGT   | GAATCAAAGGACACGA<br>TCCAA   | 60.0                             | 227                                           | DRR                                               | Ca_00288                            | R                     | --          |
| Ca1_P4_2300704   | Ca1                                     | 2300704                       | T/TG                                                          | CATTCCATTCTCATTG<br>CCT    | GCAAGTGCTGATGATG<br>CTGT    | 59.9                             | 556                                           | DRR                                               | Ca_00288                            | R                     | --          |
| Ca1_P4_2323997   | Ca1                                     | 2323997                       | GTTAATTAATTAA/GTTAATTAA                                       | GGGCCTCAACAAAGCT<br>TACA   | TCCACAAACATGCATTA<br>ATCAAC | 60.2                             | 431                                           | DRR                                               | Ca_00291                            | V                     | NAC         |
| Ca1_P4_2324632   | Ca1                                     | 2324632                       | ATTTTTTT/ATTTTTTTTTTT                                         | TTAAGCTGAGCACTTC<br>CAAGA  | GAATCCGAAACCACAC<br>GAAT    | 57.9                             | 523                                           | DRR                                               | Ca_00291                            | V                     | NAC         |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_2341397   | Ca1                                     | 2341397                       | ATCAGTT/AT                                                    | GTGACATGGTTGCAGAGGTG    | GGTTTGCTGCCACTTGAAAT    | 60.2                             | 852                                           | DRR                                               | Ca_00294                            | A                     | --  |
| Ca1_P4_2341920   | Ca1                                     | 2341920                       | G/GC                                                          | ATTTCAAGTGGCAGCAAAACC   | TCATTTTGCTCATGCTTTGG    | 60.1                             | 521                                           | DRR                                               | Ca_00294                            | A                     | --  |
| Ca1_P4_23426642  | Ca1                                     | 23426642                      | TAAA/TAAAA                                                    | AAGTTAAGGAACCACGAGTGC   | AGAGAAGTGAATGGTGCATACAA | 58.4                             | 790                                           | DRR                                               | Ca_19317                            | --                    | --  |
| Ca1_P4_2347223   | Ca1                                     | 2347223                       | TCCC/TCC                                                      | TGGCAATATCACAGCCAT      | CCCTATCACAAACCACCCAC    | 60.0                             | 826                                           | DRR                                               | Ca_00295                            | --                    | Dof |
| Ca1_P4_2347337   | Ca1                                     | 2347337                       | TTCT/TTCTCT                                                   | TGCCTGCAACAAGTAATGGA    | TGGCACAGAAGCAAAGAATG    | 60.3                             | 947                                           | DRR                                               | Ca_00295                            | --                    | Dof |
| Ca1_P4_2347502   | Ca1                                     | 2347502                       | TAAAA/TAAA                                                    | CGTATTGAAAATCCGTGCAA    | TGGCACAGAAGCAAAGAATG    | 59.6                             | 779                                           | DRR                                               | Ca_00295                            | --                    | Dof |
| Ca1_P4_2347965   | Ca1                                     | 2347965                       | C/CG                                                          | GTGGGTGGTTTGTGATAGGG    | CTGTGGGGCAAACAAAAGAT    | 60.1                             | 482                                           | DRR                                               | Ca_00295                            | --                    | Dof |
| Ca1_P4_2348870   | Ca1                                     | 2348870                       | ATAAATTTT/ATAAATTTTAAATT                                      | TTGCTTATAGGCATGGGAC     | AACCACGTTTCCGAAAATATC   | 59.9                             | 437                                           | DRR                                               | Ca_00295                            | --                    | Dof |
| Ca1_P4_23496241  | Ca1                                     | 23496241                      | CT/CTTT                                                       | AGGGTGGATCAGTTCCGATTG   | TTATATTAATTGGGTGCGCGT   | 59.9                             | 376                                           | DRR                                               | Ca_19314                            | --                    | --  |
| Ca1_P4_2358700   | Ca1                                     | 2358700                       | GAA/GAAA                                                      | TAACGGATTTTGACGATCCA    | CGCTTCGGCTTTTCTTACAG    | 59.0                             | 847                                           | DRR                                               | Ca_00296                            | L                     | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca1_P4_2360177   | Ca1                                     | 2360177                       | TGG/T                                                         | ACACCGTCGAAGAAGC<br>TGTT | CGCATGGGCTTATGAT<br>TTTT | 59.9                             | 898                                           | DRR                                               | Ca_00297                            | --                    | --   |
| Ca1_P4_2369335   | Ca1                                     | 2369335                       | ATAGTACTACTCCATTAGTACTACT<br>CCATTA/ATAGTACTACTCCATTA         | ACATCACGATTTTTCCC<br>AAA | CCTATTTAGCATGTTGC<br>CGC | 57.9                             | 165                                           | DRR                                               | Ca_00301                            | DR                    | --   |
| Ca1_P4_2369599   | Ca1                                     | 2369599                       | TTG/TTGTG                                                     | CAACTAGCGGCAACAT<br>GCTA | AGTACAACCCCTATT<br>GCCC  | 60.0                             | 496                                           | DRR                                               | Ca_00301                            | DR                    | --   |
| Ca1_P4_2399709   | Ca1                                     | 2399709                       | CCTTTT/C                                                      | TGCGAGACCAGAAGAA<br>AGGT | GCCAGCTTGAGCTGAT<br>TTCT | 60.0                             | 417                                           | DRR                                               | Ca_00306                            | O                     | --   |
| Ca1_P4_24030518  | Ca1                                     | 24030518                      | C/CATGTT                                                      | CCAATTCAAAAGCTCC<br>CAAA | CAGATCCTCCTTTCCC<br>AACA | 60.0                             | 424                                           | DRR                                               | Ca_19291                            | OK                    | --   |
| Ca1_P4_2443873   | Ca1                                     | 2443873                       | CTTT/CTT                                                      | CAATATCCATGCAGTG<br>GTCG | TAAGGTGTGTGGTGGC<br>AGAA | 59.9                             | 224                                           | DRR                                               | Ca_00309                            | --                    | --   |
| Ca1_P4_2452266   | Ca1                                     | 2452266                       | CTTTTTTTTT/CTTTTTTT                                           | TTGCAAAGCTGTTGAG<br>GTTG | TTACCGTGAGACGAAG<br>GGAC | 60.0                             | 347                                           | DRR                                               | Ca_00310                            | --                    | --   |
| Ca1_P4_24636488  | Ca1                                     | 24636488                      | ATTTT/ATTTATTTT                                               | GATGGTGTGAGTGGAG<br>CTGA | AAACACGTTGGCATT<br>GTGA  | 59.8                             | 906                                           | DRR                                               | Ca_18338                            | --                    | --   |
| Ca1_P4_2470802   | Ca1                                     | 2470802                       | ATTT/ATT                                                      | GACGTTATCGACTGGG<br>CAAT | GCGTGAGTAGCAAACG<br>AACA | 60.0                             | 320                                           | DRR                                               | Ca_00312                            | J                     | bHLH |
| Ca1_P4_2471521   | Ca1                                     | 2471521                       | ATTCTT/ATT                                                    | TTCGTTTGCTACTCAC<br>GCAC | TGACTTATTCAGGCC<br>TGCT  | 60.1                             | 310                                           | DRR                                               | Ca_00312                            | J                     | bHLH |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                           |                          |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca1_P4_24797994  | Ca1                                     | 24797994                      | GTTTT/GTTT                                                                | TGATTTTCGAAGACTT<br>GGGG | TGCATCGTTCTCCTCTT<br>CCT     | 60.0                             | 894                                           | DRR                                               | Ca_18329                            | T                     | --   |
| Ca1_P4_25539046  | Ca1                                     | 25539046                      | CATATATATATATATATATATATATA<br>TA/CATATATATATATATATATATATA<br>TATATATATATA | CTGATGTTGGTCCTGG<br>TCCT | AACCAACCCAACGAGA<br>AGTG     | 60.0                             | 684                                           | DRR                                               | Ca_25082                            | --                    | --   |
| Ca1_P4_25781138  | Ca1                                     | 25781138                      | GG/GGGAAATACTTG                                                           | GCTTCAAGAGACGAAA<br>TCCG | ACACGACCGATAGGGA<br>TCAG     | 60.0                             | 709                                           | DRR                                               | Ca_18582                            | --                    | --   |
| Ca1_P4_26473008  | Ca1                                     | 26473008                      | CTAAATT/CTAAATTCTGTAAATT                                                  | CCATTGACCCTTGCAA<br>ACTT | CTGCAGGAAGCTAAAA<br>TCCG     | 60.0                             | 368                                           | DRR                                               | Ca_18608                            | R                     | NAC  |
| Ca1_P4_2669284   | Ca1                                     | 2669284                       | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                             | CCCCAACTTTGAAGC<br>AACT  | TTTGCTGCTATGTG<br>CCTC       | 59.2                             | 344                                           | DRR                                               | Ca_00327                            | --                    | ERF  |
| Ca1_P4_2670477   | Ca1                                     | 2670477                       | AACA/AA                                                                   | TAGCAGACTCCAAATC<br>CCCA | AAACCAGCGGTTTCAA<br>TCTG     | 60.6                             | 778                                           | DRR                                               | Ca_00327                            | --                    | ERF  |
| Ca1_P4_2686396   | Ca1                                     | 2686396                       | GTT/GTTT                                                                  | AAACGCCATTGCACCT<br>TAAC | CAATTCATATCGGCAAT<br>CCC     | 60.0                             | 684                                           | DRR                                               | Ca_00328                            | --                    | MIKC |
| Ca1_P4_2686857   | Ca1                                     | 2686857                       | TG/T                                                                      | AATGTGATGCACGTTT<br>TGGA | CAATTTACGCAACAA<br>TCG       | 60.0                             | 444                                           | DRR                                               | Ca_00328                            | --                    | MIKC |
| Ca1_P4_2691980   | Ca1                                     | 2691980                       | AAGAG/AAG                                                                 | TTAGCTCAGCTTGAC<br>AGGA  | GCATTGTACATTCTCGT<br>GCG     | 59.9                             | 541                                           | DRR                                               | Ca_00330                            | --                    | --   |
| Ca1_P4_2692135   | Ca1                                     | 2692135                       | AC/ACCTC                                                                  | ACAATGCCATTTTCAAG<br>GCT | CGTGAAGACTAAAGGT<br>CAGAAAAA | 59.6                             | 532                                           | DRR                                               | Ca_00330                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca1_P4_2693052   | Ca1                                     | 2693052                       | CT/CTT                                                        | CAACCAGTAATAATGC<br>GCCA | CGTGACAGAGGACGCT<br>TGTA | 59.6                             | 468                                           | DRR                                               | Ca_00330                            | --                    | --     |
| Ca1_P4_2693080   | Ca1                                     | 2693080                       | TAAAAAAAA/TAAAAAAAAA                                          | CAACCAGTAATAATGC<br>GCCA | CGTGACAGAGGACGCT<br>TGTA | 59.6                             | 468                                           | DRR                                               | Ca_00330                            | --                    | --     |
| Ca1_P4_27597440  | Ca1                                     | 27597440                      | ATT/AT                                                        | AAATCCAACAATCTCC<br>CCC  | CCCTGAGACTCACGAA<br>GAGG | 60.0                             | 559                                           | DRR                                               | Ca_25069                            | --                    | --     |
| Ca1_P4_2802326   | Ca1                                     | 2802326                       | GTTT/GTT                                                      | GGGTTACAGACCGACC<br>TTGA | TCGGCAGTTGTGATCG<br>AATA | 60.0                             | 242                                           | DRR                                               | Ca_00344                            | --                    | NAC    |
| Ca1_P4_2802455   | Ca1                                     | 2802455                       | ATTTTT/ATTTT                                                  | GGGTTACAGACCGACC<br>TTGA | GCGGATTTGTCCATCT<br>TTGT | 60.0                             | 765                                           | DRR                                               | Ca_00344                            | --                    | NAC    |
| Ca1_P4_2808661   | Ca1                                     | 2808661                       | TAAA/TAAAAA                                                   | TCATGTTGTTGCCGT<br>TTGT  | TCAGCACAATCAACAA<br>GGGA | 60.0                             | 233                                           | DRR                                               | Ca_00345                            | T                     | M-type |
| Ca1_P4_2831499   | Ca1                                     | 2831499                       | GTTTTTTTTTTTTT/GTTTTTTTTT<br>TT                               | CCTCTGACCACATGGG<br>ACTT | TCAAAAACAAAAGCGC<br>ACTG | 60.0                             | 625                                           | DRR                                               | Ca_00347                            | --                    | ARF    |
| Ca1_P4_2831879   | Ca1                                     | 2831879                       | TAAAA/TAAAAA                                                  | TTTGAGTCTTCGAGCC<br>ACAG | CTGGTCCTTTCCTTTCC<br>CTC | 59.2                             | 342                                           | DRR                                               | Ca_00347                            | --                    | ARF    |
| Ca1_P4_2867118   | Ca1                                     | 2867118                       | CA/CAA                                                        | AGGAGCCTTTGGTTTT<br>GGTT | TCCCTCTTCCCTTTCT<br>CAT  | 60.0                             | 555                                           | DRR                                               | Ca_00348                            | R                     | --     |
| Ca1_P4_2867217   | Ca1                                     | 2867217                       | ATTTTTTT/ATTTTTTTTT                                           | AGGAGCCTTTGGTTTT<br>GGTT | TCCCTCTTCCCTTTCT<br>CAT  | 60.0                             | 555                                           | DRR                                               | Ca_00348                            | R                     | --     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca1_P4_2875002   | Ca1                                     | 2875002                       | CTTTTTTTTT/CTTTTTTTTT                                         | TGCCAAAGGTAATTTT<br>CCG  | GCCCGCAAAAGTTAAA<br>AGAA    | 59.9                             | 149                                           | DRR                                               | Ca_00349                            | --                    | --     |
| Ca1_P4_2877412   | Ca1                                     | 2877412                       | CA/CAA                                                        | TTTGGTTCAGAAGCTG<br>GACA | AATCGACGCCGATGAC<br>TAAC    | 59.4                             | 565                                           | DRR                                               | Ca_00350                            | GC                    | SBP    |
| Ca1_P4_2884045   | Ca1                                     | 2884045                       | TAAA/TAA                                                      | GAGCTTCTCCACCTCA<br>CGTC | GTGGCATTGAGGTGAG<br>GAAT    | 60.0                             | 412                                           | DRR                                               | Ca_00351                            | T                     | M-type |
| Ca1_P4_2884405   | Ca1                                     | 2884405                       | AGAGACATT/A                                                   | ATTCTCACCTGAATG<br>CCAC  | TGAAAGCATCATGCAC<br>ACAA    | 59.9                             | 511                                           | DRR                                               | Ca_00351                            | T                     | M-type |
| Ca1_P4_2884853   | Ca1                                     | 2884853                       | GTTTT/GTTT                                                    | TCTCCGTCGTGTTGTG<br>TTGT | ATTGCGGAGTTAACAA<br>TGGC    | 60.2                             | 743                                           | DRR                                               | Ca_00351                            | T                     | M-type |
| Ca1_P4_2885377   | Ca1                                     | 2885377                       | ATTTTTTT/ATTTTTTTTT                                           | GCCATTGTAACTCCG<br>CAAT  | CATTGGAGAGGGCAT<br>AGGA     | 60.0                             | 360                                           | DRR                                               | Ca_00351                            | T                     | M-type |
| Ca1_P4_2886871   | Ca1                                     | 2886871                       | ATTTTTTTTTTT/ATTTTTTTTTTTTT                                   | ACAATGACACAGTCGG<br>TGGA | CAATTGCATTTTGTAGT<br>CTTTCA | 60.0                             | 167                                           | DRR                                               | Ca_00352                            | --                    | --     |
| Ca1_P4_28910299  | Ca1                                     | 28910299                      | CATT/CATTAAATT                                                | GAAAATGATCGGTGGA<br>GGAA | CTTGCGTGTTGCACGA<br>GTAT    | 59.9                             | 620                                           | DRR                                               | Ca_18486                            | R                     | --     |
| Ca1_P4_28910417  | Ca1                                     | 28910417                      | CTTTTTTT/CTTTTTTTTTTT                                         | GAGTCATTGGTGCTT<br>GGTT  | CTTGCGTGTTGCACGA<br>GTAT    | 60.0                             | 385                                           | DRR                                               | Ca_18486                            | R                     | --     |
| Ca1_P4_28910492  | Ca1                                     | 28910492                      | GATTAA/GATTAAATTAA                                            | GAGTCATTGGTGCTT<br>GGTT  | CTTGCGTGTTGCACGA<br>GTAT    | 60.0                             | 385                                           | DRR                                               | Ca_18486                            | R                     | --     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)            | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                          |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca1_P4_2904188   | Ca1                                     | 2904188                       | TG/T                                                                     | AGGAAGCAGGTGATG<br>GGAT  | ACACGGAAGTTGGTT<br>CCTG  | 60.0                             | 602                                           | DRR                                               | Ca_00354                            | --                    | bHLH     |
| Ca1_P4_2904668   | Ca1                                     | 2904668                       | A/AAAAGAGTGG                                                             | CAGGAAACCAACTTCC<br>GTGT | GGCAAAGAAAGCAGTT<br>CCAG | 60.0                             | 849                                           | DRR                                               | Ca_00354                            | --                    | bHLH     |
| Ca1_P4_2932731   | Ca1                                     | 2932731                       | AA/AATAGGTTGA                                                            | GAATCTGGTTCGCAC<br>TCAT  | GATTCCGGTATTTGCC<br>TCAA | 60.1                             | 771                                           | DRR                                               | Ca_00358                            | E                     | --       |
| Ca1_P4_2933145   | Ca1                                     | 2933145                       | AAGA/AAGAGA                                                              | CACACGGTCACAATCG<br>AACT | AGTGCCTTGGACATTT<br>TGG  | 59.6                             | 590                                           | DRR                                               | Ca_00358                            | E                     | --       |
| Ca1_P4_29386975  | Ca1                                     | 29386975                      | AATATATATATATATATATATATAT<br>AT/AATATATATATATATATATATAT<br>TATATATATATAT | TCGTTTCCCAGAGAAG<br>CAAC | AGAAATGCGGGTTAT<br>GTCT  | 60.4                             | 743                                           | DRR                                               | Ca_22561                            | R                     | HB-other |
| Ca1_P4_29422590  | Ca1                                     | 29422590                      | TT/TTATGAT                                                               | AGTGGATCGGGTGAA<br>CAAG  | GTGCGTCGAAACTA<br>GCTC   | 60.0                             | 783                                           | DRR                                               | Ca_22560                            | --                    | --       |
| Ca1_P4_2952450   | Ca1                                     | 2952450                       | GTT/GT                                                                   | ACCTCAAATCCGCAAA<br>GATG | GTGCAAGAGTTTGCT<br>TGGT  | 60.1                             | 571                                           | DRR                                               | Ca_00360                            | --                    | ERF      |
| Ca1_P4_2952486   | Ca1                                     | 2952486                       | CAATAAATAAATAAATA/CAATAAATA<br>AATAAATAAATA                              | ACCTCAAATCCGCAAA<br>GATG | GTGCAAGAGTTTGCT<br>TGCT  | 60.1                             | 571                                           | DRR                                               | Ca_00360                            | --                    | ERF      |
| Ca1_P4_2980062   | Ca1                                     | 2980062                       | ATTTTTTTTT/ATTTTTTTTT                                                    | TTGTTCAAGATTTGTT<br>GGCA | AAGTTTGGGAGGCCAT<br>AACC | 60.1                             | 665                                           | DRR                                               | Ca_00362                            | PET                   | NAC      |
| Ca1_P4_2981588   | Ca1                                     | 2981588                       | GC/G                                                                     | TGTTCGGCCATTAGAC<br>ATCA | AATCGCCCATTTCTCCT<br>CTT | 60.1                             | 345                                           | DRR                                               | Ca_00361                            | --                    | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                              |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca1_P4_29846530  | Ca1                                     | 29846530                      | CTTTT/CTTTT                                                   | TGGATTGGGGATCATT<br>CATT     | TCAACATTGGAAGCA<br>CAAGA  | 60.0                             | 897                                           | DRR                                               | Ca_24388                            | --                    | --   |
| Ca1_P4_29846941  | Ca1                                     | 29846941                      | TAAAAAAAA/TAAAAAAAA                                           | TGTTGCCAACTGAAAA<br>TCGT     | ATACAGACACCGAATG<br>GGGA  | 59.2                             | 828                                           | DRR                                               | Ca_24388                            | --                    | --   |
| Ca1_P4_3030441   | Ca1                                     | 3030441                       | AATATATAT/AATATAT                                             | AATAGTGAGGGGTGGA<br>GGCT     | TGATGGATGAGACAAA<br>ATGCC | 60.0                             | 415                                           | DRR                                               | Ca_00367                            | --                    | --   |
| Ca1_P4_3030828   | Ca1                                     | 3030828                       | TAAAAAA/TAAAAAA                                               | TCACACACATGGTGCA<br>GCTA     | CTGCTTTGCACACGCA<br>TATT  | 59.9                             | 710                                           | DRR                                               | Ca_00367                            | --                    | --   |
| Ca1_P4_3033238   | Ca1                                     | 3033238                       | CT/CTTT                                                       | CCGCTGAAGTTGAAGC<br>AGTA     | TCAGTTGCAAAGCCAA<br>ACAC  | 59.2                             | 758                                           | DRR                                               | Ca_00369                            | --                    | --   |
| Ca1_P4_3036457   | Ca1                                     | 3036457                       | TC/T                                                          | TGAAGAGAGAATGAGG<br>GGGA     | TTGAGCCATTGATTTTG<br>TGC  | 59.7                             | 662                                           | DRR                                               | Ca_00370                            | --                    | ARF  |
| Ca1_P4_3036576   | Ca1                                     | 3036576                       | ATTTTT/ATTTTTT                                                | TGAAGAGAGAATGAGG<br>GGGA     | CCTTATTCAACGGCTG<br>GTGT  | 59.7                             | 801                                           | DRR                                               | Ca_00370                            | --                    | ARF  |
| Ca1_P4_3071285   | Ca1                                     | 3071285                       | C/CAAAAAATTTAATTG                                             | AGGCACAAATGGAGCA<br>AATC     | TCCATTGACCATTTTC<br>ACA   | 60.1                             | 623                                           | DRR                                               | Ca_00374                            | EH                    | bHLH |
| Ca1_P4_3079517   | Ca1                                     | 3079517                       | A/AAATTTTTTG                                                  | TCAAATTCGTAACCAA<br>ATCTTCAA | ATTGCCCAAGACATTA<br>TCG   | 59.2                             | 478                                           | DRR                                               | Ca_00375                            | --                    | bHLH |
| Ca1_P4_3087515   | Ca1                                     | 3087515                       | CAAA/CAAAA                                                    | GGGCAATTCTATCGCT<br>CAAA     | ACTGGTGGACGAGCAA<br>GACT  | 60.2                             | 681                                           | DRR                                               | Ca_00376                            | --                    | bHLH |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca1_P4_31498685  | Ca1                                     | 31498685                      | AGG/AG                                                        | TTGGAGCTTCAGCATT<br>TGTG | CCTCTTTTCTTCGCATT<br>TCG | 60.0                             | 747                                           | DRR                                               | Ca_21863                            | --                    | M-type |
| Ca1_P4_33105635  | Ca1                                     | 33105635                      | TC/T                                                          | TGCCAAGAACGATAAA<br>AGCA | TTCTGCATTTTCCTTGA<br>GCA | 59.4                             | 101                                           | DRR                                               | Ca_19438                            | --                    | --     |
| Ca1_P4_33388984  | Ca1                                     | 33388984                      | ATTTTTTTTTTTTTT/ATTTTTTTTTT<br>TTTTTTT                        | TGTTGACGTTTCAACG<br>GAGA | TCCCTATTCAACCCCT<br>TTC  | 60.3                             | 136                                           | DRR                                               | Ca_19442                            | --                    | --     |
| Ca1_P4_33722196  | Ca1                                     | 33722196                      | AAGA/AA                                                       | GATTTTACGAGGATGG<br>CGAA | ATGAGCGAGGTAGAAG<br>CCAA | 60.0                             | 610                                           | DRR                                               | Ca_19456                            | --                    | --     |
| Ca1_P4_338839    | Ca1                                     | 338839                        | AACA/AA                                                       | CTTTGATTTGAATTTGG<br>CCC | AGTTGGGTCCTTGCTT<br>TTTT | 59.4                             | 399                                           | DRR                                               | Ca_00034                            | S                     | B3     |
| Ca1_P4_34005765  | Ca1                                     | 34005765                      | ATA/ATAGTA                                                    | AATCGTTTCGCAAGAC<br>CTTC | CGACGCTTGATCGTTA<br>ATTG | 59.3                             | 539                                           | DRR                                               | Ca_27634                            | --                    | --     |
| Ca1_P4_34136656  | Ca1                                     | 34136656                      | ATTTTTTTT/ATTTTTTTT                                           | TTTCTTGGTGACCCAC<br>ATCA | AAGTCGAGGACAATGC<br>TTGC | 59.9                             | 338                                           | DRR                                               | Ca_25472                            | QI                    | bHLH   |
| Ca1_P4_34137295  | Ca1                                     | 34137295                      | CTTT/CTT                                                      | GCAAGCATTGTCCTCG<br>ACTT | TGTTACCAGGCTGAAC<br>CACA | 60.4                             | 845                                           | DRR                                               | Ca_25472                            | QI                    | bHLH   |
| Ca1_P4_34160353  | Ca1                                     | 34160353                      | ATT/AT                                                        | GGTTTCGCCCTGACAT<br>AAAA | ACTCTGGACACTTGGG<br>TTGC | 59.9                             | 773                                           | DRR                                               | Ca_25473                            | O                     | --     |
| Ca1_P4_34730486  | Ca1                                     | 34730486                      | TTTTA/TTTAGTCCTTTA                                            | ATATGACTCCTGAGCG<br>GTGC | TTTTTCCGACTTGGTCC<br>TTT | 60.2                             | 501                                           | DRR                                               | Ca_21419                            | --                    | C3H    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca1_P4_34865996  | Ca1                                     | 34865996                      | TAATAAAATAATAA/TAATAATAAA<br>TAAATAAA                         | TTGTTTCGAGAATTGG<br>AGGG    | TGAGGTGGTGACCAAT<br>TGAA   | 60.0                             | 462                                           | DRR                                               | Ca_21411                            | --                    | MYB_related |
| Ca1_P4_35240205  | Ca1                                     | 35240205                      | ATAT/ATATTAT                                                  | GTAGCATTTTGGCCT<br>CCCT     | GTCGAGAAGAAGGCTT<br>GCAT   | 60.5                             | 782                                           | DRR                                               | Ca_26097                            | QI                    | bHLH        |
| Ca1_P4_35240820  | Ca1                                     | 35240820                      | GTTTTTTT/GTTTTTTTTT                                           | TGCAAGCCTTCTTCTC<br>GACT    | TTGGTGGAATGTGTGC<br>ATGT   | 60.3                             | 543                                           | DRR                                               | Ca_26098                            | QI                    | --          |
| Ca1_P4_35317313  | Ca1                                     | 35317313                      | CTTTTTTT/CTTTTTTTTT                                           | CCTGATCCTCATCGTC<br>CATT    | GCCAGGTTCACTCGAT<br>TCAT   | 59.9                             | 464                                           | DRR                                               | Ca_26100                            | QI                    | bHLH        |
| Ca1_P4_355593    | Ca1                                     | 355593                        | TA/TAAAA                                                      | TTCACATTATCCGGCT<br>CCTC    | TGTGCCATTTAAGTTG<br>CCA    | 60.0                             | 430                                           | DRR                                               | Ca_00037                            | E                     | --          |
| Ca1_P4_35569645  | Ca1                                     | 35569645                      | TAAAAA/TAAAAA                                                 | TGAGTGCACCTTTTAC<br>AGCG    | TTGCACGCTTAGTATG<br>CACC   | 60.1                             | 256                                           | DRR                                               | Ca_24107                            | --                    | --          |
| Ca1_P4_355898    | Ca1                                     | 355898                        | ATTATTTAT/ATTAT                                               | TATTTGCAGGCCCACT<br>ATCC    | TCGAATTTCTTACCATG<br>ACCAA | 59.9                             | 709                                           | DRR                                               | Ca_00037                            | E                     | --          |
| Ca1_P4_3677454   | Ca1                                     | 3677454                       | GTATATATATATATATATA/GTATA<br>TATATATATATATA                   | ACACATCGTCCAACA<br>ATCG     | AATATTTGTGGGTGGC<br>CAAA   | 59.4                             | 590                                           | DRR                                               | Ca_00448                            | --                    | FAR1        |
| Ca1_P4_3708800   | Ca1                                     | 3708800                       | GTATATATATATATATATA/GTATA<br>TATATATATATATATA                 | GCCTGGTGACTTGTT<br>AGGC     | TTGAGTGGGATAGATC<br>GTTGG  | 59.7                             | 651                                           | DRR                                               | Ca_00451                            | --                    | G2-like     |
| Ca1_P4_37197766  | Ca1                                     | 37197766                      | GTTT/GTT                                                      | TGAGAGGAAAGAAGAC<br>AACCATC | TTTTCTTTTAAAGCG<br>CGA     | 59.7                             | 605                                           | DRR                                               | Ca_21831                            | L                     | C3H         |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                              |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca1_P4_37412282  | Ca1                                     | 37412282                      | CCATG/CCATGCATG                                               | CGTGGATGATGCTTT<br>CTCA      | TGCTTCTCATCTGCTTG<br>GTG  | 59.8                             | 580                                           | DRR                                               | Ca_21842                            | R                     | GRAS    |
| Ca1_P4_37693180  | Ca1                                     | 37693180                      | AATTAT/AAT                                                    | TGTGGAACATTCTCTG<br>CGTC     | TTCCCGAGAGATTTGT<br>CTTCA | 59.8                             | 593                                           | DRR                                               | Ca_23533                            | --                    | G2-like |
| Ca1_P4_37693633  | Ca1                                     | 37693633                      | TAAAAAAAAA/TAAAAAAAAA                                         | TGAAGACAAATCTCTC<br>GGGAA    | TTTTTGCCTTTCTTCCA<br>TTCA | 59.8                             | 170                                           | DRR                                               | Ca_23533                            | --                    | G2-like |
| Ca1_P4_37721004  | Ca1                                     | 37721004                      | TAAAAAAAAA/TAAAAAAAAA                                         | AAGACCTTCTTAACCTA<br>CCAATCG | ATTTCTCTCACCCGCAT<br>TTG  | 60.1                             | 481                                           | DRR                                               | Ca_23534                            | --                    | --      |
| Ca1_P4_37721057  | Ca1                                     | 37721057                      | ATTTTTTTTT/ATTTTTTTT                                          | AAAAATGCTCCCAAAG<br>TCATT    | ATTTCTCTCACCCGCAT<br>TTG  | 57.7                             | 260                                           | DRR                                               | Ca_23534                            | --                    | --      |
| Ca1_P4_37721398  | Ca1                                     | 37721398                      | TAAAAA/TAAA                                                   | CAATGCGGGTGAGAG<br>AAAT      | CATTGGTGGGGAGGTG<br>TATT  | 60.1                             | 598                                           | DRR                                               | Ca_23534                            | --                    | --      |
| Ca1_P4_37721826  | Ca1                                     | 37721826                      | AAAA/AAAATAAA                                                 | TCCATAGCACCTCTTG<br>ATTTTG   | CGTTGATGGCATCTTG<br>ATTG  | 59.2                             | 420                                           | DRR                                               | Ca_23534                            | --                    | --      |
| Ca1_P4_38184317  | Ca1                                     | 38184317                      | ATTTT/ATTTT                                                   | TGACTCGTGATCCTCA<br>CTGC     | TTAAGCGTGCTCTCAA<br>CGTG  | 60.0                             | 572                                           | DRR                                               | Ca_13975                            | --                    | --      |
| Ca1_P4_38184769  | Ca1                                     | 38184769                      | TAT/TATAAT                                                    | AAGGAGAGGCACGTTG<br>AGAG     | CCTACCACTCCTTCTG<br>CACC  | 59.6                             | 768                                           | DRR                                               | Ca_13975                            | --                    | --      |
| Ca1_P4_38265402  | Ca1                                     | 38265402                      | CAAAAAAAAAA/CAAAAAAAAAA                                       | TGGTATTACTGACCCG<br>CACA     | ACAATTGTTGAAAAGC<br>CCAG  | 60.0                             | 589                                           | DRR                                               | Ca_13970                            | --                    | --      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_38278656  | Ca1                                     | 38278656                      | C/CG                                                          | TCCAGCATTGCCTTTT<br>CTTT  | GCATGGGTGAGAATGG<br>AGTT | 59.8                             | 687                                           | DRR                                               | Ca_13968                            | O                     | --  |
| Ca1_P4_38338075  | Ca1                                     | 38338075                      | ATTTTTTTTT/ATTTTTTTTT                                         | TATGGGTCCATTTTAG<br>GCCA  | AATCCCCAATTCGAAAA<br>ACC | 60.1                             | 623                                           | DRR                                               | Ca_13967                            | --                    | --  |
| Ca1_P4_38345242  | Ca1                                     | 38345242                      | TA/TAAA                                                       | CACTCCCTCTTTGATG<br>CACTT | TGGGGTGTGGATTGT<br>TTCT  | 59.3                             | 487                                           | DRR                                               | Ca_13966                            | --                    | --  |
| Ca1_P4_38487463  | Ca1                                     | 38487463                      | ATTTTTTTTT/ATTTTTTTTT                                         | TGCTACCTGCAACCAG<br>TGAG  | GTCAACTTTAAGGGGG<br>CGTC | 60.0                             | 872                                           | DRR                                               | Ca_13962                            | --                    | --  |
| Ca1_P4_38535428  | Ca1                                     | 38535428                      | CAAAAAA/CAAAAAA                                               | AGGGCAATATCACATC<br>CGAG  | CGCATCAACGACATAT<br>GGAC | 59.9                             | 668                                           | DRR                                               | Ca_13959                            | --                    | --  |
| Ca1_P4_38597934  | Ca1                                     | 38597934                      | CAAAAA/CAAAAA                                                 | CATTGCCTCCCTTGTT<br>GTT   | TGTAGTTGCTGCAAAC<br>GAGG | 60.0                             | 551                                           | DRR                                               | Ca_13956                            | --                    | --  |
| Ca1_P4_38789465  | Ca1                                     | 38789465                      | TTATA/TTA                                                     | GGTCATGCATCATACC<br>CACA  | TCATCCAATACACCACC<br>CTT | 60.2                             | 691                                           | DRR                                               | Ca_13953                            | --                    | --  |
| Ca1_P4_38882967  | Ca1                                     | 38882967                      | GTTAGGA/GTTAGGACTTAGGA                                        | ATTAGGAACCCTGGCA<br>TG TG | GGCAGCATTTGGTGAA<br>CTTT | 59.8                             | 464                                           | DRR                                               | Ca_13949                            | G                     | --  |
| Ca1_P4_39073445  | Ca1                                     | 39073445                      | AATATATATAT/AATATATATAT                                       | GAAAACATGCCCATGG<br>ATCT  | GCATTAAGGTGCGATG<br>AATG | 59.8                             | 578                                           | DRR                                               | Ca_13946                            | --                    | --  |
| Ca1_P4_39073809  | Ca1                                     | 39073809                      | A/AC                                                          | CATTTCATCGCACCTTAA<br>TGC | TTGAAGAAGCATCCCT<br>CTGA | 59.1                             | 309                                           | DRR                                               | Ca_13946                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                          |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca1_P4_39446823  | Ca1                                     | 39446823                      | GATT/G                                                        | GTTGTAAGCTTGCAGG<br>AGGG | TTTTCGCCCCAATAAG<br>TTG        | 59.9                             | 713                                           | DRR                                               | Ca_13931                            | Z                     | NAC      |
| Ca1_P4_39447104  | Ca1                                     | 39447104                      | TTAATG/TTAATGTTGATCTAATG                                      | CAACTTTATTGGGGCG<br>AAAA | CCCTCGATTAATTCTCT<br>TGAGGT    | 59.9                             | 253                                           | DRR                                               | Ca_13931                            | Z                     | NAC      |
| Ca1_P4_39673797  | Ca1                                     | 39673797                      | ATTTTT/ATTTTTT                                                | GCCTCAAAGCGAAAT<br>TTGT  | TTGGAACACATAAAAA<br>TAATAATCCA | 59.3                             | 759                                           | DRR                                               | Ca_13921                            | --                    | --       |
| Ca1_P4_39733036  | Ca1                                     | 39733036                      | CTGAT/C                                                       | TGATTGAGAGGGGAGA<br>AAGG | AAACAGACCCCGAATG<br>TCAC       | 59.2                             | 117                                           | DRR                                               | Ca_13916                            | R                     | bZIP     |
| Ca1_P4_39743942  | Ca1                                     | 39743942                      | TAAAA/TAAAAA                                                  | TTCCATTTCTCCACAA<br>AGC  | TGCTACAACCGCATTG<br>TCAT       | 60.1                             | 563                                           | DRR                                               | Ca_13915                            | --                    | --       |
| Ca1_P4_40234096  | Ca1                                     | 40234096                      | ATTTTTTTTTTTTT/ATTTTTTTTTT<br>T                               | GAACGTGGAGGTGAG<br>GAAAA | AACAAAATTCAACAACC<br>AAAGAA    | 60.1                             | 575                                           | DRR                                               | Ca_13896                            | --                    | --       |
| Ca1_P4_40234165  | Ca1                                     | 40234165                      | TTTATTATTATTATTATTA/TTTATTA<br>TTATTA                         | GAACGTGGAGGTGAG<br>GAAAA | AACAAAATTCAACAACC<br>AAAGAA    | 60.1                             | 575                                           | DRR                                               | Ca_13896                            | --                    | --       |
| Ca1_P4_40373644  | Ca1                                     | 40373644                      | C/CG                                                          | TACCAAACTCAGCATT<br>GCG  | TTCTGTCGAAGAACTT<br>GTGGAA     | 59.9                             | 415                                           | DRR                                               | Ca_13892                            | --                    | Trihelix |
| Ca1_P4_40422016  | Ca1                                     | 40422016                      | TAAAAAAAAA/TAAAAAAAAA                                         | TATTTCCAAGCCAAAG<br>ACCG | CACGCTCAAATTCCT<br>CGAT        | 60.1                             | 558                                           | DRR                                               | Ca_13890                            | A                     | --       |
| Ca1_P4_40872000  | Ca1                                     | 40872000                      | AAATATATATATATATA/AATATATAT<br>ATA                            | GCAACCTGCCCTAA<br>CATA   | CCAAGACAACGAAAG<br>ATCCG       | 60.0                             | 468                                           | DRR                                               | Ca_18460                            | --                    | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca1_P4_409913    | Ca1                                     | 409913                        | GGAAAG/GG                                                     | GCACCACCTTGGCTCT<br>AATC  | GGCGAATTCAAAGTTC<br>CGTA | 59.7                             | 550                                           | DRR                                               | Ca_00043                            | --                    | --       |
| Ca1_P4_41167792  | Ca1                                     | 41167792                      | AATATATATATATATATATA/AATA<br>TATATATATATATATA                 | TTTTGGTCGGTATTCC<br>AATTT | GGGTCAAAATGTATGG<br>TCGG | 58.3                             | 802                                           | DRR                                               | Ca_18480                            | --                    | --       |
| Ca1_P4_413371    | Ca1                                     | 413371                        | AAAGTAAGT/AAAGT                                               | GAAGTCAGACGCGCTA<br>ATCC  | CTTTCCCAAAGGCAA<br>GTGA  | 60.0                             | 533                                           | DRR                                               | Ca_00045                            | --                    | --       |
| Ca1_P4_41774189  | Ca1                                     | 41774189                      | CAAAA/CAA                                                     | TCCATTACACTTGTG<br>GGA    | GGCACATTCATGTTCA<br>GACG | 59.9                             | 237                                           | DRR                                               | Ca_22517                            | G                     | --       |
| Ca1_P4_41935770  | Ca1                                     | 41935770                      | AGGG/AGGGG                                                    | TCGATCAGATAAAGCA<br>ACCG  | CAATGCTTCATACGTC<br>CTGC | 58.9                             | 410                                           | DRR                                               | Ca_22531                            | --                    | --       |
| Ca1_P4_425631    | Ca1                                     | 425631                        | AT/A                                                          | TACCACGTGGCGTCAC<br>TTTA  | AGCTTGGAGGTTTGCG<br>TAGA | 60.2                             | 705                                           | DRR                                               | Ca_00046                            | --                    | NF-YC    |
| Ca1_P4_42687636  | Ca1                                     | 42687636                      | ATTACAGAGTTACA/ATTACAGAGTT<br>ACAGAGTTACA                     | CTGGGCAAGGGATCTG<br>AATA  | TGCATTTTACAGCGCTT<br>TTG | 60.0                             | 500                                           | DRR                                               | Ca_13605                            | --                    | Trihelix |
| Ca1_P4_42822054  | Ca1                                     | 42822054                      | AATATATATATATATATATATAT/A<br>ATATATATATATATATATATATATA<br>TAT | AAAGGCATGACCAACT<br>CCAT  | CACCTGATTCTCGTT<br>GGTT  | 59.4                             | 671                                           | DRR                                               | Ca_13599                            | --                    | C2H2     |
| Ca1_P4_43681169  | Ca1                                     | 43681169                      | GAAAAAA/GAAAAAA                                               | GTGCAAAGATTGCAAC<br>GAAA  | AGCCATTAGGCTTTGA<br>TTGG | 59.9                             | 327                                           | DRR                                               | Ca_13559                            | --                    | NAC      |
| Ca1_P4_45003074  | Ca1                                     | 45003074                      | AA/AAATAAAATTCCGAATCA                                         | TCTTCCACATTGATTT<br>GTTGC | TGCTTATCCCCAGATA<br>CCG  | 60.0                             | 988                                           | DRR                                               | Ca_25714                            | --                    | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfI)     | Forward primers (5'-3')      | Reverse primers (5'-3') | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|------------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                   |                              |                         |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs  |
| Ca1_P4_45243775  | Ca1                                     | 45243775                      | T/TATGCACTTCTTTTCTC                                               | TGTGCCAAGGTTTCAG AACA        | CTTTTATTGCAAGACCC CGA   | 60.3                             | 605                                           | DRR                                         | Ca_26020                         | --                    | --   |
| Ca1_P4_45607074  | Ca1                                     | 45607074                      | AA/AAGCGCTA                                                       | TGCATCACTCCAAGAA CCAA        | ACTCACCTATTCCGAC CGTG   | 60.2                             | 344                                           | DRR                                         | Ca_24440                         | R                     | --   |
| Ca1_P4_46531041  | Ca1                                     | 46531041                      | T/TG                                                              | GCGAAAATAATGTTGA TGCAGA      | GTCTGCGGATAATTTT GCTT   | 60.1                             | 139                                           | DRR                                         | Ca_21551                         | M                     | --   |
| Ca1_P4_46728277  | Ca1                                     | 46728277                      | ATTT/ATT                                                          | TTCTTTAACCTGGCCAA ACG        | CCGTCTTCGAATCACC GTAT   | 60.1                             | 681                                           | DRR                                         | Ca_25109                         | --                    | --   |
| Ca1_P4_46834640  | Ca1                                     | 46834640                      | AATATATATATATATATATATATATATATATAT/AATATATATATATATATATATATATATATAT | TGAATTACAGCTATAAA ACGAAGATAA | GATCAGGATGAACCGG AAGA   | 57.1                             | 435                                           | DRR                                         | Ca_25116                         | U                     | --   |
| Ca1_P4_46867289  | Ca1                                     | 46867289                      | GCT/G                                                             | GCCCTCAGATGAGAGT CAGG        | CGTTTTTCAAAGCGAG GGTA   | 59.9                             | 439                                           | DRR                                         | Ca_25118                         | --                    | --   |
| Ca1_P4_46867363  | Ca1                                     | 46867363                      | CTTTT/CTTT                                                        | GCCCTCAGATGAGAGT CAGG        | CAAACCTTTCATGCGG GTAT   | 59.9                             | 836                                           | DRR                                         | Ca_25118                         | --                    | --   |
| Ca1_P4_46916401  | Ca1                                     | 46916401                      | GATATATATATATATATATATA/GATA TATATATATATATATATATATA                | CAGCAAGCACCAACCA CTTA        | TTGCCAGTTATTTTTCG AAGG  | 59.9                             | 363                                           | DRR                                         | Ca_12949                         | --                    | --   |
| Ca1_P4_4725547   | Ca1                                     | 4725547                       | GAAAAAAAAA/GAAAAAAAAAAAA AAA                                      | TTGCCACTCATAGGTC ACAAAAG     | TGGCTTCCTCTCTGTG TGTG   | 60.2                             | 571                                           | DRR                                         | Ca_00556                         | --                    | --   |
| Ca1_P4_47292040  | Ca1                                     | 47292040                      | CAACAA/CAACAAACAA                                                 | GTATAGCTGCGGAAGC TTGG        | CATAAACCCCTACCCCC TCCT  | 60.0                             | 669                                           | DRR                                         | Ca_12923                         | --                    | BES1 |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |           |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs       |
| Ca1_P4_47337298  | Ca1                                     | 47337298                      | CT/CAAAATATATACTT                                             | ATTGGGCATAGGAAGC<br>ACTG | AGTTGACCACGGACCC<br>ATAG  | 60.1                             | 533                                           | DRR                                               | Ca_12919                            | --                    | --        |
| Ca1_P4_48246328  | Ca1                                     | 48246328                      | CTT/CTTT                                                      | GACACCTCCTTTCCTC<br>CACA | CAATTCCACCGCTTTCA<br>AGT  | 60.1                             | 911                                           | DRR                                               | Ca_12858                            | --                    | --        |
| Ca1_P4_4899842   | Ca1                                     | 4899842                       | CTTTTT/CTTTTTTT                                               | GCACATTGGCAAACCTTCT      | CAAAAAGCATGCTGCA<br>AAGA  | 60.1                             | 445                                           | DRR                                               | Ca_00576                            | R                     | M-type    |
| Ca1_P4_4900100   | Ca1                                     | 4900100                       | TATTCAAT/TATTCAATTCAT                                         | TCTTTGCAGCATGCTTT<br>TTG | TTTCTGAAGCGACCA<br>TTCC   | 60.1                             | 561                                           | DRR                                               | Ca_00575                            | --                    | --        |
| Ca1_P4_4900435   | Ca1                                     | 4900435                       | C/CT                                                          | GGCTTCCCCCTTTCAA<br>CTAA | TCCATAAGCTGATCCC<br>CAAG  | 60.4                             | 920                                           | DRR                                               | Ca_00576                            | R                     | M-type    |
| Ca1_P4_4900555   | Ca1                                     | 4900555                       | AGAAGTAGACTCTGAAGTA/AGAAG<br>TA                               | GGAATTGGTCGCTTCA<br>GAAA | TCCATAAGCTGATCCC<br>CAAG  | 60.2                             | 428                                           | DRR                                               | Ca_00576                            | R                     | M-type    |
| Ca1_P4_4957124   | Ca1                                     | 4957124                       | CAAAAAAAAA/CAAAAAAAAA                                         | TATCACCTCAACGACC<br>CCTC | CGTGTCTGCCTTGAA<br>TTTT   | 59.9                             | 482                                           | DRR                                               | Ca_00586                            | T                     | WRKY      |
| Ca1_P4_5446706   | Ca1                                     | 5446706                       | GTTTTT/GTTTTTTT                                               | TGACGCAGTCTCATAG<br>TCGG | GCAATTGTCAAGCACC<br>ATGT  | 60.0                             | 336                                           | DRR                                               | Ca_00630                            | --                    | --        |
| Ca1_P4_5482292   | Ca1                                     | 5482292                       | A/AAG                                                         | TACAAATCCGGATCGA<br>AACA | TGTGTTTGTGTTGGGA<br>TGAGA | 59.0                             | 301                                           | DRR                                               | Ca_00633                            | --                    | S1Fa-like |
| Ca1_P4_5498637   | Ca1                                     | 5498637                       | AAATATTAATATTAATATTAATATTA<br>TA/AAATATTAATATTAATATTAATA      | TCCTATGATGGCTAGG<br>GGTG | CCATTGCAAGTAAAGG<br>CACA  | 59.9                             | 568                                           | DRR                                               | Ca_00635                            | C                     | --        |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                                                                              |                               |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca1_P4_5998961   | Ca1                                     | 5998961                       | TATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATA/TATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AAAA | ATAGCGCACCCTCTCT<br>CTGT      | ATTTTGTGGCACATGAA<br>GTCT | 60.0                             | 872                                           | DRR                                               | Ca_00687                            | --                    | --       |
| Ca1_P4_6148078   | Ca1                                     | 6148078                       | CAA/CA                                                                                                                                       | TTGCTATTCCCTTTCCC<br>CTT      | CTCTCATCTCTGGCCTT<br>TGG  | 59.9                             | 558                                           | DRR                                               | Ca_00699                            | S                     | --       |
| Ca1_P4_6205233   | Ca1                                     | 6205233                       | CAAAAAAAAA/CAAAAAAAAAA                                                                                                                       | GGGTATTGGATAAAAA<br>TTTCAAAAA | TGAAAATTAAGGGACG<br>GGTTT | 58.7                             | 604                                           | DRR                                               | Ca_07880                            | T                     | --       |
| Ca1_P4_6385666   | Ca1                                     | 6385666                       | TC/T                                                                                                                                         | TACTGTTCATGGCGGCA<br>GTTA     | CATGCGGTGTTTTCTT<br>CAAA  | 60.3                             | 419                                           | DRR                                               | Ca_07901                            | R                     | AP2      |
| Ca1_P4_638582    | Ca1                                     | 638582                        | ACTCT/ACT                                                                                                                                    | TGCCTAACAAGGAGGA<br>AACG      | CTTAGCAGCATGCATT<br>GACG  | 60.2                             | 554                                           | DRR                                               | Ca_00074                            | --                    | --       |
| Ca1_P4_6418036   | Ca1                                     | 6418036                       | TATAATAATAAT/TATAATAAT                                                                                                                       | ATTTCACTGCCAAAGG<br>ATGG      | TCGAGCCAAATTGTCC<br>TTCT  | 59.9                             | 544                                           | DRR                                               | Ca_07905                            | P                     | MIKC     |
| Ca1_P4_6523042   | Ca1                                     | 6523042                       | GAACAAACA/GAACA                                                                                                                              | GGAGCAGTTGTTCCCA<br>AAAA      | CGAGGAAGAAGCGGAT<br>ATTG  | 60.1                             | 444                                           | DRR                                               | Ca_07917                            | I                     | Trihelix |
| Ca1_P4_6538753   | Ca1                                     | 6538753                       | AT/ATT                                                                                                                                       | CAAGGAAAGGGAATGG<br>CATA      | AATTGAAGGCTGAAAC<br>GTGG  | 59.9                             | 787                                           | DRR                                               | Ca_07919                            | R                     | bZIP     |
| Ca1_P4_6538802   | Ca1                                     | 6538802                       | CTTTTT/CTTTTTTT                                                                                                                              | CAAGGAAAGGGAATGG<br>CATA      | AATTGAAGGCTGAAAC<br>GTGG  | 59.9                             | 787                                           | DRR                                               | Ca_07919                            | R                     | bZIP     |
| Ca1_P4_6593836   | Ca1                                     | 6593836                       | TT/TTATAT                                                                                                                                    | AAGTGGGTTGTCGCTA<br>CCTC      | CGTTCTTCTTCTCCAC<br>ATTCC | 59.2                             | 590                                           | DRR                                               | Ca_07923                            | R                     | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca1_P4_7649777   | Ca1                                     | 7649777                       | ATATG/A                                                       | ATGTAGGGGTGGGAAT<br>AGGC  | TTTCCATTGCACTCACT<br>CCA     | 60.0                             | 825                                           | DRR                                               | Ca_08019                            | Z                     | --       |
| Ca1_P4_7748427   | Ca1                                     | 7748427                       | CTTTT/CTTTTT                                                  | TAGTGGGTTCACCTGG<br>GGAG  | TTCTTTTTGTGCATTAA<br>GTTGGAA | 60.0                             | 460                                           | DRR                                               | Ca_08026                            | --                    | --       |
| Ca1_P4_7781791   | Ca1                                     | 7781791                       | CAA/C                                                         | TGCAATCTCCTTCACA<br>CTCG  | AAGTGTCTTTGTTTGAA<br>CGC     | 60.0                             | 324                                           | DRR                                               | Ca_08030                            | --                    | GRAS     |
| Ca1_P4_7810052   | Ca1                                     | 7810052                       | TCTAA/TCTAACTAA                                               | CTTTGTGGGCAAACCA<br>AACT  | GGGTGGTTGAAACTTC<br>AGGA     | 60.0                             | 521                                           | DRR                                               | Ca_08031                            | --                    | FAR1     |
| Ca1_P4_784516    | Ca1                                     | 784516                        | ATTTTTTTTT/ATTTTTTTTTT                                        | TTGCTTCATGCTTTCCCT<br>TGA | TGCATCATGCGACCTC<br>TTAT     | 59.5                             | 837                                           | DRR                                               | Ca_00097                            | --                    | --       |
| Ca1_P4_7926977   | Ca1                                     | 7926977                       | TG/T                                                          | GCATTGGCATTTCATTG<br>TGAG | CCCTTACCTTGAGGCA<br>AACA     | 60.1                             | 758                                           | DRR                                               | Ca_08042                            | --                    | HB-other |
| Ca1_P4_7948690   | Ca1                                     | 7948690                       | ATTTTTTT/ATTTTTTTTT                                           | TTTTGCATCTCTCCTCT<br>TCCA | CCAACAGTCCGACAT<br>CTCA      | 59.9                             | 453                                           | DRR                                               | Ca_08045                            | QI                    | B3       |
| Ca1_P4_7971447   | Ca1                                     | 7971447                       | CTTTTTTTTT/CTTTTTTTTTT                                        | CCATATTAGGGTGCTG<br>CGTT  | TGGCAACCATCAACTA<br>CCAA     | 60.0                             | 200                                           | DRR                                               | Ca_08047                            | U                     | MYB      |
| Ca1_P4_7988333   | Ca1                                     | 7988333                       | CTTAT/C                                                       | TCAATCCAAACAAGTC<br>CAGAA | AATCCAGCAAAACGAG<br>GTTG     | 58.2                             | 517                                           | DRR                                               | Ca_08049                            | --                    | WRKY     |
| Ca1_P4_7988388   | Ca1                                     | 7988388                       | ATT/ATTTT                                                     | TCAATCCAAACAAGTC<br>CAGAA | AATGCATGCTTTGGTTC<br>CTC     | 58.2                             | 761                                           | DRR                                               | Ca_08049                            | --                    | WRKY     |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca1_P4_7989526   | Ca1                                     | 7989526                       | TG/T                                                          | GCAACCTTCTGTCCT<br>CAGC   | GGGGGAGAGATTTCC<br>CTTT  | 60.0                             | 591                                           | DRR                                               | Ca_08049                            | --                    | WRKY |
| Ca1_P4_8039162   | Ca1                                     | 8039162                       | AA/ACCATAAGCTGA                                               | TAATGGCAAATGCTCA<br>ACCA  | GGTGAATGGCCAAAGA<br>AAAA | 60.1                             | 343                                           | DRR                                               | Ca_08051                            | M                     | FAR1 |
| Ca1_P4_8101006   | Ca1                                     | 8101006                       | GT/GTT                                                        | CCTCACCCGTGCATT<br>TTAT   | GGCGGAGACAAAGAGT<br>CAAG | 60.0                             | 587                                           | DRR                                               | Ca_08056                            | C                     | --   |
| Ca1_P4_8101258   | Ca1                                     | 8101258                       | AAAAAAAAATAAAAAA/AAAAAA                                       | CCTCACCCGTGCATT<br>TTAT   | GGCGGAGACAAAGAGT<br>CAAG | 60.0                             | 587                                           | DRR                                               | Ca_08056                            | C                     | --   |
| Ca1_P4_8115168   | Ca1                                     | 8115168                       | TG/T                                                          | AGTTTGTCCCGTCCA<br>ACAC   | CACATGGGAGGTGAGT<br>GGTA | 59.9                             | 435                                           | DRR                                               | Ca_08057                            | A                     | --   |
| Ca1_P4_8124056   | Ca1                                     | 8124056                       | AATATATATATATA/AATATATATATA<br>TATATATA                       | TGTTGAGAAGCATGCG<br>AAAG  | TCGAATCGAACACAAT<br>CCAA | 60.1                             | 918                                           | DRR                                               | Ca_08058                            | R                     | --   |
| Ca1_P4_8433346   | Ca1                                     | 8433346                       | AAAAAAAAAAATTAAAAA/AAAAA<br>AA                                | GGATCGCGGAGACTAT<br>TTTG  | AGATCCAAGAGCGGAT<br>GAGA | 59.7                             | 290                                           | DRR                                               | Ca_08078                            | --                    | --   |
| Ca1_P4_8909387   | Ca1                                     | 8909387                       | T/TCC                                                         | AGGCAAAAGGTTTTTG<br>GGTT  | GTGAGGCGTGAAGTGG<br>TTTT | 59.9                             | 806                                           | DRR                                               | Ca_02914                            | --                    | --   |
| Ca1_P4_9106412   | Ca1                                     | 9106412                       | TAAAAAAAA/TAAAAAAAA                                           | GTGCTCGATGCTGTCA<br>AAAA  | CGGGTGCAAAATCAAA<br>AGAT | 60.0                             | 667                                           | DRR                                               | Ca_02885                            | --                    | --   |
| Ca1_P4_9371422   | Ca1                                     | 9371422                       | TAAAAAAAA/TAAAAAAAA                                           | TCAATTTGGTGAATTG<br>GTGAA | TGGAACACAAACAATC<br>AGGA | 58.9                             | 215                                           | DRR                                               | Ca_02861                            | --                    | C3H  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca1_P4_9492143   | Ca1                                     | 9492143                       | CATATATATATATATATATA/CATA<br>TATATATATATATATATATA             | TCCGATTGTTAGCGCT<br>TTTT  | GGCTGCAACCATTCCT<br>CTTC     | 59.9                             | 180                                           | DRR                                               | Ca_02848                            | Q                     | E2F/DP  |
| Ca1_P4_987900    | Ca1                                     | 987900                        | CAGGAAGGAA/CAGGAA                                             | ACCATTTTGTGGGATG<br>ATGG  | TGCCACATCACCTTAA<br>TCAA     | 60.4                             | 689                                           | DRR                                               | Ca_00122                            | T                     | --      |
| Ca1_P4_9930936   | Ca1                                     | 9930936                       | TAATAC/TAATACAACAATAC                                         | TTTGAATGCCATGCA<br>GTTA   | ATGGATGCTGTGGTGA<br>ATGA     | 60.1                             | 424                                           | DRR                                               | Ca_02792                            | O                     | WRKY    |
| Ca2_P4_10097433  | Ca2                                     | 10097433                      | CG/C                                                          | GCTAAATTCGTCTTCG<br>ACGC  | CATTCAAATGGCAATG<br>CAAC     | 60.0                             | 139                                           | DRR                                               | Ca_20377                            | J                     | --      |
| Ca2_P4_10532302  | Ca2                                     | 10532302                      | ATTTTTTTTT/ATTTTTTTTT                                         | CCGAAGAGAATGGAGA<br>AAGTT | TCAAATTCGTAACCAA<br>ATCTTCAA | 57.5                             | 381                                           | DRR                                               | Ca_17578                            | --                    | --      |
| Ca2_P4_10594707  | Ca2                                     | 10594707                      | CTTTTTTTTT/CTTTTTTTTT                                         | TGACATGATCTTGCG<br>ATCC   | CAATGTTCTGGTTGCA<br>CAGG     | 59.6                             | 455                                           | DRR                                               | Ca_17574                            | O                     | bHLH    |
| Ca2_P4_17046294  | Ca2                                     | 17046294                      | AATAAATT/AAAATTATAAATT                                        | CTATTCCATCCACGAAT<br>GCC  | TCCATGGAGGATATTTA<br>TGTCG   | 60.3                             | 523                                           | DRR                                               | Ca_24768                            | --                    | G2-like |
| Ca2_P4_20761456  | Ca2                                     | 20761456                      | A/AT                                                          | AAAATCCAACAATCTCC<br>CCC  | TGTTTTCTGCCTTTTTG<br>CCT     | 60.0                             | 342                                           | DRR                                               | Ca_23762                            | --                    | --      |
| Ca2_P4_20761850  | Ca2                                     | 20761850                      | CATA/CATATATA                                                 | AAAATCCAACAATCTCC<br>CCC  | ACTCCTCCACAAGCCT<br>CTGA     | 60.0                             | 939                                           | DRR                                               | Ca_23762                            | --                    | --      |
| Ca2_P4_21783996  | Ca2                                     | 21783996                      | ATTTTT/ATTTTTTTTT                                             | ATCTCGTGGGTGGATC<br>TGAC  | GCTATGGGACCTATCA<br>GGCA     | 59.9                             | 381                                           | DRR                                               | Ca_23057                            | --                    | --      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                     |                               |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_22812516  | Ca2                                     | 22812516                      | ATTTTTTT/ATTTT                                                      | GGGGGAGAAAATTTG<br>TGTT       | TTGATCTTGCTGCATTG<br>TCC    | 60.0                             | 215                                           | DRR                                               | Ca_14986                            | --                    | --  |
| Ca2_P4_2373367   | Ca2                                     | 2373367                       | AATATATATATATATATATATA/AA<br>TATATATATATATATATATATATAT<br>ATATA     | AAAATTGTCAGGTTCA<br>CCGC      | GGTGGTGATTTGGTGC<br>TCTT    | 60.0                             | 896                                           | DRR                                               | Ca_12541                            | R                     | DBB |
| Ca2_P4_2382639   | Ca2                                     | 2382639                       | T/TCATA                                                             | TTGGAATGCCAGAGG<br>TATTAGA    | TGTGATTTGGTTTCGC<br>AAAG    | 60.0                             | 658                                           | DRR                                               | Ca_12540                            | R                     | --  |
| Ca2_P4_25352886  | Ca2                                     | 25352886                      | ATTTTTTTTT/ATTTTTTTTTTT                                             | AAAGAGACACATGACA<br>TAACCTCTC | ATGGGGGATGGACCTA<br>GAAC    | 57.9                             | 685                                           | DRR                                               | Ca_14268                            | --                    | --  |
| Ca2_P4_25535051  | Ca2                                     | 25535051                      | TTTTTTTT/TTTTTTTTTTTTTT                                             | CCAGATTGAACTGGG<br>GAAA       | AATCAAGTGGGTTCTGA<br>GTGG   | 59.9                             | 551                                           | DRR                                               | Ca_14283                            | R                     | MYB |
| Ca2_P4_2726175   | Ca2                                     | 2726175                       | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATAT                   | CGTTTCGGGTTTCGTA<br>AAAA      | TTGTTGACAAATTCGATC<br>CAAAG | 60.0                             | 302                                           | DRR                                               | Ca_10571                            | Q                     | B3  |
| Ca2_P4_28723013  | Ca2                                     | 28723013                      | GTTT/GCTTTTTT                                                       | ATCATCCCGTCCATTA<br>CGAA      | ATGCCATTACTCCGTG<br>CTTT    | 60.2                             | 507                                           | DRR                                               | Ca_14359                            | R                     | --  |
| Ca2_P4_29072040  | Ca2                                     | 29072040                      | ATCTGCAGACTTT/ATCTGCAGACTT<br>TCTGCAGACTTT                          | TTGCTGGCAGAACAAT<br>CAAG      | TGTGGGAAGCACCATG<br>TTTA    | 60.0                             | 546                                           | DRR                                               | Ca_14332                            | --                    | --  |
| Ca2_P4_29072081  | Ca2                                     | 29072081                      | TTATATATATATATATATATATATA<br>TATA/TTATATATATATATATATATAT<br>ATATATA | TTGCTGGCAGAACAAT<br>CAAG      | TGTGGGAAGCACCATG<br>TTTA    | 60.0                             | 546                                           | DRR                                               | Ca_14332                            | --                    | --  |
| Ca2_P4_29195958  | Ca2                                     | 29195958                      | CATATATATATATATATA/CATATA<br>TATATATATATATA                         | TTGTTTCGGAGGGTTG<br>ACTC      | CCACCGATTGAAACAT<br>ACCA    | 60.1                             | 612                                           | DRR                                               | Ca_14321                            | PT                    | C3H |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                        | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                                                                      |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca2_P4_29238503  | Ca2                                     | 29238503                      | A/AGTT                                                                                               | TGTGGAACACCAACGA<br>ATGT   | ACCTCCCGCTAATGTC<br>AATG  | 59.9                             | 746                                           | DRR                                               | Ca_14317                            | --                    | --     |
| Ca2_P4_29238544  | Ca2                                     | 29238544                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAA/A<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAA | TGTGGAACACCAACGA<br>ATGT   | ACCTCCCGCTAATGTC<br>AATG  | 59.9                             | 746                                           | DRR                                               | Ca_14317                            | --                    | --     |
| Ca2_P4_30259949  | Ca2                                     | 30259949                      | GAAAAAAAA/GAAAAAAAAA                                                                                 | TCAAATTTTCAAACAA<br>AATCCA | AATATCACCGTGGTC<br>CCTT   | 58.6                             | 403                                           | DRR                                               | Ca_12523                            | A                     | MYB    |
| Ca2_P4_30349843  | Ca2                                     | 30349843                      | GAGACAGACA/GAGACA                                                                                    | TGTCCAGAAACAGCTC<br>ATGG   | AACTCCTCAAAGTGAC<br>GGACA | 59.8                             | 638                                           | DRR                                               | Ca_12518                            | GE                    | bZIP   |
| Ca2_P4_30356368  | Ca2                                     | 30356368                      | AATATATA/AATATATATA                                                                                  | CCACATGGCTGCTTAT<br>GATG   | AGCGCATGGTAATGT<br>GAGA   | 60.1                             | 459                                           | DRR                                               | Ca_12517                            | --                    | ERF    |
| Ca2_P4_30369374  | Ca2                                     | 30369374                      | TAAAA/TAAAAA                                                                                         | TGTACTTCTCCGATT<br>CCAAA   | TGAATGACGACGACGG<br>TAAA  | 59.6                             | 632                                           | DRR                                               | Ca_12515                            | Q                     | --     |
| Ca2_P4_30402091  | Ca2                                     | 30402091                      | CAAAAA/CAAAAA                                                                                        | TGATTTTAGAAATTGCG<br>TGGC  | TTGGGCTTTTATTGTCC<br>ACC  | 60.1                             | 217                                           | DRR                                               | Ca_12511                            | --                    | --     |
| Ca2_P4_30402988  | Ca2                                     | 30402988                      | ATT/AT                                                                                               | TACCGGATTGGTAACG<br>TGGT   | GCGTTTGATGCATATT<br>TCG   | 60.1                             | 419                                           | DRR                                               | Ca_12511                            | --                    | --     |
| Ca2_P4_30403193  | Ca2                                     | 30403193                      | ATTGAGTT/ATTGAGTTGAGTT                                                                               | AAAGTTGCACCAAGAG<br>GTGG   | TCTCTGGCCTTCGTTA<br>GTCAA | 60.1                             | 989                                           | DRR                                               | Ca_12511                            | --                    | --     |
| Ca2_P4_30419368  | Ca2                                     | 30419368                      | TTCATCAT/TTCAT                                                                                       | GTTGCAATCATCACCA<br>CACC   | TGAGTGTCTTGGTGA<br>TTTGG  | 59.8                             | 568                                           | DRR                                               | Ca_12509                            | C                     | M-type |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30448281  | Ca2                                     | 30448281                      | AT/A                                                          | AGCGACAATGCTGAGG<br>AGAT    | TTATGGGTCGTTTGA<br>TGGT  | 60.0                             | 262                                           | DRR                                               | Ca_12507                            | --                    | --  |
| Ca2_P4_30448973  | Ca2                                     | 30448973                      | GAAAAA/GAAAAAA                                                | GCTTTTGATTTTCTAAA<br>GGATGG | TCTTCCTTGTGGTTCT<br>TTGG | 58.4                             | 759                                           | DRR                                               | Ca_12507                            | --                    | --  |
| Ca2_P4_30449164  | Ca2                                     | 30449164                      | TAAAAAA/TAAAAAA                                               | TGTTGCAAAGAGAAAG<br>AACTTCA | TGACGGTGGCAATCGA<br>TATT | 59.2                             | 557                                           | DRR                                               | Ca_12507                            | --                    | --  |
| Ca2_P4_30465917  | Ca2                                     | 30465917                      | GAAAAAAA/GAAAAAAA                                             | TCCATGATTGAGTGAC<br>TAGGGA  | GCAGTCAACCAGCGAC<br>AATA | 59.6                             | 322                                           | DRR                                               | Ca_12503                            | J                     | --  |
| Ca2_P4_30478151  | Ca2                                     | 30478151                      | CAATAAATAAATAAATAA/CAATAAA<br>TAAATAAA                        | GTGCGTGAAGGGATGA<br>AAAT    | CATCATAGCCCCGAGA<br>AAAA | 59.9                             | 758                                           | DRR                                               | Ca_12502                            | G                     | --  |
| Ca2_P4_30478867  | Ca2                                     | 30478867                      | AATATATATAT/AATATATATATAT                                     | TTTTTCTCGGGGCTAT<br>GATG    | GTAGGGCATGTGTGTG<br>TTGC | 60.0                             | 640                                           | DRR                                               | Ca_12502                            | G                     | --  |
| Ca2_P4_30510130  | Ca2                                     | 30510130                      | ATTTTTTTTTTTTT/ATTTTTTTTT<br>TTT                              | AGACCCACGGTTAAC<br>ATGA     | AGCACCTTACAAGGGG<br>GAGT | 60.2                             | 700                                           | DRR                                               | Ca_12500                            | --                    | --  |
| Ca2_P4_30510322  | Ca2                                     | 30510322                      | G/GATAACT                                                     | CTAGCTTCGCTGCACA<br>AATG    | AGCACCTTACAAGGGG<br>GAGT | 59.8                             | 200                                           | DRR                                               | Ca_12501                            | GMW                   | --  |
| Ca2_P4_30573602  | Ca2                                     | 30573602                      | CGGG/CGGGG                                                    | TGGCTCATGACCCCTT<br>TATC    | GGCCCTTTTCATTTTC<br>ATT  | 59.9                             | 709                                           | DRR                                               | Ca_12495                            | E                     | --  |
| Ca2_P4_30573670  | Ca2                                     | 30573670                      | TAAAAAAA/TAAAAAAA                                             | TGCATGCAAAAGAATT<br>GTCC    | GGCCCTTTTCATTTTC<br>ATT  | 59.7                             | 534                                           | DRR                                               | Ca_12495                            | E                     | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca2_P4_30576695  | Ca2                                     | 30576695                      | TGTGTTGGTGTGGTGTGGTGT/TTGTGTTGGTGTGGTGT                       | GCATTCAACACTCACAAGGG    | GAGTCCTGAGCCACGAAC      | 59.1                             | 430                                           | DRR                                               | Ca_12493                            | --                    | --   |
| Ca2_P4_30578105  | Ca2                                     | 30578105                      | AC/A                                                          | GCCCCTGCACTAGTTTGAAG    | GGCTTGTTAGTCTGCTTGCC    | 59.9                             | 583                                           | DRR                                               | Ca_12493                            | --                    | --   |
| Ca2_P4_30578122  | Ca2                                     | 30578122                      | TAAAAA/TAAAAA                                                 | GCCCCTGCACTAGTTTGAAG    | GGCTTGTTAGTCTGCTTGCC    | 59.9                             | 583                                           | DRR                                               | Ca_12493                            | --                    | --   |
| Ca2_P4_30618375  | Ca2                                     | 30618375                      | AT/A                                                          | TGGTCACCGGATATTTTG      | ACCTTGAAGAGCGAATGAGC    | 60.6                             | 506                                           | DRR                                               | Ca_12490                            | R                     | --   |
| Ca2_P4_30671540  | Ca2                                     | 30671540                      | TAAAAA/TAAAAA                                                 | TTGATTGATGGTTAAGAGACA   | ATAACGTGTTGGATCAGCCC    | 57.4                             | 697                                           | DRR                                               | Ca_12489                            | QI                    | bHLH |
| Ca2_P4_30681354  | Ca2                                     | 30681354                      | ATTATTTATTTATTTAT/ATTATTTATTTAT                               | CACATTTCAATAATTGCATCCG  | GCATTTTGTGTGGGTGATT     | 60.2                             | 805                                           | DRR                                               | Ca_12488                            | F                     | --   |
| Ca2_P4_30737874  | Ca2                                     | 30737874                      | CATCATGATCA/CATCATGATCATGATCA                                 | AGGGTTGGCAATTTTCTTGA    | TGTAAAGAGGAGGCCGTGAC    | 59.5                             | 428                                           | DRR                                               | Ca_12484                            | T                     | RAV  |
| Ca2_P4_30739062  | Ca2                                     | 30739062                      | AC/ACC                                                        | TTGTGTGTGGGCTCAACTTC    | TGGCCTACCTCTTGATGA      | 59.7                             | 569                                           | DRR                                               | Ca_12483                            | T                     | FAR1 |
| Ca2_P4_30767153  | Ca2                                     | 30767153                      | TAAAAAAAAA/TAAAAAAAAA                                         | TCAAGGATTCCAGATCAGG     | CAAAATGCGGTGTAATGCTG    | 60.0                             | 142                                           | DRR                                               | Ca_12479                            | K                     | ERF  |
| Ca2_P4_30840476  | Ca2                                     | 30840476                      | AG/A                                                          | GCATGCGAACATGAATTTG     | CCGGTGGATTGGATGTAAAA    | 60.1                             | 589                                           | DRR                                               | Ca_12475                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca2_P4_30840563  | Ca2                                     | 30840563                      | TAAAAA/TAAAAA                                                 | GCATGCGAACATGAAT<br>TTTG  | CCGGTGGATTGGATGT<br>TAAA   | 60.1                             | 589                                           | DRR                                               | Ca_12475                            | --                    | --   |
| Ca2_P4_30840723  | Ca2                                     | 30840723                      | TC/T                                                          | GCATGCGAACATGAAT<br>TTTG  | GGCCACTCATGTTGTC<br>TCCT   | 60.1                             | 788                                           | DRR                                               | Ca_12475                            | --                    | --   |
| Ca2_P4_30869262  | Ca2                                     | 30869262                      | AATATA/AATA                                                   | TCAAGGGCGACTTTTA<br>TTGG  | CGAATTTAGGGGATCC<br>AGGT   | 60.1                             | 130                                           | DRR                                               | Ca_12473                            | U                     | --   |
| Ca2_P4_30902428  | Ca2                                     | 30902428                      | CTGT/CT                                                       | CCCCATATTGCAAAG<br>GCTA   | CAATGGGTTTGCAAG<br>TGTG    | 59.9                             | 385                                           | DRR                                               | Ca_12471                            | --                    | --   |
| Ca2_P4_30957679  | Ca2                                     | 30957679                      | ATTTTT/ATTTTTTT                                               | TCGGTTGTAGCCGAGC<br>TAGT  | TTTTGCTTGGGTCGAG<br>AGAT   | 60.0                             | 791                                           | DRR                                               | Ca_12469                            | U                     | bHLH |
| Ca2_P4_30957722  | Ca2                                     | 30957722                      | CCA/CCACA                                                     | TCGGTTGTAGCCGAGC<br>TAGT  | TTTTGCTTGGGTCGAG<br>AGAT   | 60.0                             | 791                                           | DRR                                               | Ca_12469                            | U                     | bHLH |
| Ca2_P4_30979139  | Ca2                                     | 30979139                      | TTTTTATTT/TTTT                                                | CTCGCCAACCTTACCGA<br>TTGT | TCATTATTGTGAAATAG<br>GGCCA | 60.1                             | 554                                           | DRR                                               | Ca_12466                            | O                     | TCP  |
| Ca2_P4_31004687  | Ca2                                     | 31004687                      | TCACA/TCA                                                     | TGGTCTTTGGATTCCC<br>ATGT  | TATTGCGGAGTCTCGT<br>GTGA   | 60.2                             | 414                                           | DRR                                               | Ca_12464                            | --                    | LBD  |
| Ca2_P4_31004710  | Ca2                                     | 31004710                      | TG/T                                                          | TGGTCTTTGGATTCCC<br>ATGT  | TATTGCGGAGTCTCGT<br>GTGA   | 60.2                             | 414                                           | DRR                                               | Ca_12464                            | --                    | LBD  |
| Ca2_P4_31926358  | Ca2                                     | 31926358                      | CCTTT/C                                                       | GTGGGAGATGCAATCC<br>AAGT  | TGTCACAAATGTGTCG<br>TGAAAA | 59.9                             | 652                                           | DRR                                               | Ca_17824                            | --                    | ERF  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca2_P4_31939044  | Ca2                                     | 31939044                      | ATTTTTTTT/ATTTTTTTT                                           | ATCACATTGCAAAGCA<br>ACGA  | TGTATTCACGGTTTG<br>GTTTT  | 60.3                             | 586                                           | DRR                                               | Ca_17823                            | R                     | C3H    |
| Ca2_P4_31939517  | Ca2                                     | 31939517                      | ACT/ACTCT                                                     | TCTTAAACCCAAACC<br>GTGAA  | GAGCTTTTGGGGGATA<br>GAGG  | 59.5                             | 490                                           | DRR                                               | Ca_17823                            | R                     | C3H    |
| Ca2_P4_3201185   | Ca2                                     | 3201185                       | ATTTTTTTTT/ATTTTTTTTTT                                        | TTTGCAAATGTTTCCT<br>TCA   | GAGTGGGGGTTGGAG<br>GTAGT  | 59.1                             | 405                                           | DRR                                               | Ca_10527                            | K                     | HD-ZIP |
| Ca2_P4_32048288  | Ca2                                     | 32048288                      | AC/A                                                          | CCAAATCGAACTCTCT<br>CCTCA | CGTGATGCACCGATAA<br>ATTG  | 59.4                             | 634                                           | DRR                                               | Ca_17817                            | R                     | --     |
| Ca2_P4_32048344  | Ca2                                     | 32048344                      | CTTTTT/CTTTTTT                                                | CCAAATCGAACTCTCT<br>CCTCA | CGTGATGCACCGATAA<br>ATTG  | 59.4                             | 634                                           | DRR                                               | Ca_17817                            | R                     | --     |
| Ca2_P4_32069395  | Ca2                                     | 32069395                      | TTATATATATATATAT/TTATATATAT<br>ATATATATAT                     | ACCCCGTTGATCATAA<br>GTCG  | AAATCCTGGCAGTCA<br>TCGT   | 59.8                             | 922                                           | DRR                                               | Ca_17815                            | U                     | --     |
| Ca2_P4_32074725  | Ca2                                     | 32074725                      | AGTGTGTGT/AGTGTGT                                             | TTCCTATGTGCAAAAGT<br>GCAT | TCCCTTGAGTGGCAGT<br>AACC  | 58.3                             | 474                                           | DRR                                               | Ca_17814                            | S                     | --     |
| Ca2_P4_32118444  | Ca2                                     | 32118444                      | GACGAACG/GACG                                                 | ACCATGCCACATCATC<br>TTGA  | TGCAATTGAGAAATTTG<br>CGT  | 59.9                             | 342                                           | DRR                                               | Ca_17813                            | --                    | ERF    |
| Ca2_P4_32129360  | Ca2                                     | 32129360                      | CATTGAATTGAATTGAATTG/CATTGAATTGAATTGAATTG                     | CTCCTAATTTGCGTTT<br>CCG   | GTTCAAGCTCGCAACAA<br>TTCA | 59.7                             | 368                                           | DRR                                               | Ca_17812                            | O                     | --     |
| Ca2_P4_32173774  | Ca2                                     | 32173774                      | TC/T                                                          | ATGTTTTGATTGGGGC<br>TTTG  | TAAATCAGCCCTTTTGG<br>TGG  | 59.8                             | 631                                           | DRR                                               | Ca_17806                            | --                    | WRKY   |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca2_P4_32175488  | Ca2                                     | 32175488                      | AAT/AATAT                                                     | CACAACATCATCAAGA<br>AACCAAA | GGCATCGCTAACGCA<br>TTAT  | 59.9                             | 681                                           | DRR                                               | Ca_17806                            | --                    | WRKY    |
| Ca2_P4_32199784  | Ca2                                     | 32199784                      | ATT/ATTT                                                      | TCCCATTACCACCAAA<br>GACA    | TGCCATAACCACCAAA<br>GACA | 58.8                             | 413                                           | DRR                                               | Ca_10295                            | --                    | G2-like |
| Ca2_P4_32241009  | Ca2                                     | 32241009                      | GAAAAAAAAA/GAAAAAAAAA                                         | TGAGACGTCACCCCTCA<br>GTTG   | GAGGCCAAAGGTCCAA<br>TATG | 59.9                             | 568                                           | DRR                                               | Ca_10293                            | --                    | --      |
| Ca2_P4_32241234  | Ca2                                     | 32241234                      | AATATATATATATAT/AATATATAT<br>ATATAT                           | CATATTGGACCTTTGG<br>CCTC    | TGCTTGCCAATTCATGT<br>CTC | 59.4                             | 434                                           | DRR                                               | Ca_10293                            | --                    | --      |
| Ca2_P4_32327707  | Ca2                                     | 32327707                      | GT/GTAATGATAT                                                 | TTCCCTTCACTATCG<br>GTGC     | CAAAATTGCAATTGTGC<br>CTG | 60.1                             | 660                                           | DRR                                               | Ca_10285                            | R                     | --      |
| Ca2_P4_32327737  | Ca2                                     | 32327737                      | A/ATC                                                         | TTCCCTTCACTATCG<br>GTGC     | CAAAATTGCAATTGTGC<br>CTG | 60.1                             | 660                                           | DRR                                               | Ca_10285                            | R                     | --      |
| Ca2_P4_32354755  | Ca2                                     | 32354755                      | TAGTTGTCAA/TAGTTGTCAAAGTTG<br>TCAA                            | TTCCAGCCAACTCCTG<br>ATTC    | TTTAGTGGTCCCTTGC<br>CAAC | 60.2                             | 548                                           | DRR                                               | Ca_10283                            | --                    | --      |
| Ca2_P4_32412446  | Ca2                                     | 32412446                      | ATTTTTTTTT/ATTTTTTTTTT                                        | GGCTCATTACAGTGGA<br>GGGA    | TAATGGGACCAAACT<br>GCAC  | 60.1                             | 688                                           | DRR                                               | Ca_10279                            | --                    | bHLH    |
| Ca2_P4_32435073  | Ca2                                     | 32435073                      | GTTTTT/GTTTTTTT                                               | TCGCTCAGTGATGTTG<br>AAGG    | GCCTCAAATCTTTTC<br>GTTTC | 60.0                             | 695                                           | DRR                                               | Ca_10275                            | O                     | C2H2    |
| Ca2_P4_32436418  | Ca2                                     | 32436418                      | CG/C                                                          | TCACATGGTGGCATCC<br>TAGA    | CGAGTCATCCATGCTC<br>TGTT | 60.1                             | 302                                           | DRR                                               | Ca_10275                            | O                     | C2H2    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca2_P4_32477117  | Ca2                                     | 32477117                      | TTTGTT/TTTGTTGTT                                              | CTGCAATGATAATTGG<br>GGCT     | CAACTGCAATGTTCCAT<br>ATTCTG | 59.9                             | 555                                           | DRR                                               | Ca_10273                            | R                     | C3H      |
| Ca2_P4_32673561  | Ca2                                     | 32673561                      | ATTTTTTTTTT/ATTTTTTTTTT                                       | TTCAACCAAGCCTACC<br>CTTC     | TGGCCAACAAAATTTAA<br>CCA    | 59.2                             | 449                                           | DRR                                               | Ca_10254                            | DR                    | --       |
| Ca2_P4_33058448  | Ca2                                     | 33058448                      | CATATTAGTATATTAGTA/CATATTA<br>GTA                             | CCTTACCATGACCCCA<br>AATG     | TGCCTGGGTTTCTTTAA<br>TGG    | 60.0                             | 630                                           | DRR                                               | Ca_10218                            | R                     | B3       |
| Ca2_P4_33076756  | Ca2                                     | 33076756                      | CAAAAAAAAA/CAAAAAAAAAA                                        | TGCACAATTACCATAAA<br>ACAATTT | TGGTGGTAATGGAGGC<br>AGTT    | 57.7                             | 558                                           | DRR                                               | Ca_10215                            | K                     | MYB      |
| Ca2_P4_33147399  | Ca2                                     | 33147399                      | AGT/A                                                         | CAACCCAAACATTGGA<br>CAAA     | CGGTACAGGATAGGG<br>ATGT     | 59.3                             | 771                                           | DRR                                               | Ca_10205                            | D                     | M-type   |
| Ca2_P4_33398226  | Ca2                                     | 33398226                      | CTAGTA/CTAGTAGTA                                              | AAACGTGCCTTGAAAA<br>TTGG     | AAATGCAGGGTCACAA<br>CACA    | 60.0                             | 727                                           | DRR                                               | Ca_10186                            | T                     | M-type   |
| Ca2_P4_33398441  | Ca2                                     | 33398441                      | TACACAC/TACAC                                                 | AGAGCCTACAGCAAGC<br>CAAA     | AAATGCAGGGTCACAA<br>CACA    | 60.2                             | 205                                           | DRR                                               | Ca_10186                            | T                     | M-type   |
| Ca2_P4_33661751  | Ca2                                     | 33661751                      | ATTTTTTTTT/ATTTTTTTTT                                         | GTTTGTGGTAGGGGCT<br>TCAA     | TTGTCTATGCAACATG<br>CCC     | 60.0                             | 388                                           | DRR                                               | Ca_10172                            | --                    | HB-other |
| Ca2_P4_34272124  | Ca2                                     | 34272124                      | AATATATATATATATATATATATA/<br>AATATATATATATATATATATA           | GGCACCTCATATGCAA<br>CCTT     | TGGCACCAAACTTACA<br>CCAA    | 60.0                             | 652                                           | DRR                                               | Ca_15251                            | --                    | WRKY     |
| Ca2_P4_34864878  | Ca2                                     | 34864878                      | GTATA/GTA                                                     | CTTCAGTCTGACGCTC<br>TCCC     | TTGCTGCCAAAATAAAC<br>AACA   | 60.1                             | 651                                           | DRR                                               | Ca_16882                            | --                    | FAR1     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                                   |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca2_P4_34945283  | Ca2                                     | 34945283                      | GAAAAA/GAAAAAA                                                    | ACACAGTGAGCACACC<br>CAAA   | ACGATCGCACTTCGTC<br>TTCT | 60.2                             | 443                                           | DRR                                               | Ca_16876                            | --                    | --    |
| Ca2_P4_35559233  | Ca2                                     | 35559233                      | CAA/CAAA                                                          | CCAAAATATCCACCGT<br>GTTT   | TTCCTGGACGAAAATG<br>AACC | 57.3                             | 582                                           | DRR                                               | Ca_09721                            | K                     | NF-YB |
| Ca2_P4_35839544  | Ca2                                     | 35839544                      | AATATATATATATATATATATAT<br>ATA/AATATATATATATATATATAT<br>ATATATATA | CTGCACAGGCTCTACA<br>ACCA   | GGACCTGCAATCCAAC<br>CTAA | 60.0                             | 783                                           | DRR                                               | Ca_09758                            | O                     | MYB   |
| Ca2_P4_35843737  | Ca2                                     | 35843737                      | TATGATA/TATGATAATGATA                                             | TTTGTGTCTTTTGGC<br>CTT     | GGAGAGAGAGACACG<br>GTTGC | 57.4                             | 699                                           | DRR                                               | Ca_09759                            | E                     | MYB   |
| Ca2_P4_35843945  | Ca2                                     | 35843945                      | ATTTTT/ATTT                                                       | TGTGATTTAACATTAC<br>TTGGCA | GGAGAGAGAGACACG<br>GTTGC | 60.4                             | 274                                           | DRR                                               | Ca_09759                            | E                     | MYB   |
| Ca2_P4_35846531  | Ca2                                     | 35846531                      | ATT/ATTT                                                          | TTATTTGTCGGTGGC<br>AACA    | TGATCGGAATGCGAAT<br>AACA | 60.0                             | 455                                           | DRR                                               | Ca_09760                            | J                     | --    |
| Ca2_P4_35857180  | Ca2                                     | 35857180                      | GTATATATATATATATATAT/GTAT<br>ATATATATATATATAT                     | TTTGATTGCCTTCCTCC<br>ATC   | TTCGGGATTAAACATT<br>CGG  | 60.0                             | 509                                           | DRR                                               | Ca_09762                            | R                     | --    |
| Ca2_P4_35858374  | Ca2                                     | 35858374                      | AAAGCAAGCAA/AAAGCAA                                               | CCCCTCAACATTACC<br>CCTT    | TTTCGCCGTCAGAGAG<br>AAAT | 60.0                             | 762                                           | DRR                                               | Ca_09762                            | R                     | --    |
| Ca2_P4_35914172  | Ca2                                     | 35914172                      | AAAAATAA/AAAA                                                     | ACAAATGCATGGGAAT<br>GACA   | GGGGGAGACTCATCAC<br>TCAA | 59.8                             | 182                                           | DRR                                               | Ca_09766                            | --                    | ERF   |
| Ca2_P4_35918468  | Ca2                                     | 35918468                      | TAAAAAAA/TAAAAAATAA                                               | AGCTGCAAGAGAAACA<br>GATGG  | TTTCAACGCTACCTTC<br>ATCA | 59.6                             | 804                                           | DRR                                               | Ca_09767                            | M                     | --    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                 |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_35965637  | Ca2                                     | 35965637                      | CTT/CT                                                                          | TGGAAGAATGCTTTCA<br>AGGG   | ACATTCCATGGGCTGC<br>TTAG | 60.2                             | 636                                           | DRR                                               | Ca_09771                            | J                     | NAC |
| Ca2_P4_35965829  | Ca2                                     | 35965829                      | CAAAAA/CA                                                                       | ATTTTCTGCTAGCGG<br>GACC    | ACATTCCATGGGCTGC<br>TTAG | 60.6                             | 260                                           | DRR                                               | Ca_09771                            | J                     | NAC |
| Ca2_P4_35966301  | Ca2                                     | 35966301                      | CT/CTT                                                                          | AGCCCATGGAATGTGA<br>AAAG   | CCAAAACCTTTGCCTT<br>GAAA | 59.9                             | 506                                           | DRR                                               | Ca_09771                            | J                     | NAC |
| Ca2_P4_35987956  | Ca2                                     | 35987956                      | ATGTTGT/ATGT                                                                    | GGATTGGCTCCCAT<br>ATTT     | GCGTTTTCAAGGTTGG<br>ATGT | 60.0                             | 851                                           | DRR                                               | Ca_09772                            | T                     | LBD |
| Ca2_P4_36401773  | Ca2                                     | 36401773                      | TATAATAATAATAATA/TATAATAATA<br>ATA                                              | GGATAAGGATCTGCAT<br>CGGA   | ATCCATTTTGTGGAAC<br>CAA  | 60.0                             | 434                                           | DRR                                               | Ca_09829                            | R                     | --  |
| Ca2_P4_3758160   | Ca2                                     | 3758160                       | ACTCTCTCTCTCTCTCTCTCTCTCT<br>CTCT/ACTCTCTCTCTCTCTCTCTCTCT<br>CTCTCTCTCTCT       | GGTGTGTTGTGCTCCAT<br>AGGC  | GAAACAGCACTGCCCA<br>ATTT | 60.5                             | 200                                           | DRR                                               | Ca_10485                            | J                     | --  |
| Ca2_P4_3809184   | Ca2                                     | 3809184                       | TTATATATATATATATATATATATATA<br>TATAT/TTATATATATATATATATATA<br>TATATATATATATATAT | TCTTCGAGCAATTGTG<br>TGCT   | CTAAAAAAGGCACGC<br>CGAA  | 59.6                             | 538                                           | DRR                                               | Ca_10479                            | --                    | --  |
| Ca2_P4_3901584   | Ca2                                     | 3901584                       | C/CGAG                                                                          | TTCAAGTTCAGCAGTG<br>ACCG   | ACAGCAAATTATGGG<br>CACC  | 60.0                             | 565                                           | DRR                                               | Ca_10467                            | G                     | --  |
| Ca2_P4_3901844   | Ca2                                     | 3901844                       | AC/ACTTCACGAGC                                                                  | GTCGCTATCTCCCCAG<br>TGAA   | CATTCTGTGCCGCTAT<br>CTGA | 60.2                             | 248                                           | DRR                                               | Ca_10466                            | GT                    | --  |
| Ca2_P4_453297    | Ca2                                     | 453297                        | TTATATATATATATATATAT/TTATAT<br>ATATATATATATATAT                                 | TTCAAACCAAATGATCC<br>AATGA | ATAAATGTTGGGTGGC<br>CAAA | 60.2                             | 685                                           | DRR                                               | Ca_16985                            | L                     | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                         | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                       |                             |                             |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_4812881   | Ca2                                     | 4812881                       | ATTTTTTT/ATTTTTTTTT                                                                                   | AACCAGTTCGTTCCA<br>AGTG     | TCCCCCAACAGAATTT<br>GAG     | 60.0                             | 731                                           | DRR                                                  | Ca_21090                            | --                    | MYB |
| Ca2_P4_5095861   | Ca2                                     | 5095861                       | GC/G                                                                                                  | GCCCGTTTGATTCACT<br>TTTC    | TCCAAACTGCACCACA<br>AAAC    | 59.6                             | 611                                           | DRR                                                  | Ca_14700                            | K                     | --  |
| Ca2_P4_5163788   | Ca2                                     | 5163788                       | CAAAAAAAAA/CAAAAAAAAA                                                                                 | TGCGAGAAAGTGAATT<br>CCAG    | GGAATGATGATGGGGT<br>TTTG    | 59.0                             | 658                                           | DRR                                                  | Ca_14696                            | --                    | --  |
| Ca2_P4_5373619   | Ca2                                     | 5373619                       | CATATATATATATATATATATATA<br>TATATATATATATATATATATAT/CAT<br>ATATATATATATATATATATATATA<br>TATATATATATAT | CGGAGGCTTAAGGACA<br>ATCA    | CGTTGCTCCAAATTTTA<br>TAATGG | 60.2                             | 784                                           | DRR                                                  | Ca_14670                            | E                     | MYB |
| Ca2_P4_753916    | Ca2                                     | 753916                        | CTTTTTTTTT/CTTTTTTTTT                                                                                 | TTGCCCATTAAC TTAC<br>CCG    | ACTTGTGCATTGCA TT<br>AGTTC  | 59.8                             | 555                                           | DRR                                                  | Ca_17000                            | --                    | ARF |
| Ca2_P4_7626448   | Ca2                                     | 7626448                       | AAATTATAATTATAATTA/AAATTATA<br>ATTATAATTATAATTA                                                       | AACAAGCATTTTGTGA<br>GGGC    | ATTCGACTAGTGGTGG<br>TGCC    | 60.1                             | 931                                           | DRR                                                  | Ca_18119                            | --                    | --  |
| Ca2_P4_7684658   | Ca2                                     | 7684658                       | CAA/CAAA                                                                                              | GCGCTTTTGGGTGTAC<br>ATTT    | GGGAAATAGCATGTTG<br>TGGG    | 60.0                             | 553                                           | DRR                                                  | Ca_18122                            | --                    | --  |
| Ca2_P4_7684720   | Ca2                                     | 7684720                       | ATTTTTTTTT/ATTTTTTTTT                                                                                 | GCGCTTTTGGGTGTAC<br>ATTT    | GGGAAATAGCATGTTG<br>TGGG    | 60.0                             | 553                                           | DRR                                                  | Ca_18122                            | --                    | --  |
| Ca2_P4_7801863   | Ca2                                     | 7801863                       | AA/AACA                                                                                               | TTCGGAGTTGCAGATG<br>ATTG    | TCATTCTTCACCTTGA<br>ACCA    | 59.8                             | 203                                           | DRR                                                  | Ca_18127                            | --                    | ERF |
| Ca2_P4_7818010   | Ca2                                     | 7818010                       | GATA/GATATTCTAATA                                                                                     | TGGACATAGAAAAACC<br>AAATGGA | ATGTGGAAGTTGAACC<br>CCAA    | 60.6                             | 598                                           | DRR                                                  | Ca_18128                            | QR                    | B3  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_7819525   | Ca2                                     | 7819525                       | TAACAA/TAA                                                    | GCCACAAATCATGTGT<br>TCCA     | GCATCCTCCAAGGTAT<br>CGAA  | 60.4                             | 539                                           | DRR                                               | Ca_18128                            | QR                    | B3  |
| Ca2_P4_7821264   | Ca2                                     | 7821264                       | CTTTTTTTTT/CTTTTTTTTTTT                                       | TTCAGGAACACCATGG<br>TTCA     | GAGGTTTCTGAAAGCG<br>TTGC  | 59.9                             | 948                                           | DRR                                               | Ca_18129                            | R                     | CPP |
| Ca2_P4_7881740   | Ca2                                     | 7881740                       | ATATTCC/ATATTCTATTCC                                          | TCATCTCCATGTGGTC<br>TCCA     | TGCAAATGACCACCCA<br>CTTA  | 60.0                             | 642                                           | DRR                                               | Ca_18136                            | --                    | --  |
| Ca2_P4_7886311   | Ca2                                     | 7886311                       | CAAAA/CAA                                                     | TTGTGGTCAAATTGGA<br>ACAAGT   | GCGAATCCCATAGGTA<br>AAAGC | 59.4                             | 742                                           | DRR                                               | Ca_18137                            | E                     | --  |
| Ca2_P4_7886536   | Ca2                                     | 7886536                       | CTTTT/CTTT                                                    | AAAAGGCAGACAACAT<br>GGAT     | GTCCTTTTGCTCCTCT<br>GCAC  | 57.1                             | 461                                           | DRR                                               | Ca_18137                            | E                     | --  |
| Ca2_P4_7887518   | Ca2                                     | 7887518                       | ATTTTTTT/ATTTTTTTT                                            | AAGCAAATACATCTC<br>GAAGTTCT  | TCCCAAGAAAAGCTTC<br>AACC  | 57.8                             | 550                                           | DRR                                               | Ca_18137                            | E                     | --  |
| Ca2_P4_7896699   | Ca2                                     | 7896699                       | TGGG/TGGGG                                                    | TTGGACGCATCCTGAT<br>TGTA     | CCGGACGACGATTAGT<br>GATT  | 60.1                             | 847                                           | DRR                                               | Ca_18138                            | --                    | Dof |
| Ca2_P4_7896829   | Ca2                                     | 7896829                       | GAAA/GAAAA                                                    | CTTTGAGCTAGTGTGT<br>GCCG     | GCTGAGCTTGACGTA<br>GGGC   | 59.7                             | 477                                           | DRR                                               | Ca_18138                            | --                    | Dof |
| Ca2_P4_7913902   | Ca2                                     | 7913902                       | GAAAAAAAAA/GAAAAAAAAA                                         | TCAAATCTACCTTAAC<br>GATTCACA | AAGGACAGTTGTCCCA<br>ATGC  | 59.2                             | 326                                           | DRR                                               | Ca_18139                            | FE                    | --  |
| Ca2_P4_7935559   | Ca2                                     | 7935559                       | TCTA/T                                                        | AACCGTTTGAGGAATT<br>GACG     | TCGAACTTGCATTGCC<br>ATAA  | 60.0                             | 865                                           | DRR                                               | Ca_18144                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca2_P4_7935610   | Ca2                                     | 7935610                       | TATTAT/TATTATTAT                                              | GGTGATGGGTAGGT<br>GAATG      | TCGAACTGCATTGCC<br>ATAA    | 60.1                             | 590                                           | DRR                                               | Ca_18144                            | --                    | --   |
| Ca2_P4_7936230   | Ca2                                     | 7936230                       | AT/ATT                                                        | TATGGCAATGCAAGTT<br>CGAC     | TCGCAAACTTCAAGA<br>GTGG    | 59.7                             | 443                                           | DRR                                               | Ca_18144                            | --                    | --   |
| Ca2_P4_8362914   | Ca2                                     | 8362914                       | GAATGAAATGAAA/GAATGAAATGAA<br>ATGAAATGAAA                     | GTGGGTATCCGGAGGT<br>ATCA     | TCCAAACACTCCCAAAA<br>AGC   | 59.6                             | 307                                           | DRR                                               | Ca_21465                            | --                    | --   |
| Ca2_P4_8597078   | Ca2                                     | 8597078                       | CCT/C                                                         | TCACGTTTTGAATTG<br>CGA       | GACCCATCCATGTGGA<br>GTTT   | 60.2                             | 514                                           | DRR                                               | Ca_22316                            | A                     | --   |
| Ca3_P4_10398321  | Ca3                                     | 10398321                      | G/GATTGATCTTTCCC                                              | CGGATTGCCAAGTACA<br>AGGT     | CAAACCACAACCAGCA<br>CAAC   | 60.0                             | 770                                           | DRR                                               | Ca_18819                            | J                     | --   |
| Ca3_P4_11249483  | Ca3                                     | 11249483                      | TAAA/TAA                                                      | GCAATTGTGGTTGCTG<br>ACTG     | TTCATCTTCCAAAGGCA<br>TTTTA | 60.3                             | 607                                           | DRR                                               | Ca_19372                            | --                    | C2H2 |
| Ca3_P4_11250270  | Ca3                                     | 11250270                      | TT/TTAT                                                       | AACAATTGATTCGTGT<br>GATTGG   | TTGGGTCCAATAGGAA<br>GTCG   | 59.7                             | 806                                           | DRR                                               | Ca_19372                            | --                    | C2H2 |
| Ca3_P4_11250530  | Ca3                                     | 11250530                      | TTTATTATTATTATTATTATT/TTT<br>ATTATTATTATTATTATTATTATT         | TGGTAACAAATTGATTA<br>ATCGCAA | TTGGGTCCAATAGGAA<br>GTCG   | 60.6                             | 609                                           | DRR                                               | Ca_19372                            | --                    | C2H2 |
| Ca3_P4_11590236  | Ca3                                     | 11590236                      | ATT/A                                                         | TTGCTCCTACGTATCT<br>CCCG     | CCTTTTGTCATTTGGG<br>CTC    | 60.2                             | 800                                           | DRR                                               | Ca_19380                            | --                    | --   |
| Ca3_P4_12402301  | Ca3                                     | 12402301                      | T/TG                                                          | GAAGGTTGAGCAAC<br>GAGC       | GAATGATTTTGAAGTG<br>GGGG   | 60.0                             | 880                                           | DRR                                               | Ca_21030                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                               | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                                                             |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca3_P4_15072147  | Ca3                                     | 15072147                      | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>A                                                 | GAGTGGTGTGGAGTC<br>ATGTTT   | AGACATGTGTTCCCTT<br>CCG   | 59.0                             | 424                                           | DRR                                               | Ca_17011                            | --                    | --          |
| Ca3_P4_15072299  | Ca3                                     | 15072299                      | ATT/ATTT                                                                                                    | GCGAAATCCAACTTTT<br>CCAA    | AGACATGTGTTCCCTT<br>CCG   | 60.1                             | 211                                           | DRR                                               | Ca_17011                            | --                    | --          |
| Ca3_P4_15073326  | Ca3                                     | 15073326                      | GAAAAAAAAA/GAAAAAAAAA                                                                                       | TGTGTGTGCATCCAAA<br>AGGT    | TTTGGGAGTAGGCCTT<br>CCTT  | 60.0                             | 205                                           | DRR                                               | Ca_17012                            | R                     | --          |
| Ca3_P4_15396841  | Ca3                                     | 15396841                      | CATATATATATATATATATATATA<br>TATATATATATATATATA/CATATATA<br>TATATATATATATATATATATATAT<br>ATATATATATATATATATA | TCAATGCGGTCTCTGA<br>AGTG    | CACATGCTAATCGACA<br>CCGT  | 60.0                             | 412                                           | DRR                                               | Ca_17029                            | --                    | Trihelix    |
| Ca3_P4_15658487  | Ca3                                     | 15658487                      | TTCCA/TTCCACTCCA                                                                                            | AAAGCATTCCCACTAC<br>GGTG    | TTGTCACAGCCTAAAAC<br>CCC  | 60.0                             | 343                                           | DRR                                               | Ca_17043                            | --                    | --          |
| Ca3_P4_15658525  | Ca3                                     | 15658525                      | TC/TCATTCC                                                                                                  | AAAGCATTCCCACTAC<br>GGTG    | TTGTCACAGCCTAAAAC<br>CCC  | 60.0                             | 343                                           | DRR                                               | Ca_17043                            | --                    | --          |
| Ca3_P4_16094863  | Ca3                                     | 16094863                      | CTTTTTT/CTTTTTTT                                                                                            | TCTCCGCATAAGCTTT<br>CGAT    | TGATTGCAAAATAGCAC<br>CCAA | 59.9                             | 248                                           | DRR                                               | Ca_17065                            | --                    | --          |
| Ca3_P4_16879725  | Ca3                                     | 16879725                      | T/TCCCACTGGTCA                                                                                              | AAGCGTACCTGTGGGA<br>ATTG    | GCGGATCCACTCACTA<br>AAGG  | 60.0                             | 818                                           | DRR                                               | Ca_18286                            | R                     | MYB         |
| Ca3_P4_18089824  | Ca3                                     | 18089824                      | AATATATATATATATATATATATAT<br>ATATA/AATATATATATATATATATAT<br>ATATATATATATATATA                               | TGCGTGATTATCTGTTT<br>AACGAA | CCGACAGCGGATGATT<br>TTAT  | 59.7                             | 791                                           | DRR                                               | Ca_21136                            | --                    | MYB_related |
| Ca3_P4_18345308  | Ca3                                     | 18345308                      | TAAAAAAA/TAAAAAAA                                                                                           | GGTTTCCCTCCTAAGT<br>TAAGGGT | GCGGTGCAATCAGTAA<br>ACCT  | 60.1                             | 271                                           | DRR                                               | Ca_19619                            | O                     | --          |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |           |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----------|
|                  |                                         |                               |                                                               |                              |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs       |
| Ca3_P4_19366983  | Ca3                                     | 19366983                      | ATTTTTTTTT/ATTTTTTTTT                                         | AGCTACTCGTCATCCT<br>CCGA     | TAAAAAGTGAACACAC<br>GCCG  | 60.0                             | 807                                           | DRR                                               | Ca_19336                            | --                    | --        |
| Ca3_P4_19368565  | Ca3                                     | 19368565                      | GTTTTT/GTTTTT                                                 | GGTGATGCATGATGAT<br>TTGC     | TGGGTTAGCTTTTGGG<br>ATTG  | 59.9                             | 630                                           | DRR                                               | Ca_19336                            | --                    | --        |
| Ca3_P4_19383912  | Ca3                                     | 19383912                      | CAAA/CAA                                                      | GTCAGGTCAGGCTGGA<br>AAAA     | TCGTCTTAATCCACTTG<br>GTGC | 60.2                             | 436                                           | DRR                                               | Ca_19337                            | --                    | --        |
| Ca3_P4_20011560  | Ca3                                     | 20011560                      | GTTGACACTT/GTTGACACTTGACA<br>CTT                              | GCAATTGCAAGAGCGT<br>GATA     | TTTGGCATGCAATCAAA<br>CAT  | 60.0                             | 277                                           | DRR                                               | Ca_09404                            | --                    | --        |
| Ca3_P4_21276082  | Ca3                                     | 21276082                      | AT/ATTATTATTATTATTT                                           | TTGATCTTTTGTCGGT<br>TGC      | TCTTGGACATCATCAAA<br>GCG  | 58.7                             | 530                                           | DRR                                               | Ca_09490                            | --                    | S1Fa-like |
| Ca3_P4_22165237  | Ca3                                     | 22165237                      | AG/A                                                          | TTTGAAATGCCAATAAA<br>GTTTGAA | CATGCAATGCACGAGA<br>TCAT  | 59.9                             | 502                                           | DRR                                               | Ca_20412                            | U                     | --        |
| Ca3_P4_22553987  | Ca3                                     | 22553987                      | CGAC/CGACGTATTGAGAC                                           | CCACATGAGTGTGTG<br>AGGG      | GGCTATCGCTTATGCA<br>GGAC  | 60.0                             | 588                                           | DRR                                               | Ca_06259                            | --                    | SAP       |
| Ca3_P4_23016776  | Ca3                                     | 23016776                      | TCCTACCT/TCCT                                                 | GCACACCTATGTGGTC<br>TTGC     | CCATTTTGTGGAAGTTT<br>GGTT | 59.2                             | 615                                           | DRR                                               | Ca_06208                            | QR                    | B3        |
| Ca3_P4_23356020  | Ca3                                     | 23356020                      | GA/G                                                          | TCGTTTCCGGAGTCAA<br>GTTT     | TGGGCTGGTATGTGAC<br>TTTG  | 60.2                             | 718                                           | DRR                                               | Ca_06185                            | O                     | --        |
| Ca3_P4_23876448  | Ca3                                     | 23876448                      | AATATATATATATAT/AATATATAT<br>ATATATATATATAT                   | CATAATCCCATCGCTC<br>TCGT     | TCGGTAACTGGCCAA<br>ACTC   | 60.1                             | 568                                           | DRR                                               | Ca_06137                            | --                    | --        |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                  | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                                                                                                |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca3_P4_29263411  | Ca3                                     | 29263411                      | TAAAAAAAA/TAAAAAAAA                                                                                                                                            | TTCAAAATGGACCGT<br>GAAA    | TTGCAACTTTACGAAAC<br>CCC | 59.9                             | 537                                           | DRR                                               | Ca_07235                            | IR                    | Nin-like |
| Ca3_P4_29263688  | Ca3                                     | 29263688                      | A/AAAGGT                                                                                                                                                       | TTGAAGATCTCTGTGG<br>CGAA   | CTTCTCTCCCCAGCTT<br>GTTG | 59.5                             | 762                                           | DRR                                               | Ca_07235                            | IR                    | Nin-like |
| Ca3_P4_30017715  | Ca3                                     | 30017715                      | ATTTTTTTTT/ATTTTTTTTT                                                                                                                                          | TTCATTTTCATCTGCC<br>CTC    | AACCCTGCCTCAGTGT<br>CAAC | 60.0                             | 707                                           | DRR                                               | Ca_07315                            | T                     | --       |
| Ca3_P4_30559364  | Ca3                                     | 30559364                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATAATTATTATTATTATT<br>TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATA<br>ATTATTATTATTATTATT | TTATCGTAACGTGGGT<br>GTCG   | AATTTCCAAGTGGTCC<br>CCTC | 59.5                             | 576                                           | DRR                                               | Ca_07376                            | --                    | --       |
| Ca3_P4_31126519  | Ca3                                     | 31126519                      | ATTTTTTTTT/ATTTTTTTTT                                                                                                                                          | TATCGCTTTAAGGTGC<br>CGTT   | AAAATTCATCACCCCAT<br>TCG | 59.9                             | 406                                           | DRR                                               | Ca_12210                            | R                     | HD-ZIP   |
| Ca3_P4_31206870  | Ca3                                     | 31206870                      | GTTTTTTTTT/GTTTTTTTTT                                                                                                                                          | CAATTCATCTGTTGGG<br>AGATCA | CCTGCATTACTTGCTC<br>CACA | 59.9                             | 727                                           | DRR                                               | Ca_12217                            | O                     | TCP      |
| Ca3_P4_31290388  | Ca3                                     | 31290388                      | AG/A                                                                                                                                                           | TTTAAAGAAGGGAGGT<br>CGCTC  | TTGAAGCAGTGTGTG<br>GGAA  | 59.8                             | 632                                           | DRR                                               | Ca_12225                            | P                     | ERF      |
| Ca3_P4_31290755  | Ca3                                     | 31290755                      | ATATT/AT                                                                                                                                                       | GATGGTCGATTGAGA<br>GCGT    | AAAAACACACGCAAC<br>CAACA | 60.2                             | 725                                           | DRR                                               | Ca_12225                            | P                     | ERF      |
| Ca3_P4_31298029  | Ca3                                     | 31298029                      | TAAAAAAAAA/TAAAAAAAAA                                                                                                                                          | GGACTTTTGGCACGAT<br>GTTT   | TTTGCAACTTTTGACGG<br>ACA | 60.0                             | 716                                           | DRR                                               | Ca_12226                            | K                     | MYB      |
| Ca3_P4_31306026  | Ca3                                     | 31306026                      | GAAAAA/GAAAAA                                                                                                                                                  | GTCGCATCCCTCAAAA<br>GTGT   | ACTTGAAGCAACGGCT<br>AGGA | 60.1                             | 521                                           | DRR                                               | Ca_12229                            | --                    | Dof      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca3_P4_31356584  | Ca3                                     | 31356584                      | A/AG                                                          | TCAATCACCCAAGCAT<br>TTCA | TTTGAAGGCGGTACAA<br>GTCC | 60.0                             | 896                                           | DRR                                               | Ca_12235                            | --                    | Whirly  |
| Ca3_P4_31413249  | Ca3                                     | 31413249                      | AA/AATA                                                       | TGTTGCACGTTGGACA<br>AGTT | GACTGCTACCAACCCA<br>GCAT | 60.2                             | 374                                           | DRR                                               | Ca_12238                            | A                     | --      |
| Ca3_P4_31490470  | Ca3                                     | 31490470                      | CTT/CTTT                                                      | GTCCCCCTCCATTTTG<br>GATT | ACTTTTGAAGGTTTGG<br>GGG  | 60.0                             | 369                                           | DRR                                               | Ca_12247                            | T                     | --      |
| Ca3_P4_31498522  | Ca3                                     | 31498522                      | GC/G                                                          | CTAGCTCGGGTTTCT<br>GACG  | TTGGCCACAGTTTAAC<br>CACA | 60.0                             | 531                                           | DRR                                               | Ca_12248                            | T                     | --      |
| Ca3_P4_31499264  | Ca3                                     | 31499264                      | TAAGC/T                                                       | TTAAAGGGATTTTCGA<br>GGCA | CACATGTTATTTGCCG<br>CTGT | 59.7                             | 476                                           | DRR                                               | Ca_12249                            | I                     | --      |
| Ca3_P4_31499806  | Ca3                                     | 31499806                      | CATATCAATATCAATATCAATATCAA<br>TAT/CATATCAATATCAATATCAATAT     | GCGGCAAATAACATGT<br>GAAA | TCCTAGACTTGTGGG<br>GCAC  | 59.6                             | 565                                           | DRR                                               | Ca_12248                            | T                     | --      |
| Ca3_P4_31588239  | Ca3                                     | 31588239                      | TACAAC/TAC                                                    | CTTCCAAATACCTCCC<br>CCAT | CCGTGGCCTTCTCTAC<br>TCTG | 60.0                             | 346                                           | DRR                                               | Ca_12258                            | BK                    | G2-like |
| Ca3_P4_31588307  | Ca3                                     | 31588307                      | T/TC                                                          | CTTCCAAATACCTCCC<br>CCAT | CCGTGGCCTTCTCTAC<br>TCTG | 60.0                             | 346                                           | DRR                                               | Ca_12258                            | BK                    | G2-like |
| Ca3_P4_31609545  | Ca3                                     | 31609545                      | T/TTA                                                         | GACAAAGCCAGAACCT<br>TTGC | ACCCAAGCAGGCATAC<br>AAAC | 59.9                             | 538                                           | DRR                                               | Ca_12260                            | --                    | --      |
| Ca3_P4_31635608  | Ca3                                     | 31635608                      | GTTTTTTTTTTT/GTTTTTTTTT                                       | AATGGGTTCCCTGGAT<br>TTTC | CTTTGGTGGGATCAGA<br>GAGC | 60.0                             | 222                                           | DRR                                               | Ca_12262                            | T                     | --      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                                           |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca3_P4_31637117  | Ca3                                     | 31637117                      | TGA/TGAGGA                                                                | TGCGTAAAAGCCAAAC<br>AAAA  | GCACAAGCAGAGCAAA<br>ATGA  | 59.4                             | 943                                           | DRR                                               | Ca_12264                            | --                    | NF-YB |
| Ca3_P4_31672462  | Ca3                                     | 31672462                      | AG/AGG                                                                    | AAGGCCGATTAGCCAA<br>AAAT  | TAGGAGGTCGCTTCTC<br>CAAA  | 59.9                             | 211                                           | DRR                                               | Ca_12269                            | --                    | NF-YB |
| Ca3_P4_32486522  | Ca3                                     | 32486522                      | AAATAATAATAATAATAATA<br>ATAATAATAAT/AAATAATAATAATA<br>TAATAATAATAATAATAAT | AACCACTTTTAAATCGA<br>TGCG | TGCAGTAGTTTGCTGC<br>CATC  | 59.1                             | 498                                           | DRR                                               | Ca_11974                            | --                    | --    |
| Ca3_P4_32582344  | Ca3                                     | 32582344                      | CGTGT/CGT                                                                 | CAGAACTGATTCTTCC<br>CCCA  | TCTCGGGTAAGTAAAG<br>GGCA  | 60.0                             | 408                                           | DRR                                               | Ca_11984                            | P                     | --    |
| Ca3_P4_32671018  | Ca3                                     | 32671018                      | CATATATATATATATATATATATA<br>TA/CATATATATATATATATATATA<br>TATATATATATA     | TGGTTGGAGAGCAAG<br>AAGG   | TTAGTGGAATTGCTTCC<br>CTGG | 60.4                             | 655                                           | DRR                                               | Ca_11996                            | --                    | --    |
| Ca3_P4_34821669  | Ca3                                     | 34821669                      | C/CGTTGAGTGA                                                              | TGTCCTTTGATGTGCA<br>GGAC  | CCAGCAACTCACGTGA<br>CAAT  | 59.7                             | 521                                           | DRR                                               | Ca_00758                            | --                    | --    |
| Ca3_P4_35006302  | Ca3                                     | 35006302                      | CTCTTCTTCTT/CTCTTCTT                                                      | CGATTGTTGATCCTCC<br>TCGT  | CTGCACACTTTGAGGC<br>TGAG  | 60.1                             | 460                                           | DRR                                               | Ca_00774                            | R                     | ZF-HD |
| Ca3_P4_3524015   | Ca3                                     | 3524015                       | AATATATATATATAT/AATATATATAT<br>ATATATAT                                   | GTTTGCAGGAAGAGGC<br>AAAG  | GCCAGCAGCCTTCAAG<br>ATAG  | 60.0                             | 712                                           | DRR                                               | Ca_21350                            | J                     | --    |
| Ca3_P4_35341749  | Ca3                                     | 35341749                      | ATTTTTTTT/ATTTTTTTT                                                       | CTGCCAGAAAGTTGAG<br>AAGGA | AAGGTTGTGTTTGAAA<br>CCGC  | 59.6                             | 779                                           | DRR                                               | Ca_00813                            | G                     | --    |
| Ca3_P4_35466145  | Ca3                                     | 35466145                      | TCACGAC/TC                                                                | CAATTTTTGCCGCCAT<br>TAT   | GGGCTGTCAGAGCAGA<br>AAAG  | 59.8                             | 743                                           | DRR                                               | Ca_00829                            | R                     | NAC   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca3_P4_35691450  | Ca3                                     | 35691450                      | TTATATATATATATATA/TTATATATA<br>TATATA                         | TCGTTACCCCTCTCGT<br>CATC    | CATTTCATACACTTGC<br>GCT   | 60.1                             | 594                                           | DRR                                               | Ca_00858                            | R                     | ZF-HD |
| Ca3_P4_35954208  | Ca3                                     | 35954208                      | A/AT                                                          | ATCCGTCTCTATACCC<br>GCAA    | ATCTACCCCGCACCCA<br>TAAT  | 59.6                             | 607                                           | DRR                                               | Ca_00890                            | V                     | --    |
| Ca3_P4_35955479  | Ca3                                     | 35955479                      | TAAAA/TAAAAA                                                  | AAATCGGCCCAACCT<br>AATC     | TCACAAATTCACAATCA<br>ACCG | 60.2                             | 238                                           | DRR                                               | Ca_00890                            | V                     | --    |
| Ca3_P4_35959327  | Ca3                                     | 35959327                      | GAAAAAA/GAAAAAAA                                              | TGTTGACCAATAAGCA<br>AAATTGA | TGACACACAACATACAA<br>GCCA | 59.5                             | 360                                           | DRR                                               | Ca_00891                            | V                     | GRAS  |
| Ca3_P4_35959933  | Ca3                                     | 35959933                      | GTTTTTT/GTTTTTTT                                              | TCTGAACAAATGATCG<br>GGTG    | ACATGCAATTTCCATCC<br>ACA  | 59.5                             | 164                                           | DRR                                               | Ca_00891                            | V                     | GRAS  |
| Ca3_P4_35959985  | Ca3                                     | 35959985                      | CAAAAAAAAAAAAA/CAAAAAA<br>AAAAA                               | TCTGAACAAATGATCG<br>GGTG    | ACATGCAATTTCCATCC<br>ACA  | 59.5                             | 164                                           | DRR                                               | Ca_00891                            | V                     | GRAS  |
| Ca3_P4_35967790  | Ca3                                     | 35967790                      | GAAAATAGAAA/GAAAATAGAAACA<br>AAATAGAAA                        | TTGATTATGAGCACCA<br>AGCG    | TGCTCGGATTTTGT<br>TTGAGA  | 59.8                             | 335                                           | DRR                                               | Ca_00892                            | C                     | --    |
| Ca3_P4_35981261  | Ca3                                     | 35981261                      | GT/G                                                          | TACCGGGAGAATTGAC<br>GACT    | TTGGGTCCATTTGGTTT<br>GAT  | 59.6                             | 317                                           | DRR                                               | Ca_00893                            | --                    | --    |
| Ca3_P4_35992938  | Ca3                                     | 35992938                      | ATT/AT                                                        | AGAAGCACAAAGTCCCC<br>TGAA   | GCTCATGTGTAAAGCC<br>GTGA  | 59.8                             | 710                                           | DRR                                               | Ca_00894                            | --                    | --    |
| Ca3_P4_35993475  | Ca3                                     | 35993475                      | CATATA/CATA                                                   | TCACGGCTTTACACAT<br>GAGC    | TTGATTGCAACCCAAAA<br>TCT  | 59.9                             | 515                                           | DRR                                               | Ca_00894                            | --                    | --    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                               |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca3_P4_36016163  | Ca3                                     | 36016163                      | TAAAAAAAAA/TAAAAAAAAA                                         | CAACTGCACAGATGGA<br>TTGG      | AATTTGCAATTTGATCC<br>CCA | 60.1                             | 650                                           | DRR                                               | Ca_00900                            | O                     | CAMTA |
| Ca3_P4_36022347  | Ca3                                     | 36022347                      | AC/ACC                                                        | AACATTTACAAACATAA<br>ACGACGAA | TGGAGATGGAAATGGA<br>GAGG | 59.0                             | 524                                           | DRR                                               | Ca_00901                            | O                     | CAMTA |
| Ca3_P4_36022379  | Ca3                                     | 36022379                      | TCC/TC                                                        | AACATTTACAAACATAA<br>ACGACGAA | TGGAGATGGAAATGGA<br>GAGG | 59.0                             | 524                                           | DRR                                               | Ca_00901                            | O                     | CAMTA |
| Ca3_P4_36032382  | Ca3                                     | 36032382                      | ATTTTTTTTT/ATTTTTT                                            | GCTTTGCTCCACATC<br>TCTC       | AACGCTGAACCAAAT<br>GACC  | 60.0                             | 217                                           | DRR                                               | Ca_00902                            | S                     | bZIP  |
| Ca3_P4_36033507  | Ca3                                     | 36033507                      | TAGAGA/TAGAGAGA                                               | CTTCTACCCCCCTCAA<br>AACA      | AGGCTTGATGACAGT<br>GATG  | 60.1                             | 696                                           | DRR                                               | Ca_00902                            | S                     | bZIP  |
| Ca3_P4_36098742  | Ca3                                     | 36098742                      | TC/T                                                          | TATGCTGATTCGGCCA<br>TTTT      | CTCGGTTGTTGTTGGA<br>GGTT | 60.4                             | 379                                           | DRR                                               | Ca_00908                            | K                     | --    |
| Ca3_P4_36116492  | Ca3                                     | 36116492                      | T/TC                                                          | TTGTGCTCAAACAGAG<br>TCGG      | ATGTGTCTGCCATGCT<br>TCTG | 60.0                             | 510                                           | DRR                                               | Ca_00911                            | D                     | --    |
| Ca3_P4_36116714  | Ca3                                     | 36116714                      | AATGGCAGAAGCATGGCAGAAGCA<br>TGGCAGA/AATGGCAGAAGCATGGC<br>AGA  | TTGTGCTCAAACAGAG<br>TCGG      | TGGCTCAATCATTATC<br>TGC  | 60.0                             | 770                                           | DRR                                               | Ca_00911                            | D                     | --    |
| Ca3_P4_36116816  | Ca3                                     | 36116816                      | CT/CTCATTAT                                                   | CGAAAAACCGCCATAA<br>ACAT      | TGGCTCAATCATTATC<br>TGC  | 59.8                             | 337                                           | DRR                                               | Ca_00911                            | D                     | --    |
| Ca3_P4_36129194  | Ca3                                     | 36129194                      | GTAAATTA/GTAAATTAATTA                                         | GCAAAAAGCACCTCGA<br>CTTT      | CACACCAATCAAACGA<br>GCAA | 59.5                             | 696                                           | DRR                                               | Ca_00912                            | YU                    | --    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca3_P4_36152348  | Ca3                                     | 36152348                      | ATTT/ATT                                                      | TGGCTGTCAATTTGGA<br>AAAA | GGTTGATGCTGTCGTG<br>TTTG     | 59.1                             | 297                                           | DRR                                               | Ca_00916                            | A                     | GeBP |
| Ca3_P4_36152949  | Ca3                                     | 36152949                      | TAAAAAAA/TAAAAAAA                                             | CAACACGACAGCATC<br>AACC  | GGTGCTTTGAAGATTG<br>GAGG     | 60.2                             | 578                                           | DRR                                               | Ca_00916                            | A                     | GeBP |
| Ca3_P4_36153695  | Ca3                                     | 36153695                      | TT/TTAT                                                       | TTATTTTCGGGCTTTT<br>GTCA | ATTGATTGATTGGCATG<br>CTG     | 59.6                             | 514                                           | DRR                                               | Ca_00916                            | A                     | GeBP |
| Ca3_P4_36167042  | Ca3                                     | 36167042                      | GTTTTTTTTT/GTTTTTTTTT                                         | TTTTGACCCATCCAAG<br>AAGG | CCCCGTCTAATTAGCC<br>AACA     | 59.9                             | 459                                           | DRR                                               | Ca_00918                            | KTDL                  | --   |
| Ca3_P4_36178800  | Ca3                                     | 36178800                      | TATTTTAATTTTAATTT/TATTTTAAT<br>TTTAATTTTAATTT                 | TGGATAAGACCGGAGA<br>ATGC | TCTCGAAACTAGAAAA<br>GAACAAAA | 60.0                             | 812                                           | DRR                                               | Ca_00921                            | Q                     | B3   |
| Ca3_P4_36178910  | Ca3                                     | 36178910                      | AAT/A                                                         | TGGATAAGACCGGAGA<br>ATGC | TCTCGAAACTAGAAAA<br>GAACAAAA | 60.0                             | 812                                           | DRR                                               | Ca_00921                            | Q                     | B3   |
| Ca3_P4_36188427  | Ca3                                     | 36188427                      | TAA/TAAA                                                      | GCATAGGACTAGGCCC<br>AAAA | GGGAAGCGTCACACTA<br>AAGC     | 59.2                             | 521                                           | DRR                                               | Ca_00922                            | Q                     | B3   |
| Ca3_P4_36189478  | Ca3                                     | 36189478                      | AATAT/AATATTCACATTATAT                                        | CAACCGTTCAAATCAC<br>ATCG | GCCAAGGCCAAATCAA<br>CTTA     | 60.0                             | 690                                           | DRR                                               | Ca_00922                            | Q                     | B3   |
| Ca3_P4_36193918  | Ca3                                     | 36193918                      | GATATA/GATATATA                                               | TGAGGGACAAAAGGTT<br>CAGC | TGAAATATGGCTTCCT<br>TCG      | 60.2                             | 558                                           | DRR                                               | Ca_00923                            | --                    | bHLH |
| Ca3_P4_36194243  | Ca3                                     | 36194243                      | TAT/TATATGTAAAAAAT                                            | TGCCATAAGATGCGA<br>AACA  | TGAAATATGGCTTCCT<br>TCG      | 60.2                             | 249                                           | DRR                                               | Ca_00923                            | --                    | bHLH |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca3_P4_36198404  | Ca3                                     | 36198404                      | TAAAAAAAA/TAAAAAA                                             | TTCTTGCAATCAAAGCA<br>TCG | AACAGAGGCGGTGTCA<br>CTCT   | 60.0                             | 469                                           | DRR                                               | Ca_00924                            | --                    | --      |
| Ca3_P4_36198453  | Ca3                                     | 36198453                      | AATA/AA                                                       | TTCTTGCAATCAAAGCA<br>TCG | AACAGAGGCGGTGTCA<br>CTCT   | 60.0                             | 469                                           | DRR                                               | Ca_00924                            | --                    | --      |
| Ca3_P4_36199218  | Ca3                                     | 36199218                      | TTTCTTCTT/TTTCTTCTTCTT                                        | CACTCAAGGGACTAGG<br>AGCG | GGTTTATGGGTCTTGG<br>GGAT   | 60.0                             | 482                                           | DRR                                               | Ca_00924                            | --                    | --      |
| Ca3_P4_36204205  | Ca3                                     | 36204205                      | ATTT/ATTTT                                                    | ACATGCACAAATCCCT<br>CACA | GGTAGCAAAGCAATTT<br>CGGA   | 60.0                             | 435                                           | DRR                                               | Ca_00925                            | --                    | --      |
| Ca3_P4_36204911  | Ca3                                     | 36204911                      | ATATTAAATTT/ATATTAAATTTATTA<br>AATTT                          | GTCGTTGGAGTCTTTG<br>CGAT | TTCACCAAATGTTGACC<br>GAA   | 60.3                             | 452                                           | DRR                                               | Ca_00925                            | --                    | --      |
| Ca3_P4_36205222  | Ca3                                     | 36205222                      | GA/G                                                          | AAAATTGGAATTGTCAC<br>GCC | CATTCTTGTTGATGCCA<br>TGC   | 59.8                             | 548                                           | DRR                                               | Ca_00925                            | --                    | --      |
| Ca3_P4_36205967  | Ca3                                     | 36205967                      | GT/GTCT                                                       | GCATGGCATCAACAAG<br>AATG | CATCAGAAAGTCTGTTG<br>CCGA  | 60.1                             | 467                                           | DRR                                               | Ca_00925                            | --                    | --      |
| Ca3_P4_36213829  | Ca3                                     | 36213829                      | ATG/ATGAAAAAGTG                                               | AAAATTATTGTGGCCG<br>AGCA | ACAGGGGATGCAGACT<br>TTTT   | 60.5                             | 845                                           | DRR                                               | Ca_00926                            | --                    | LSD     |
| Ca3_P4_36215526  | Ca3                                     | 36215526                      | TA/TAA                                                        | TTGATTGCCGACAGTC<br>TTTG | CGCAATTTTGAATGTCA<br>TCATC | 59.8                             | 622                                           | DRR                                               | Ca_00927                            | --                    | CO-like |
| Ca3_P4_36215688  | Ca3                                     | 36215688                      | ATTTTT/ATTTT                                                  | TGCTGTAACGATGATG<br>CCAC | CAATGTGGATGCCTTT<br>GTTG   | 60.7                             | 981                                           | DRR                                               | Ca_00927                            | --                    | CO-like |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca3_P4_36220876  | Ca3                                     | 36220876                      | TAGA/TA                                                       | AATCCTAAAGCGCCGA<br>ATT   | GCTGGCACATTGTGAA<br>AAGA  | 60.1                             | 565                                           | DRR                                               | Ca_00928                            | --                    | --          |
| Ca3_P4_36221155  | Ca3                                     | 36221155                      | CAAAA/CAAA                                                    | TTTTTCAATGTGCCA<br>GCTC   | AAATCCATCCCCGTATC<br>TCC  | 59.8                             | 405                                           | DRR                                               | Ca_00928                            | --                    | --          |
| Ca3_P4_36236843  | Ca3                                     | 36236843                      | CATTCCA/CATTCCATATTCCA                                        | GAGTGGCTGGGAATCA<br>ACAT  | CACCAAGACTCATCTT<br>GCGA  | 59.9                             | 511                                           | DRR                                               | Ca_00931                            | O                     | --          |
| Ca3_P4_36256005  | Ca3                                     | 36256005                      | CTAAAGATA/CTAAAGATATAAAGAT<br>A                               | CCCTCCCTTGTGACG<br>AATA   | ATTGGCGAAGAAATGC<br>AATC  | 59.9                             | 705                                           | DRR                                               | Ca_00935                            | --                    | --          |
| Ca3_P4_36257974  | Ca3                                     | 36257974                      | AATATATAT/AATAT                                               | CGAGCATGGTGCAACT<br>TCTA  | CCTATTCCGTTTTTCATG<br>CGT | 60.0                             | 583                                           | DRR                                               | Ca_00936                            | --                    | MYB_related |
| Ca3_P4_36273608  | Ca3                                     | 36273608                      | ATTT/ATTTT                                                    | TTCACCTGCTTGGGC<br>TTTT   | GCGGGACATATTCAGG<br>AGAA  | 60.0                             | 405                                           | DRR                                               | Ca_00937                            | J                     | Dof         |
| Ca3_P4_36274277  | Ca3                                     | 36274277                      | T/TA                                                          | TGGGTTTTTCATTGGTTT<br>GGT | AAGCCGACTTCAAGAA<br>GGAC  | 60.1                             | 419                                           | DRR                                               | Ca_00937                            | J                     | Dof         |
| Ca3_P4_36340133  | Ca3                                     | 36340133                      | A/AGTAGAGATATAATTG                                            | TAGCCCGTCACAATTT<br>AGGG  | CTCTTTCTTCCCTCCG<br>CTC   | 60.0                             | 910                                           | DRR                                               | Ca_00942                            | --                    | HB-other    |
| Ca3_P4_36343651  | Ca3                                     | 36343651                      | TAAAAAAAA/TAAAAAAAAA                                          | GGGGTGATCGAATTAG<br>GGTT  | CCTAGAGGATCAAAAG<br>GCCC  | 60.0                             | 608                                           | DRR                                               | Ca_00943                            | R                     | C2H2        |
| Ca3_P4_36343819  | Ca3                                     | 36343819                      | ATTTT/ATTT                                                    | GGCCTTTTGATCCTCT<br>AGGC  | TGCATTGAATTGCCAA<br>CAT   | 60.2                             | 320                                           | DRR                                               | Ca_00943                            | R                     | C2H2        |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca3_P4_36344189  | Ca3                                     | 36344189                      | GCCC/GCC                                                      | GGCCTTTTGATCCTCT<br>AGGC | TGCAATTTTATCACAT<br>CCCC    | 60.2                             | 777                                           | DRR                                               | Ca_00943                            | R                     | C2H2  |
| Ca3_P4_36363400  | Ca3                                     | 36363400                      | ATTTTTTTT/ATTTTTTTT                                           | CAATGCATATGGACGG<br>AATG | GACGACAAAGGATATT<br>CATGAGC | 59.8                             | 352                                           | DRR                                               | Ca_00945                            | --                    | NF-X1 |
| Ca3_P4_36403564  | Ca3                                     | 36403564                      | TCA/T                                                         | TGAGGTGCTAACCCG<br>AAGA  | AGTGACAACCCCTCAA<br>TTCG    | 59.4                             | 223                                           | DRR                                               | Ca_00951                            | H                     | --    |
| Ca3_P4_36404085  | Ca3                                     | 36404085                      | GTT/GT                                                        | CGAATTGAGGGTTGT<br>CACT  | TGAATCTTATGCGTGA<br>GCG     | 60.0                             | 803                                           | DRR                                               | Ca_00951                            | H                     | --    |
| Ca3_P4_36424396  | Ca3                                     | 36424396                      | AA/AAAAATATA                                                  | GGACTGGGATTGAAC<br>GAAA  | TGCAAAGCCAAATGCT<br>ACAC    | 59.9                             | 586                                           | DRR                                               | Ca_00955                            | --                    | --    |
| Ca3_P4_36445861  | Ca3                                     | 36445861                      | ATTTTTTTTT/ATTTTTTTTT                                         | CGAAGGTTGTTCTCTG<br>ACAT | ACCGACACGTCTACAC<br>ACCA    | 60.1                             | 267                                           | DRR                                               | Ca_00960                            | O                     | --    |
| Ca3_P4_36446253  | Ca3                                     | 36446253                      | CAG/CAGAG                                                     | ATCCCAATCACCTCAC<br>TTGC | CCCAGATTCTATGCG<br>GAAA     | 59.9                             | 533                                           | DRR                                               | Ca_00960                            | O                     | --    |
| Ca3_P4_36447139  | Ca3                                     | 36447139                      | CAT/CATAT                                                     | GGATGAGTGCAATTG<br>GGAT  | AATGAATGGCTGCGCT<br>AGTT    | 59.8                             | 473                                           | DRR                                               | Ca_00960                            | O                     | --    |
| Ca3_P4_36526857  | Ca3                                     | 36526857                      | CAAAAAAAAA/CAAAAAAAAA                                         | AAGTCGCCAACGCAAT<br>AAAC | CTCTTTGTGCAACAG<br>GCAA     | 60.1                             | 827                                           | DRR                                               | Ca_00970                            | --                    | --    |
| Ca3_P4_36932559  | Ca3                                     | 36932559                      | GAIAAAAAAAAA/AAAAAAAAAA                                       | GTTACGATTTTCATTGG<br>CGA | CTTTGGTATGTTGGGC<br>CTGT    | 58.6                             | 917                                           | DRR                                               | Ca_01018                            | --                    | WRKY  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                          | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                                        |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca3_P4_36986782  | Ca3                                     | 36986782                      | AACT/A                                                                                 | TTTCAAGGTGTGTCA<br>CCGA      | TCTTACACCTCTTCGG<br>GTGC   | 60.1                             | 502                                           | DRR                                               | Ca_01027                            | U                     | C2H2        |
| Ca3_P4_37030222  | Ca3                                     | 37030222                      | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>ATATATA                      | GAAAAGCCCATTTTGT<br>CTCG     | AAAGGTTTGAAAATGG<br>ATGGTC | 59.7                             | 593                                           | DRR                                               | Ca_01031                            | G                     | C3H         |
| Ca3_P4_3703442   | Ca3                                     | 3703442                       | TAAAAAAAAA/TAAAAAAAAA                                                                  | GCGGAGATATTGCTG<br>CGTA      | TGGGCCCATTTACGTC<br>TAAG   | 61.3                             | 649                                           | DRR                                               | Ca_21344                            | --                    | --          |
| Ca3_P4_3704345   | Ca3                                     | 3704345                       | TAAAAA/TAAAAA                                                                          | TGGCAAGGAAATGACT<br>CACA     | GCAGATTGTGGGTTTG<br>ATTG   | 60.2                             | 944                                           | DRR                                               | Ca_21343                            | A                     | --          |
| Ca3_P4_37736258  | Ca3                                     | 37736258                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATA/AAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATA | TTTTGTCATTTGGTATT<br>CATTTCA | TCTCATTTACATCCGG<br>ACA    | 58.5                             | 595                                           | DRR                                               | Ca_01110                            | O                     | --          |
| Ca3_P4_37991623  | Ca3                                     | 37991623                      | TAAAAAAAAA/TAAAAAAAAA                                                                  | TAGATTCCCCACCAGT<br>CCAG     | TGGTACGCGACAATTT<br>TTGTT  | 59.9                             | 793                                           | DRR                                               | Ca_01140                            | --                    | --          |
| Ca3_P4_38073514  | Ca3                                     | 38073514                      | CAAAAAAAAAAAAA/CAAAAAAAAA<br>AAAA                                                      | CTTCTGAATGGGTTTG<br>GTGG     | ATGGACTCAATTGGGA<br>GTGG   | 60.3                             | 439                                           | DRR                                               | Ca_01151                            | DL                    | --          |
| Ca3_P4_38155393  | Ca3                                     | 38155393                      | ATTTT/ATTT                                                                             | GTTTTGCGCCAATTTT<br>ATT      | AGGGTGTTACATTCCGT<br>GCAT  | 60.0                             | 484                                           | DRR                                               | Ca_01160                            | L                     | MYB_related |
| Ca3_P4_38174096  | Ca3                                     | 38174096                      | AGG/AG                                                                                 | CGAAACACGTTACCAT<br>CATCC    | CCGATGAGTGTGGATG<br>TGAA   | 60.2                             | 410                                           | DRR                                               | Ca_01161                            | --                    | NF-YA       |
| Ca3_P4_38174447  | Ca3                                     | 38174447                      | A/AT                                                                                   | TTCACATCCCACTCAT<br>CGG      | CTGGCACTGGCATTCC<br>TAAT   | 60.5                             | 628                                           | DRR                                               | Ca_01161                            | --                    | NF-YA       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca3_P4_38184409  | Ca3                                     | 38184409                      | TGAAAA/TGAAAAGAAAA                                            | TCCACGAAACGAAGAA<br>GGTT | AGTGCGAAACCCCTTA<br>TCCC | 59.7                             | 603                                           | DRR                                               | Ca_01162                            | --                    | --   |
| Ca3_P4_38184714  | Ca3                                     | 38184714                      | ATTTTTTTT/ATTTTTTTTTTT                                        | GGGATTAAGGGTTTGC<br>CACT | CTGGCTTGTGAACCCA<br>AAAT | 60.2                             | 298                                           | DRR                                               | Ca_01162                            | --                    | --   |
| Ca3_P4_38184945  | Ca3                                     | 38184945                      | T/TG                                                          | AAGAAGAGAGGTTGGA<br>GCCC | CTGGCTTGTGAACCCA<br>AAAT | 59.8                             | 143                                           | DRR                                               | Ca_01162                            | --                    | --   |
| Ca3_P4_38185351  | Ca3                                     | 38185351                      | TAAACAAAACAA/TAAACAA                                          | ATTTTGGGTTCAACG<br>CCAG  | CAATTGGTGTAGGCC<br>ACCT  | 60.0                             | 497                                           | DRR                                               | Ca_01162                            | --                    | --   |
| Ca3_P4_38206155  | Ca3                                     | 38206155                      | TGGGGGG/TGGGGGGG                                              | GCATGCTGCCCATACC<br>TATT | CTCCCCCTTCTCCAGG<br>ATAG | 60.0                             | 691                                           | DRR                                               | Ca_01163                            | E                     | --   |
| Ca3_P4_38215897  | Ca3                                     | 38215897                      | CTT/CTTCTCTTCATT                                              | TGTTGCCTGGAAATGA<br>GTTG | TGCTGCATTGAAATCG<br>AGTC | 59.7                             | 688                                           | DRR                                               | Ca_01165                            | R                     | --   |
| Ca3_P4_38226965  | Ca3                                     | 38226965                      | A/AC                                                          | GGCTGGAAAAGATGTG<br>GAAA | CTATTTGGCACGTCTG<br>GGTT | 60.1                             | 281                                           | DRR                                               | Ca_01167                            | R                     | --   |
| Ca3_P4_38228316  | Ca3                                     | 38228316                      | T/TC                                                          | ATGATCCACTGAGATT<br>CCGC | CCAGAGTGTGACGCTT<br>TTGA | 60.0                             | 472                                           | DRR                                               | Ca_01168                            | R                     | bHLH |
| Ca3_P4_38228566  | Ca3                                     | 38228566                      | GAA/GAAA                                                      | AAATGTGAAAGCATGA<br>GGGG | TGTCCACTTCCTCGGC<br>TTAC | 59.9                             | 796                                           | DRR                                               | Ca_01168                            | R                     | bHLH |
| Ca3_P4_38230070  | Ca3                                     | 38230070                      | CTTTATAAGCCGGTTTTTTATAAGC<br>CGGTTTT/CTTTATAAGCCGGTTTT        | CCCTGGCTACCAAGTA<br>CCAA | TCCGAGACGGGTAAAT<br>ATGC | 60.0                             | 610                                           | DRR                                               | Ca_01168                            | R                     | bHLH |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)        | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                      |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca3_P4_38333156  | Ca3                                     | 38333156                      | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATAT                    | CCTGCCTTGCACCTAT<br>CAGT    | TAGTGTGATTGCCCT<br>TTTT     | 60.3                             | 683                                           | DRR                                               | Ca_01182                            | R                     | --       |
| Ca3_P4_38612369  | Ca3                                     | 38612369                      | TAAAAA/TAAAA                                                         | TTTTGAAAGCTCTCGC<br>TTGA    | TGCGACCTCATGAAGA<br>CTAAAA  | 58.9                             | 423                                           | DRR                                               | Ca_01216                            | --                    | GeBP     |
| Ca3_P4_38690322  | Ca3                                     | 38690322                      | AATATATATATATATATATATA/AATA<br>TATATATATATATATATATATATAT<br>ATA      | GAAGCAGGGAGGAGG<br>AAAAC    | TGCTCAATGAGGATTAT<br>GCCAA  | 60.2                             | 910                                           | DRR                                               | Ca_01224                            | K                     | Trihelix |
| Ca3_P4_38970415  | Ca3                                     | 38970415                      | GTTTTTT/GTTTTTTT                                                     | CGCAACCTCGTAATCC<br>ATTT    | CATCCCTAGAAATGCGA<br>CCAT   | 60.0                             | 565                                           | DRR                                               | Ca_01259                            | --                    | --       |
| Ca3_P4_39547263  | Ca3                                     | 39547263                      | CTTTATTTTTTTTTATTTTTTTTT/CT<br>TTATTTTTTTTTTATTTTTTTTTATT<br>TTTTTTT | GGGTGAGAAGTCTGAC<br>GGAG    | TGGA AAAACCAAGAAAT<br>GTTGA | 59.8                             | 806                                           | DRR                                               | Ca_01325                            | --                    | ERF      |
| Ca3_P4_39848936  | Ca3                                     | 39848936                      | AATATATATATATATATATATATAT<br>AT/AATATATATATATATATATATATA<br>TATATAT  | GAAACAGTGAATGCCA<br>CCCT    | GGTTTTGAATTGCCAT<br>GCTT    | 60.0                             | 325                                           | DRR                                               | Ca_01370                            | P                     | GRAS     |
| Ca3_P4_4121386   | Ca3                                     | 4121386                       | CTTT/CTTTT                                                           | GACTGGACGTAACCCA<br>CGTT    | AGCATTGTGCTTACGA<br>CGAA    | 59.9                             | 379                                           | DRR                                               | Ca_22386                            | --                    | --       |
| Ca3_P4_5070771   | Ca3                                     | 5070771                       | ATTTTTTTTTTTTT/ATTTTTTTTTTT<br>TT                                    | AACCTTGATGCTCACA<br>TGAAA   | TTACACTGTTAGCCG<br>GATGC    | 58.2                             | 696                                           | DRR                                               | Ca_23878                            | --                    | --       |
| Ca3_P4_5414883   | Ca3                                     | 5414883                       | ATGTTTGG/ATGTTTGGTTTTTTGTT<br>TGG                                    | CTCACATATGCACCTG<br>CTCG    | TTCTGAAGGTCAAAC<br>GTGC     | 60.4                             | 470                                           | DRR                                               | Ca_20660                            | --                    | --       |
| Ca3_P4_5692377   | Ca3                                     | 5692377                       | GTT/GT                                                               | TGTGCAATTAAGAGAG<br>GACACAA | CGAGAAATAGCTCACG<br>AGGC    | 59.8                             | 268                                           | DRR                                               | Ca_20648                            | --                    | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca3_P4_6345015   | Ca3                                     | 6345015                       | CAAAAAAAAA/CAAAAAAAAA                                         | CAGCTGTTCCGATGCTTCA     | GCTCATGGGATGTCAACCTT    | 60.0                             | 979                                           | DRR                                               | Ca_24832                            | --                    | B3       |
| Ca3_P4_6772905   | Ca3                                     | 6772905                       | GTTT/GTT                                                      | TCCCTTTGTCTTTTCGCTACT   | CACTGCCGTTCTTCACCTCA    | 59.9                             | 383                                           | DRR                                               | Ca_16559                            | R                     | NAC      |
| Ca3_P4_6774064   | Ca3                                     | 6774064                       | T/TTAA                                                        | TTTGCTGGACTTTGAAGCCT    | CCCGGTCCTAGAGAGAAAGA    | 60.0                             | 640                                           | DRR                                               | Ca_16559                            | R                     | NAC      |
| Ca3_P4_7228177   | Ca3                                     | 7228177                       | GAGTTACATAGTTACATA/GAGTTACATA                                 | CTGTTGGGCAAGGGATCTAA    | ACAGCGCTTTTGTGCTTTTT    | 60.1                             | 463                                           | DRR                                               | Ca_16534                            | --                    | --       |
| Ca3_P4_7312652   | Ca3                                     | 7312652                       | TAAAAAAAA/TAAAAAAAA                                           | CGCAAGATTTTACCTACCTGTG  | TGATCAAGCTTCCAGTCCAA    | 58.8                             | 720                                           | DRR                                               | Ca_16529                            | --                    | LFY      |
| Ca3_P4_781722    | Ca3                                     | 781722                        | CAA/CAAAA                                                     | AAAACGCGCCACTAATGACT    | AGCAAGAGTGCAAAGTCGGT    | 59.8                             | 546                                           | DRR                                               | Ca_22643                            | V                     | B3       |
| Ca3_P4_8081601   | Ca3                                     | 8081601                       | CATATATATATATATATA/CATATATATATATATA                           | AAAGCGCTGTAAAATGCACA    | GAAATAGCTTGCTGTTGGGC    | 59.5                             | 580                                           | DRR                                               | Ca_24371                            | --                    | Trihelix |
| Ca3_P4_8730393   | Ca3                                     | 8730393                       | AAA/AAACCAACAA                                                | GCCAAACAAATTGAAACCCA    | ATCTCCGAACCCCTTCTAA     | 60.7                             | 414                                           | DRR                                               | Ca_23717                            | --                    | B3       |
| Ca3_P4_8900151   | Ca3                                     | 8900151                       | TAAAAA/TAAAAA                                                 | GTGAAATCCACCCTCGACT     | TCAAACCTGCCATTTCTCA     | 59.0                             | 156                                           | DRR                                               | Ca_25279                            | R                     | --       |
| Ca3_P4_9306348   | Ca3                                     | 9306348                       | AATATATATATATATATATA/AAATATATATATATATATA                      | TCCAGGTGAAAAGTAACGCC    | TGCTGAGCAAAACACTCTGG    | 60.1                             | 432                                           | DRR                                               | Ca_20961                            | --                    | Trihelix |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca3_P4_9649838   | Ca3                                     | 9649838                       | ATTT/ATT                                                      | TAAGGCAGATTGCCCA<br>AAAC  | TTTCGGGAATGAAACT<br>GGAC    | 60.1                             | 462                                           | DRR                                               | Ca_20979                            | --                    | --     |
| Ca3_P4_9651257   | Ca3                                     | 9651257                       | CTTTTT/CTTTTT                                                 | CTCCAAACTGGGGTGT<br>CACT  | CGGTCTCAACCTCTCC<br>CATA    | 60.0                             | 882                                           | DRR                                               | Ca_20979                            | --                    | --     |
| Ca4_P4_10784287  | Ca4                                     | 10784287                      | TAAAAAAAAA/TAAAAAAAAA                                         | TGGGCCGAATTTTGTG<br>ATAG  | CGCACAATTGATACATC<br>AACAC  | 60.8                             | 486                                           | DRR                                               | Ca_04314                            | U                     | --     |
| Ca4_P4_11070438  | Ca4                                     | 11070438                      | T/TATTATTATTACG                                               | TTTGCCCAATAAAGA<br>GCAC   | AACAACTTTTCGAACC<br>ACC     | 60.1                             | 701                                           | DRR                                               | Ca_04340                            | J                     | --     |
| Ca4_P4_11216218  | Ca4                                     | 11216218                      | TAAAAAAAAA/TAAAAA                                             | GCATAACCAATGCTCT<br>TGGAA | TCAAACCAAGGATGAT<br>GCAA    | 60.1                             | 853                                           | DRR                                               | Ca_04353                            | U                     | M-type |
| Ca4_P4_11222847  | Ca4                                     | 11222847                      | A/AC                                                          | AATCTCCGAATCATTGT<br>CGG  | ACTGTCTCACGAGTCG<br>GCTT    | 59.9                             | 584                                           | DRR                                               | Ca_04354                            | A                     | --     |
| Ca4_P4_11280849  | Ca4                                     | 11280849                      | TC/TCC                                                        | GCTCAGCAGCTTTGAC<br>TTTG  | TTCGAATTGAACTCCT<br>CCA     | 59.0                             | 733                                           | DRR                                               | Ca_04359                            | --                    | --     |
| Ca4_P4_11281622  | Ca4                                     | 11281622                      | TG/T                                                          | TTTAAGGCATGTGAGT<br>TCAGC | TGCAAAATCAATACATG<br>GTTTCG | 58.0                             | 641                                           | DRR                                               | Ca_04359                            | --                    | --     |
| Ca4_P4_11285447  | Ca4                                     | 11285447                      | C/CAA                                                         | TCCACATGCACCTGTG<br>AACT  | AGTAGTGCCTCAAACC<br>ACGG    | 60.2                             | 382                                           | DRR                                               | Ca_04361                            | GE                    | GATA   |
| Ca4_P4_11310573  | Ca4                                     | 11310573                      | TAAAAA/TAAAA                                                  | TACGAGAACATCCACG<br>GTGA  | GAGGGACGGCACATAA<br>ACAT    | 60.1                             | 564                                           | DRR                                               | Ca_04363                            | --                    | --     |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_11311504  | Ca4                                     | 11311504                      | A/ACAC                                                        | TGATGGTTGGCCTAAATGGT    | TTGCTGAAGACTGATGCCAC    | 60.2                             | 463                                           | DRR                                               | Ca_04363                            | --                    | --   |
| Ca4_P4_11317243  | Ca4                                     | 11317243                      | ATCTCTCTCTCTCTCTC/ATCTCTCTCTCTCTC                             | CCTTCCACTGCCAAAACATT    | CAATTGGTCGGTTTCTGGTT    | 60.0                             | 430                                           | DRR                                               | Ca_04364                            | D                     | WRKY |
| Ca4_P4_11331252  | Ca4                                     | 11331252                      | TAAA/TAAAA                                                    | AGAGGGAAAAAGGGGTGAA     | TCTCTTCTCGCCCCAGTTTA    | 59.9                             | 742                                           | DRR                                               | Ca_04367                            | U                     | FAR1 |
| Ca4_P4_11346851  | Ca4                                     | 11346851                      | GTTTTTTT/GTTTTTTTT                                            | AACAGAAAAGATTGCATGCGT   | TGCAATGACTCCCATTCGA     | 59.8                             | 323                                           | DRR                                               | Ca_04368                            | R                     | --   |
| Ca4_P4_11347660  | Ca4                                     | 11347660                      | TTATA/TTA                                                     | CCGAATGAGCCTTCACAAGT    | TTAGGGGTGGACAAAGTTCG    | 60.3                             | 595                                           | DRR                                               | Ca_04368                            | R                     | --   |
| Ca4_P4_11362167  | Ca4                                     | 11362167                      | AAAAATAAA/AAAAATAAAATAAG<br>AAAAATAAA                         | TCCCAACCTAGACCGGAA      | TTGCATGCTGCTGGAACTAC    | 59.5                             | 265                                           | DRR                                               | Ca_04370                            | --                    | ERF  |
| Ca4_P4_11394293  | Ca4                                     | 11394293                      | AATATATATATA/AATATATATATATA<br>TATATATA                       | TCAACACATCGCAAATATCCA   | GCCGCAAAACCAAATACATC    | 59.9                             | 522                                           | DRR                                               | Ca_04373                            | J                     | --   |
| Ca4_P4_11395658  | Ca4                                     | 11395658                      | GTAACATATTA/GTAACATATTAACA<br>TATTA                           | CCAAGTTCCAATGGCTTGAT    | CGCTTCAGACAACACAAGA     | 59.9                             | 587                                           | DRR                                               | Ca_04373                            | J                     | --   |
| Ca4_P4_11425739  | Ca4                                     | 11425739                      | A/AT                                                          | CAAAAAGACATCGAATGGCA    | CAACCAACGGATCATATGAATTT | 59.7                             | 778                                           | DRR                                               | Ca_04376                            | GC                    | bHLH |
| Ca4_P4_11437417  | Ca4                                     | 11437417                      | TTATTAT/TT                                                    | AAGGGAGTCTGGTGAGCAAA    | CATTGAAAAACCATTCGCCT    | 59.8                             | 811                                           | DRR                                               | Ca_04378                            | S                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                   | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                                                                 |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca4_P4_11440445  | Ca4                                     | 11440445                      | ACTCT/ACT                                                                                                                       | CGATGCTGCCATAAT<br>TCTT  | AAAAACCGTTGTCGAAT<br>GCT    | 60.1                             | 757                                           | DRR                                               | Ca_04380                            | J                     | --       |
| Ca4_P4_11453608  | Ca4                                     | 11453608                      | ATATATTAT/ATAT                                                                                                                  | CTCCATTTTGCACGAA<br>GACA | CCCATGTTACCCCTA<br>ATTG     | 59.8                             | 556                                           | DRR                                               | Ca_04381                            | --                    | --       |
| Ca4_P4_11462375  | Ca4                                     | 11462375                      | AC/A                                                                                                                            | GCATGTGGGTGTTTGT<br>TTGA | TCAAGCTTGAAGTTG<br>CTTG     | 60.4                             | 612                                           | DRR                                               | Ca_04382                            | --                    | --       |
| Ca4_P4_11555971  | Ca4                                     | 11555971                      | CATATATATAT/CATATAT                                                                                                             | CATTATTGGATTCGTTG<br>GGG | GGGTGATAGATTCTTG<br>ATGCAAT | 60.0                             | 362                                           | DRR                                               | Ca_04385                            | K                     | Trihelix |
| Ca4_P4_11556235  | Ca4                                     | 11556235                      | ATTTTTTTTT/ATTTTTTTT                                                                                                            | CATTATTGGATTCGTTG<br>GGG | AAGCTCGCTTTTTGAAA<br>TGG    | 60.0                             | 790                                           | DRR                                               | Ca_04385                            | K                     | Trihelix |
| Ca4_P4_1169667   | Ca4                                     | 1169667                       | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTAT           | TTTTAGCCCCGTTTTGT<br>TCA | TAAGGTGTCCGACATC<br>AGATT   | 60.5                             | 701                                           | DRR                                               | Ca_07748                            | OU                    | --       |
| Ca4_P4_11849287  | Ca4                                     | 11849287                      | TTTAGTCATT/TTTAGTCATTAGTCA<br>TT                                                                                                | TTTAGCTGACTTGTGG<br>GGCT | TGAAATTATCCACCCAC<br>CAA    | 59.9                             | 777                                           | DRR                                               | Ca_04405                            | M                     | C2H2     |
| Ca4_P4_12011085  | Ca4                                     | 12011085                      | CTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTA/CTTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTA | TCATGCGATTGTGATG<br>ACCT | TGATTGTGCTTGAGTT<br>GGGA    | 60.1                             | 671                                           | DRR                                               | Ca_04426                            | --                    | --       |
| Ca4_P4_12174371  | Ca4                                     | 12174371                      | T/TA                                                                                                                            | ACCAAACAGCGACCAA<br>ACTC | AAGGTAGAGATCGCGT<br>CGAA    | 60.2                             | 544                                           | DRR                                               | Ca_04442                            | --                    | GRAS     |
| Ca4_P4_12225286  | Ca4                                     | 12225286                      | G/GAGTCTC                                                                                                                       | TCATGGAGGCAAAGAA<br>GGAG | TGACATGTGGATCGTG<br>GTTT    | 60.3                             | 724                                           | DRR                                               | Ca_04444                            | --                    | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_12393377  | Ca4                                     | 12393377                      | TAAAAAAAAAAAAAAAAA/TAAAAAAA<br>AAAAAA                         | TGTGCTGTTGTGATTA<br>GGGG   | AGCGTTCAAGGTGCAA<br>AAGT | 59.6                             | 659                                           | DRR                                               | Ca_04463                            | QI                    | bHLH |
| Ca4_P4_12472732  | Ca4                                     | 12472732                      | GAAAAAAAAA/GAAAAAAAAAAAAA                                     | GGGGAGTTTGGTTCCT<br>TATTTT | GATCAACGGCGAGAGA<br>AAAG | 59.6                             | 465                                           | DRR                                               | Ca_04469                            | Z                     | bHLH |
| Ca4_P4_12493651  | Ca4                                     | 12493651                      | ATTTTTT/ATTTTTTTT                                             | ATTCCTCGTCCGTTTTT<br>AGA   | TTTTTCTTCTGATTG<br>GTCC  | 59.7                             | 293                                           | DRR                                               | Ca_04473                            | --                    | --   |
| Ca4_P4_12528630  | Ca4                                     | 12528630                      | TAAAAA/TAAAAA                                                 | TAACGCTAGGGTCCCA<br>TGTC   | AGCTTCTTGAGCCAT<br>GTCA  | 60.0                             | 211                                           | DRR                                               | Ca_04475                            | C                     | bZIP |
| Ca4_P4_12535193  | Ca4                                     | 12535193                      | GAAAAAAA/GAAAAAA                                              | CGAAGCCTGCAACTTT<br>TACC   | CCAAACATGCAGGTTC<br>CTCT | 59.9                             | 231                                           | DRR                                               | Ca_04476                            | --                    | --   |
| Ca4_P4_12554607  | Ca4                                     | 12554607                      | A/AC                                                          | CCAAAGCAAAACAAGC<br>CATT   | TGCTTCTTAGGGTAAG<br>CCGA | 60.1                             | 508                                           | DRR                                               | Ca_04478                            | A                     | EIL  |
| Ca4_P4_12571013  | Ca4                                     | 12571013                      | GTATATA/GTATA                                                 | GGCTCACATCAGGAAT<br>GGAT   | GGCTCTTGGTCATTGG<br>ATGT | 59.9                             | 968                                           | DRR                                               | Ca_04479                            | E                     | --   |
| Ca4_P4_12583830  | Ca4                                     | 12583830                      | ATTTTTTTT/ATTTTTTTTTT                                         | TGTTGTTGGATGCACC<br>TGTT   | GATACATGGGCATTCA<br>GGCT | 60.0                             | 835                                           | DRR                                               | Ca_04480                            | L                     | --   |
| Ca4_P4_12592291  | Ca4                                     | 12592291                      | ATA/ATACAAATACTTGATGTA                                        | TGACTGCCGCTTTGTC<br>ATTA   | TTTCGATTCAAACCCAA<br>ACC | 60.4                             | 588                                           | DRR                                               | Ca_04481                            | R                     | --   |
| Ca4_P4_12597000  | Ca4                                     | 12597000                      | AT/ATCTAATGGT                                                 | CACATGGTTCAGGTT<br>CCTT    | CTTATGGCGTGGCCTT<br>AAAC | 59.8                             | 820                                           | DRR                                               | Ca_04482                            | R                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca4_P4_12866217  | Ca4                                     | 12866217                      | GGG/GGGAGCTTTATTTTTTGG                                        | TAGACTCCACTAAGCC<br>CCCA | CCTTCCAACGCAACATT<br>TCT | 59.7                             | 294                                           | DRR                                               | Ca_04506                            | T                     | FAR1     |
| Ca4_P4_13546142  | Ca4                                     | 13546142                      | TAAA/TAA                                                      | GAGATTACGAAGACC<br>GAGG  | GCCAATGCTAATCTGC<br>AACA | 59.8                             | 665                                           | DRR                                               | Ca_04571                            | T                     | --       |
| Ca4_P4_13555418  | Ca4                                     | 13555418                      | ATTTTTTTTT/ATTTTTTTTT                                         | CTTCTACTGGCATGTG<br>GCTG | TTGCATTGGAGATGA<br>CAAA  | 59.5                             | 640                                           | DRR                                               | Ca_04572                            | --                    | --       |
| Ca4_P4_13555921  | Ca4                                     | 13555921                      | CCTCGTTCAATC/CCTCGTTCAATCT<br>CGTTCAATC                       | AAGCATTCTTCTCGGG<br>TCAA | CATCCCTAAGATGCGA<br>CCAT | 59.8                             | 333                                           | DRR                                               | Ca_04572                            | --                    | --       |
| Ca4_P4_13586319  | Ca4                                     | 13586319                      | CTT/CTTT                                                      | CCTTCAACGAGCAGCC<br>TTAG | TTCACACCTTGCAGCT<br>ATCG | 60.1                             | 511                                           | DRR                                               | Ca_04576                            | --                    | --       |
| Ca4_P4_13586598  | Ca4                                     | 13586598                      | ATTTTT/ATTTTT                                                 | CCTTCAACGAGCAGCC<br>TTAG | AAATTGGGAAATTGG<br>AGGG  | 60.1                             | 678                                           | DRR                                               | Ca_04576                            | --                    | --       |
| Ca4_P4_13593543  | Ca4                                     | 13593543                      | TA/T                                                          | TGGTTCTCATTGCTTG<br>CTTG | ACCCATGAATTTCCC<br>TCC   | 60.0                             | 565                                           | DRR                                               | Ca_04577                            | --                    | HB-other |
| Ca4_P4_13617448  | Ca4                                     | 13617448                      | TG/TGG                                                        | GGGCCTTTTCTTCAGC<br>TTTT | TGCATGTTATCCGCAAT<br>CTC | 59.8                             | 713                                           | DRR                                               | Ca_04579                            | --                    | --       |
| Ca4_P4_13618875  | Ca4                                     | 13618875                      | C/CG                                                          | AATGCATTTTCGCTAC<br>CTTC | CAACATATGCATTTCCG<br>TGG | 60.1                             | 329                                           | DRR                                               | Ca_04579                            | --                    | --       |
| Ca4_P4_13624309  | Ca4                                     | 13624309                      | CTTT/CTT                                                      | CTGGAAAAGAAGAGGG<br>GGAC | CAGGTTGGTCGAATCA<br>TGTG | 60.0                             | 748                                           | DRR                                               | Ca_04580                            | --                    | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_13624341  | Ca4                                     | 13624341                      | CAAAA/CAAAA                                                   | CTGGAAAAGAAGAGGG<br>GGAC | CAGTTGGTCAATCA<br>TGTG   | 60.0                             | 748                                           | DRR                                               | Ca_04580                            | --                    | --    |
| Ca4_P4_13663032  | Ca4                                     | 13663032                      | TAAAA/TAAA                                                    | AGTACCTTCGTCGTGT<br>TCGC | GGACTTTTCAAACGG<br>CTCA  | 60.3                             | 231                                           | DRR                                               | Ca_04585                            | R                     | bHLH  |
| Ca4_P4_13663581  | Ca4                                     | 13663581                      | T/TG                                                          | AACGAAGACCCTGTGA<br>CCTG | GCCGGCTTGTAGGTTG<br>AATA | 60.2                             | 168                                           | DRR                                               | Ca_04585                            | R                     | bHLH  |
| Ca4_P4_13667763  | Ca4                                     | 13667763                      | T/TA                                                          | CTCAAGATTCAATGGG<br>ACGA | TTGTGATGGTGATGG<br>GTTG  | 58.6                             | 275                                           | DRR                                               | Ca_04586                            | Q                     | B3    |
| Ca4_P4_13667908  | Ca4                                     | 13667908                      | TGG/TGGG                                                      | CAACCCATCACCATCA<br>CAAA | AAATCGACGCCACTTT<br>CATC | 60.2                             | 148                                           | DRR                                               | Ca_04586                            | Q                     | B3    |
| Ca4_P4_13678246  | Ca4                                     | 13678246                      | C/CT                                                          | CCGACGAATTCCTTC<br>AAAA  | TGTTGAGTCGGTGAG<br>ACAG  | 60.0                             | 583                                           | DRR                                               | Ca_04588                            | E                     | --    |
| Ca4_P4_13697619  | Ca4                                     | 13697619                      | AAAGAAGAAG/AAAGAAG                                            | ACACACAAAGGCAAAC<br>CACA | ATCAGCTGACCCCAA<br>AATG  | 60.0                             | 934                                           | DRR                                               | Ca_04591                            | --                    | --    |
| Ca4_P4_13735535  | Ca4                                     | 13735535                      | TAGAATTCAGAAT/TAGAATTCAGAA<br>TTCAGAAT                        | TTGTTCTTGACCTTTT<br>GGG  | TGGTTCTGAAATCTGC<br>CTGA | 59.9                             | 745                                           | DRR                                               | Ca_04597                            | U                     | --    |
| Ca4_P4_13756219  | Ca4                                     | 13756219                      | GTTT/GTTTT                                                    | TACCGGAAATTCAGC<br>AAGG  | GGCATGGTATTCCCTC<br>CTTT | 60.1                             | 599                                           | DRR                                               | Ca_04600                            | --                    | NF-YB |
| Ca4_P4_13788471  | Ca4                                     | 13788471                      | ATGTTGT/ATGTTGTTGT                                            | CAGGCCAGCTAACTTT<br>TTCG | GCCAACTTTGAGTGGT<br>GGAT | 60.0                             | 600                                           | DRR                                               | Ca_04603                            | Q                     | --    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                    | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                                                                  |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_13788854  | Ca4                                     | 13788854                      | CA/CAAA                                                                                          | AAGTGCAATTAGGCCA<br>GTGC | GCCAACTTTGAGTGGT<br>GGAT  | 60.3                             | 105                                           | DRR                                               | Ca_04603                            | Q                     | --    |
| Ca4_P4_13789143  | Ca4                                     | 13789143                      | CAA/CAAA                                                                                         | ATCCACCACTCAAAGT<br>TGGC | TTGGTACGAAACATCC<br>ATCAA | 60.0                             | 517                                           | DRR                                               | Ca_04603                            | Q                     | --    |
| Ca4_P4_13798628  | Ca4                                     | 13798628                      | CGG/CGGG                                                                                         | GCGATTGTTTAGGTTG<br>GGAA | TTTTCAACACGAGGGA<br>ATCA  | 59.9                             | 443                                           | DRR                                               | Ca_04605                            | R                     | --    |
| Ca4_P4_14090717  | Ca4                                     | 14090717                      | TGAGAGAG/TGAGAG                                                                                  | GTTGGTTTGAATGGAG<br>GGAA | AGTTCCAGCTCTTAAC<br>CGCA  | 59.8                             | 660                                           | DRR                                               | Ca_04636                            | OR                    | YABBY |
| Ca4_P4_14405624  | Ca4                                     | 14405624                      | ATGTTGTT/ATGTTGTTGT                                                                              | CGGTGGTTGCTCTCTC<br>TTTC | GGGGTACAATGTGGAA<br>CCAA  | 60.0                             | 440                                           | DRR                                               | Ca_05663                            | E                     | MYB   |
| Ca4_P4_14405755  | Ca4                                     | 14405755                      | ATCTCTCTCT/ATCTCTCT                                                                              | ATGTGCATGCCAAGTT<br>GTGT | ACCTATAAGCCCTTTG<br>CGCT  | 60.0                             | 963                                           | DRR                                               | Ca_05663                            | E                     | MYB   |
| Ca4_P4_14406037  | Ca4                                     | 14406037                      | GTCITT/GT                                                                                        | TTGGTTCCACATTGTA<br>CCCC | TTGTGCTGGAGTTGG<br>ATCA   | 60.5                             | 639                                           | DRR                                               | Ca_05663                            | E                     | MYB   |
| Ca4_P4_14406133  | Ca4                                     | 14406133                      | CAAA/CAAAA                                                                                       | TTGGTTCCACATTGTA<br>CCCC | CCATTGGTTGGGATAT<br>GGAG  | 60.5                             | 892                                           | DRR                                               | Ca_05663                            | E                     | MYB   |
| Ca4_P4_15396694  | Ca4                                     | 15396694                      | GATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAA/GATAA<br>TAATAATAATAATAATAATAATAA<br>ATAATAATAA | TCCCTCGTGAGAACTT<br>GTCT | AGGGGACCAAAATTGT<br>GAAT  | 57.4                             | 514                                           | DRR                                               | Ca_05556                            | R                     | B3    |
| Ca4_P4_15916952  | Ca4                                     | 15916952                      | TA/TAAA                                                                                          | CCACCAGCGATTATCA<br>ACCT | TGTCTTCCTTCCCTGTC<br>TGG  | 60.0                             | 490                                           | DRR                                               | Ca_05516                            | --                    | bHLH  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_15920083  | Ca4                                     | 15920083                      | AGGTG/AGGTGGTG                                                | TGATTTTCATGCCTAATG<br>CCA    | AATGAAAATGGGGTCC<br>AATG   | 60.0                             | 495                                           | DRR                                               | Ca_05514                            | --                    | SBP   |
| Ca4_P4_15920382  | Ca4                                     | 15920382                      | TAAAAA/TAAAAA                                                 | AATTGTCTTGCAATTGG<br>ACCC    | GTGCCGCTCCAGCTAC<br>TATC   | 59.8                             | 324                                           | DRR                                               | Ca_05514                            | --                    | SBP   |
| Ca4_P4_15921827  | Ca4                                     | 15921827                      | GAAAAAAAAA/GAAAAAAAAA                                         | GGGGGCCAATTGATTC<br>TTAC     | GGTCCACATCCAGCTC<br>ATT    | 60.5                             | 455                                           | DRR                                               | Ca_05515                            | --                    | ERF   |
| Ca4_P4_15926036  | Ca4                                     | 15926036                      | AAAGA/AAAGAAGA                                                | GTTTCCCTTACGCCAG<br>ATGA     | GCATTGCTGTATTGGT<br>GCAT   | 60.1                             | 532                                           | DRR                                               | Ca_05513                            | R                     | --    |
| Ca4_P4_15958358  | Ca4                                     | 15958358                      | CT/C                                                          | ACAAAGCTCAAACCTG<br>CCAT     | CCCCTATTACCCGCAT<br>AAGA   | 59.9                             | 342                                           | DRR                                               | Ca_05511                            | --                    | C2H2  |
| Ca4_P4_15958886  | Ca4                                     | 15958886                      | CTT/C                                                         | CTTATGCGGTGAATAG<br>GGGA     | GCATGTTATTGGTCCC<br>ACCT   | 59.9                             | 372                                           | DRR                                               | Ca_05511                            | --                    | C2H2  |
| Ca4_P4_15969199  | Ca4                                     | 15969199                      | TAA/TA                                                        | TAAGGCGTTAACTTGC<br>ACCC     | TGGTTGTGGCGATTAC<br>AAGA   | 60.1                             | 494                                           | DRR                                               | Ca_05510                            | J                     | NF-YA |
| Ca4_P4_16097791  | Ca4                                     | 16097791                      | TTATATATAT/TTATATATATAT                                       | GTGGAATGTAAGATCG<br>CCGT     | GCAAACAGAGGAAGAG<br>AAGGAA | 60.0                             | 535                                           | DRR                                               | Ca_05500                            | --                    | --    |
| Ca4_P4_16098339  | Ca4                                     | 16098339                      | TAAAAAAAAA/TAAAAAAAAA                                         | CCTTCTCTTCTCTGTT<br>TGCTC    | CTCATACATGAGGGGA<br>AAGCA  | 59.6                             | 674                                           | DRR                                               | Ca_05500                            | --                    | --    |
| Ca4_P4_16098449  | Ca4                                     | 16098449                      | C/CT                                                          | CAATTCCAAAATATGAC<br>AACAACC | TCATACATGAGGGGAA<br>AGCA   | 59.5                             | 528                                           | DRR                                               | Ca_05500                            | --                    | --    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca4_P4_16146480  | Ca4                                     | 16146480                      | CT/C                                                          | AAAGAAGCAGAGGAAG<br>CGTG    | GCAAACGTATGATGGG<br>GACT | 59.8                             | 337                                           | DRR                                               | Ca_05497                            | I                     | bHLH    |
| Ca4_P4_1641697   | Ca4                                     | 1641697                       | AATATATATATA/AATATATATATATA                                   | GTTGCTGGTTGAACAA<br>GGGT    | TGGCCTGTATGATGGA<br>ACAA | 60.0                             | 633                                           | DRR                                               | Ca_07792                            | B                     | NF-YC   |
| Ca4_P4_16728592  | Ca4                                     | 16728592                      | TAAAAAAAAA/TAAAAAAAAA                                         | CATGGGGATGCTGCTA<br>TTTT    | CAACTTCCTCTTTTGGC<br>ACA | 59.9                             | 388                                           | DRR                                               | Ca_05454                            | O                     | MYB     |
| Ca4_P4_16813063  | Ca4                                     | 16813063                      | CTAGAAGCTTTAGAAGCTTTA/CTAG<br>AAGCTTTA                        | GTAAGTGATGGGTGCG<br>TGTG    | TGTGAACCCAGCTGCT<br>CTAA | 60.0                             | 700                                           | DRR                                               | Ca_05442                            | --                    | --      |
| Ca4_P4_16826129  | Ca4                                     | 16826129                      | A/AAATT                                                       | TTTTATCCACCAAAAT<br>TCAAAAA | TGATTTTTCAGGAGGC<br>CACT | 58.9                             | 521                                           | DRR                                               | Ca_05439                            | --                    | --      |
| Ca4_P4_16826292  | Ca4                                     | 16826292                      | CAAAAAA/CAAAAAA                                               | GCGACCATCTGTTGCA<br>GTTA    | TGATTTTTCAGGAGGC<br>CACT | 59.9                             | 459                                           | DRR                                               | Ca_05439                            | --                    | --      |
| Ca4_P4_16960625  | Ca4                                     | 16960625                      | GTT/GTTT                                                      | GCGAATTGCAGACTGA<br>AACA    | CTGGAATCCTCCTC<br>CTCC   | 60.0                             | 925                                           | DRR                                               | Ca_05428                            | --                    | --      |
| Ca4_P4_16997698  | Ca4                                     | 16997698                      | GTT/GTTTTT                                                    | CAAACCTCAAGTCCCC<br>ATTG    | TCCGAAGCCACCACTT<br>CTAC | 60.3                             | 651                                           | DRR                                               | Ca_05426                            | U                     | --      |
| Ca4_P4_17010005  | Ca4                                     | 17010005                      | AAAAAATAATATC/AAAAAATAATATC<br>ATTTAAAAATAATATC               | ACGGCCTAGCTTATTC<br>CCAT    | GTATGCAATGGGTGC<br>TGTG  | 60.0                             | 690                                           | DRR                                               | Ca_05423                            | --                    | --      |
| Ca4_P4_17010261  | Ca4                                     | 17010261                      | GAGACA/GAGACAGACA                                             | GTTAGCCTCACAGCAC<br>CCAT    | GCTTCTAACTCGGCAA<br>GTGG | 60.1                             | 342                                           | DRR                                               | Ca_05422                            | --                    | G2-like |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca4_P4_17030182  | Ca4                                     | 17030182                      | TAA/TAAAA                                                     | AAGATTTTGTGTTTGAA<br>CCCTCA  | TCTCGCCTTTGTATCG<br>TCA     | 59.9                             | 426                                           | DRR                                               | Ca_05420                            | R                     | bHLH     |
| Ca4_P4_17030352  | Ca4                                     | 17030352                      | T/TTGGAAATC                                                   | AAGATTTTGTGTTTGAA<br>CCCTCA  | CTTCATCGTTGAATTTG<br>GGG    | 59.9                             | 596                                           | DRR                                               | Ca_05420                            | R                     | bHLH     |
| Ca4_P4_17036708  | Ca4                                     | 17036708                      | GAAAAAA/GAAAAAA                                               | TTGTGTATGTGACGGG<br>AAGA     | CCGAGGAGAGGTATG<br>GATT     | 60.1                             | 574                                           | DRR                                               | Ca_05419                            | C                     | bHLH     |
| Ca4_P4_17047964  | Ca4                                     | 17047964                      | GAAAAAAAA/GAAAAAAAA                                           | AGAGGTCATTGGGTG<br>GACA      | AAGCGACCAGTTGAAG<br>GAAA    | 60.4                             | 453                                           | DRR                                               | Ca_05418                            | DA                    | --       |
| Ca4_P4_17048228  | Ca4                                     | 17048228                      | CTTTTTTTTT/CTTTTTTTTT                                         | TTTCCTCAACTGGTC<br>GCTT      | TCATCATCTTGCTCTCC<br>ACG    | 59.9                             | 527                                           | DRR                                               | Ca_05418                            | DA                    | --       |
| Ca4_P4_17082004  | Ca4                                     | 17082004                      | TGAT/TGATCGAT                                                 | TTTTGACAATGGGCAC<br>TCAA     | CTGCAGGTAAGCATCC<br>CAAT    | 60.1                             | 295                                           | DRR                                               | Ca_05415                            | --                    | --       |
| Ca4_P4_17101658  | Ca4                                     | 17101658                      | ATTTT/ATTTT                                                   | TGATGTAACTGACAAA<br>TGCTGTTT | GTCGAGAGTTGGGTCA<br>TGGT    | 60.0                             | 322                                           | DRR                                               | Ca_05414                            | --                    | --       |
| Ca4_P4_17115270  | Ca4                                     | 17115270                      | ATTTT/ATTTT                                                   | GGGACCGTTCGTTTCA<br>AATA     | AACATGATTCGAATTCA<br>ATTCTC | 59.8                             | 221                                           | DRR                                               | Ca_05412                            | CR                    | Nin-like |
| Ca4_P4_17141313  | Ca4                                     | 17141313                      | T/TC                                                          | TTTCAATCGTATCAAGT<br>TTTTGC  | AAACTGAAAGGCCTAA<br>TTCCAA  | 58.4                             | 682                                           | DRR                                               | Ca_05410                            | CR                    | Nin-like |
| Ca4_P4_17142439  | Ca4                                     | 17142439                      | TAA/T                                                         | CACGAACCCTGCCAAA<br>TTAT     | TTGTGCTTTAGAGGAT<br>GGGG    | 59.8                             | 603                                           | DRR                                               | Ca_05410                            | CR                    | Nin-like |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_17146199  | Ca4                                     | 17146199                      | TTTTTTTTTATTATTATTTT/TTTTT                                    | ATTCCAGCTCCACAA<br>TCAC  | GGCTCTTGATGGGTTG<br>TGTT  | 59.9                             | 442                                           | DRR                                               | Ca_05409                            | K                     | --  |
| Ca4_P4_17146270  | Ca4                                     | 17146270                      | AGGGG/AGGG                                                    | ATTCCAGCTCCACAA<br>TCAC  | GGCTCTTGATGGGTTG<br>TGTT  | 59.9                             | 442                                           | DRR                                               | Ca_05409                            | K                     | --  |
| Ca4_P4_17152700  | Ca4                                     | 17152700                      | TAACAACA/TAACA                                                | CTGCAAATGTCAAGGC<br>AGAA | TGCTTTTGGTGCACTCT<br>CTGG | 60.0                             | 617                                           | DRR                                               | Ca_05408                            | K                     | ERF |
| Ca4_P4_17158347  | Ca4                                     | 17158347                      | TAAAAAAA/TAAAAAAA                                             | CCAATCTTGCCACAC<br>CATGT | TCACCTAATGCCAAACA<br>CACA | 60.7                             | 300                                           | DRR                                               | Ca_05407                            | --                    | --  |
| Ca4_P4_17159336  | Ca4                                     | 17159336                      | A/AC                                                          | GCCACGCTCTAGGTTG<br>AGAT | CCTCAGGCCTGCAACT<br>GTAT  | 59.5                             | 222                                           | DRR                                               | Ca_05407                            | --                    | --  |
| Ca4_P4_17193639  | Ca4                                     | 17193639                      | ATTTT/ATTT                                                    | AAGCAGCAAGGATCAC<br>CAAT | CCCCATTAGTATTGCC<br>GCTA  | 59.7                             | 532                                           | DRR                                               | Ca_05405                            | T                     | --  |
| Ca4_P4_17200546  | Ca4                                     | 17200546                      | GTT/GTTT                                                      | GCATTAGGGGTGCTTT<br>GTGT | ATGGGCGAATGCAAAA<br>GTTA  | 60.0                             | 763                                           | DRR                                               | Ca_05404                            | --                    | --  |
| Ca4_P4_17214261  | Ca4                                     | 17214261                      | GCTATC/G                                                      | GCTTTTTAGGCTGGGG<br>AATC | AATAATTTGGTCAGGC<br>GTGC  | 60.0                             | 194                                           | DRR                                               | Ca_05402                            | C                     | --  |
| Ca4_P4_17214540  | Ca4                                     | 17214540                      | A/ATATAG                                                      | GCTTTTTAGGCTGGGG<br>AATC | TTGGTCAATGCGGAAG<br>TGTA  | 60.0                             | 627                                           | DRR                                               | Ca_05402                            | C                     | --  |
| Ca4_P4_17214599  | Ca4                                     | 17214599                      | AC/ACTTC                                                      | GCTTTTTAGGCTGGGG<br>AATC | TTGGTCAATGCGGAAG<br>TGTA  | 60.0                             | 627                                           | DRR                                               | Ca_05402                            | C                     | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_17238317  | Ca4                                     | 17238317                      | CTTTATTT/CTTTATTTATTT                                         | AAAAATGGGGTGGATG<br>AACA   | TTCCAATGTTGCAGAA<br>GCAG     | 60.0                             | 439                                           | DRR                                               | Ca_05400                            | YU                    | --  |
| Ca4_P4_17268685  | Ca4                                     | 17268685                      | TGG/TGGG                                                      | CATCCCATCCAGGACC<br>TTTA   | CTGGTTCGCGTTGAA<br>CTTA      | 59.7                             | 308                                           | DRR                                               | Ca_05398                            | R                     | --  |
| Ca4_P4_17293581  | Ca4                                     | 17293581                      | GTAT/GTATAT                                                   | TCACATCCGTTGAACG<br>AAGA   | TTTGTTTTATTAGTTTT<br>GGTGTGG | 60.2                             | 652                                           | DRR                                               | Ca_05392                            | R                     | --  |
| Ca4_P4_17293735  | Ca4                                     | 17293735                      | GGAGAGAG/GGAGAG                                               | TCACATCCGTTGAACG<br>AAGA   | TTTGTTTTATTAGTTTT<br>GGTGTGG | 60.2                             | 652                                           | DRR                                               | Ca_05392                            | R                     | --  |
| Ca4_P4_17299142  | Ca4                                     | 17299142                      | TTTA/TTTAATTA                                                 | GGCCCCAAAGAGGAAA<br>AATA   | AATCCTTGTTGCGTTG<br>GTC      | 60.3                             | 171                                           | DRR                                               | Ca_05391                            | TBLD                  | --  |
| Ca4_P4_17314848  | Ca4                                     | 17314848                      | CAA/CAAACCGAACTAGAA                                           | TTGTAAAACTGCATCA<br>ATCGAA | CTCCCCACTCACAGT<br>CCAT      | 59.7                             | 488                                           | DRR                                               | Ca_05390                            | M                     | --  |
| Ca4_P4_17315192  | Ca4                                     | 17315192                      | TAAA/TAAAA                                                    | ATGGACTGTGAGTGGG<br>GAAG   | TTGGTCCAACAGCTTG<br>ATGA     | 60.0                             | 716                                           | DRR                                               | Ca_05390                            | M                     | --  |
| Ca4_P4_17342101  | Ca4                                     | 17342101                      | ATTTTT/ATTT                                                   | CTTCCTCTAGCACCAG<br>CACC   | CACGATGAGTTTTCGT<br>GTCA     | 60.0                             | 572                                           | DRR                                               | Ca_05389                            | A                     | --  |
| Ca4_P4_17376716  | Ca4                                     | 17376716                      | ATTTTTTTTT/ATTTTTTTTTT                                        | CCCCCATCTTCAAATG<br>TGTT   | AGATGTAGCAACGCAA<br>ACCA     | 59.6                             | 698                                           | DRR                                               | Ca_05387                            | R                     | --  |
| Ca4_P4_17471371  | Ca4                                     | 17471371                      | TG/T                                                          | CACAGTGGCTGAGAGT<br>GGAA   | AGTAGTGGTGGTTTG<br>CCTG      | 60.0                             | 625                                           | DRR                                               | Ca_05380                            | AB                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_17494891  | Ca4                                     | 17494891                      | GAAAAAAAAA/GAAAAAAAAA                                         | AGATCTCCGAACGATG<br>ATGG | AAGCAACCCCACTTC<br>ACAC  | 60.0                             | 245                                           | DRR                                               | Ca_05377                            | R                     | B3   |
| Ca4_P4_17495202  | Ca4                                     | 17495202                      | GT/G                                                          | GTGTGAAGTGGGGTTT<br>GCTT | CGAAATTCATGCATTCA<br>ACG | 60.0                             | 476                                           | DRR                                               | Ca_05377                            | R                     | B3   |
| Ca4_P4_17495331  | Ca4                                     | 17495331                      | TATACTCA/TA                                                   | GTGTGAAGTGGGGTTT<br>GCTT | CGAAATTCATGCATTCA<br>ACG | 60.0                             | 476                                           | DRR                                               | Ca_05377                            | R                     | B3   |
| Ca4_P4_17495385  | Ca4                                     | 17495385                      | AAT/A                                                         | GTGTGAAGTGGGGTTT<br>GCTT | CGAAATTCATGCATTCA<br>ACG | 60.0                             | 476                                           | DRR                                               | Ca_05377                            | R                     | B3   |
| Ca4_P4_17495441  | Ca4                                     | 17495441                      | AG/A                                                          | GTGTGAAGTGGGGTTT<br>GCTT | CGAAATTCATGCATTCA<br>ACG | 60.0                             | 476                                           | DRR                                               | Ca_05377                            | R                     | B3   |
| Ca4_P4_17495949  | Ca4                                     | 17495949                      | C/CTT                                                         | TCATTGCTGAAGAGCA<br>CGAT | TGCTCAACAACAGGAA<br>GTGG | 59.6                             | 728                                           | DRR                                               | Ca_05377                            | R                     | B3   |
| Ca4_P4_17524638  | Ca4                                     | 17524638                      | GTATTATTATTATTA/GTATTATTATT<br>ATTATTA                        | GGAGATGGAGATGGCT<br>GTGT | GGGTATCAAGCCGAAT<br>CAAA | 60.1                             | 862                                           | DRR                                               | Ca_05374                            | R                     | NAC  |
| Ca4_P4_17608586  | Ca4                                     | 17608586                      | CAATTTTAATTTTA/CAATTTTAATTT<br>TAATTTTA                       | CTGACAGTTGAGCACT<br>CCCA | TGTCACCCCGTTCTTG<br>TGTA | 60.0                             | 634                                           | DRR                                               | Ca_05370                            | O                     | --   |
| Ca4_P4_17626592  | Ca4                                     | 17626592                      | A/AG                                                          | TGTCCTTTTCTCGTGC<br>TCTT | TGCACGGAAGAGTGTG<br>AATC | 60.0                             | 813                                           | DRR                                               | Ca_05368                            | F                     | --   |
| Ca4_P4_17640423  | Ca4                                     | 17640423                      | CTTTTTTT/CTTTTTT                                              | CAAGAAGAAGTGGTGG<br>GGAA | GAACCTTTTCCATCGA<br>GTCA | 60.1                             | 524                                           | DRR                                               | Ca_05367                            | Z                     | WRKY |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_17645039  | Ca4                                     | 17645039                      | ATCT/AT                                                       | GGGAGAGCCCTAGTTG<br>GTTT  | TGGTTGCTTTGAGCTTT<br>TGA     | 59.6                             | 262                                           | DRR                                               | Ca_05366                            | --                    | --   |
| Ca4_P4_17649601  | Ca4                                     | 17649601                      | TAAAAAAA/TAAAAA                                               | GCCTTAGTTTTTTCGGC<br>TTCC | CAAAATAAGCACCAAC<br>CTCTCA   | 60.2                             | 945                                           | DRR                                               | Ca_05365                            | H                     | --   |
| Ca4_P4_17653817  | Ca4                                     | 17653817                      | AATATA/AATA                                                   | GATGTGAGGGCTTGCA<br>ATTT  | GGTGCAACTTTATTTG<br>GTCG     | 60.1                             | 870                                           | DRR                                               | Ca_05364                            | S                     | --   |
| Ca4_P4_17654597  | Ca4                                     | 17654597                      | TCACACAC/TCACACACAC                                           | TCCAATTGACACCACT<br>GCTC  | TTTTC AACATTCTAAAA<br>ATGGGC | 59.7                             | 542                                           | DRR                                               | Ca_05364                            | S                     | --   |
| Ca4_P4_17661717  | Ca4                                     | 17661717                      | ATT/AT                                                        | TGATCCGGTCGGTTGT<br>AAAT  | AAGCTCGACATTTCAAA<br>GGC     | 60.2                             | 840                                           | DRR                                               | Ca_05363                            | R                     | WRKY |
| Ca4_P4_17661910  | Ca4                                     | 17661910                      | ATTTTT/ATTTTTTT                                               | AACATGTGAAATGGGA<br>AGGC  | TTAACGGTTCGTTTTCC<br>AGG     | 59.8                             | 982                                           | DRR                                               | Ca_05363                            | R                     | WRKY |
| Ca4_P4_17672684  | Ca4                                     | 17672684                      | GATA/GA                                                       | TGTAGTCCCTCTGTCC<br>CAAAA | CGGAAGATACCAAGTC<br>GCAT     | 59.6                             | 433                                           | DRR                                               | Ca_05360                            | --                    | --   |
| Ca4_P4_17704939  | Ca4                                     | 17704939                      | CATATATAT/CATATATATATAT                                       | AAGTCGAACCCCAATA<br>ACCC  | TTTAGGGATGATTGCTT<br>GGG     | 60.1                             | 600                                           | DRR                                               | Ca_05355                            | R                     | SBP  |
| Ca4_P4_17705462  | Ca4                                     | 17705462                      | GAAAAA/GAAAAAA                                                | GTGCTTTCCCAAGCAA<br>TCAT  | TCTGAGATGGGTTTGC<br>CTTT     | 60.1                             | 885                                           | DRR                                               | Ca_05355                            | R                     | SBP  |
| Ca4_P4_17707066  | Ca4                                     | 17707066                      | ATTTTT/ATTTTTTT                                               | TTGCATGCTTGGATTG<br>AAAA  | CCATCGAAAAGGAATG<br>GCTA     | 60.2                             | 413                                           | DRR                                               | Ca_05354                            | O                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_17721218  | Ca4                                     | 17721218                      | ATTCATG/A                                                     | CAAGACTTTGTTGGGG<br>GAAA  | TCAGTTCTGTCACAGT<br>CGGC    | 59.9                             | 413                                           | DRR                                               | Ca_05353                            | O                     | SRS |
| Ca4_P4_17758892  | Ca4                                     | 17758892                      | GTTTTTTTT/GTTTTTTT                                            | TTTGATGCAAACAAGTT<br>CCTG | CGATGAAGGAGTTCTC<br>AGCC    | 58.8                             | 499                                           | DRR                                               | Ca_05349                            | O                     | --  |
| Ca4_P4_17759068  | Ca4                                     | 17759068                      | GAAAA/GAAA                                                    | GGCTGAGAACTCCTTC<br>ATCG  | CGCACCACCTTTACATT<br>CCT    | 60.0                             | 431                                           | DRR                                               | Ca_05349                            | O                     | --  |
| Ca4_P4_17766593  | Ca4                                     | 17766593                      | TAAAA/TAAA                                                    | ATTGCATTGTGCTCCA<br>CTTG  | AGGGGTTGGTATAGTA<br>GAAGGAA | 59.7                             | 512                                           | DRR                                               | Ca_05348                            | --                    | --  |
| Ca4_P4_17766645  | Ca4                                     | 17766645                      | CTTTTT/CTTTTTT                                                | ATTGCATTGTGCTCCA<br>CTTG  | GGCTCTGTTTGATACA<br>GCCA    | 59.7                             | 744                                           | DRR                                               | Ca_05348                            | --                    | --  |
| Ca4_P4_17766884  | Ca4                                     | 17766884                      | A/AAAT                                                        | TGCACCAGACATATTTT<br>CGC  | AAAAGCCACACAGGAT<br>GGAC    | 59.7                             | 873                                           | DRR                                               | Ca_05348                            | --                    | --  |
| Ca4_P4_17775093  | Ca4                                     | 17775093                      | A/AC                                                          | AAGAGTTGCCAAAGTG<br>GTGC  | ACGCGGAGAAATTTGC<br>TATT    | 60.3                             | 519                                           | DRR                                               | Ca_05347                            | R                     | --  |
| Ca4_P4_17863849  | Ca4                                     | 17863849                      | AA/AATAACCAATA                                                | TTTGATTGTGGCTTTTG<br>CAG  | AAATCTGCCAATCATGC<br>CTC    | 59.8                             | 563                                           | DRR                                               | Ca_18623                            | --                    | WOX |
| Ca4_P4_17864168  | Ca4                                     | 17864168                      | ACGTAACC/AC                                                   | GAGGCATGATTGGCAG<br>ATTT  | TCGTCATTCCAAATAGC<br>GAC    | 60.0                             | 536                                           | DRR                                               | Ca_18623                            | --                    | WOX |
| Ca4_P4_17864334  | Ca4                                     | 17864334                      | ATTTTTT/ATTTTTTTT                                             | GAGGCATGATTGGCAG<br>ATTT  | TCGTCATTCCAAATAGC<br>GAC    | 60.0                             | 536                                           | DRR                                               | Ca_18623                            | --                    | WOX |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')       | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|-------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                                             |                               |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_18295337  | Ca4                                     | 18295337                      | A/ATT                                                                       | TTCTATTGCTCACCC<br>CTTG       | GAAAAACAAGACCCGC<br>GATA | 60.1                             | 539                                           | DRR                                               | Ca_18662                            | --                    | --    |
| Ca4_P4_1831456   | Ca4                                     | 1831456                       | TTA/TTATA                                                                   | TCCAATAAGGTTGCCT<br>AAGGA     | GAGATTAAGCCGGAAG<br>ACCC | 58.7                             | 256                                           | DRR                                               | Ca_07804                            | --                    | --    |
| Ca4_P4_1840388   | Ca4                                     | 1840388                       | C/CA                                                                        | GCGAACCAAAGTGTGA<br>GTGA      | TTCTCTCCATCTGCTG<br>GCT  | 59.9                             | 654                                           | DRR                                               | Ca_07805                            | --                    | --    |
| Ca4_P4_1843722   | Ca4                                     | 1843722                       | ATACTACTACTACTAC/ATACTACTA<br>CTACTACTACTAC                                 | CAAGTGTGGGCATCTC<br>AGAA      | CTGCTGTTTCAAGCCA<br>ATCA | 59.8                             | 418                                           | DRR                                               | Ca_07806                            | R                     | WRKY  |
| Ca4_P4_18883677  | Ca4                                     | 18883677                      | AATATATATATATATATATATATAT<br>ATATA/AATATATATATATATATAT<br>ATATATATATATATATA | AAATGTAGGGTGGAC<br>GGTG       | TATCCCCCAATGAAG<br>GACA  | 59.7                             | 750                                           | DRR                                               | Ca_13985                            | E                     | WRKY  |
| Ca4_P4_18943390  | Ca4                                     | 18943390                      | TATAATAATAATAATAATA/TATAATA<br>ATAATAATAATAATA                              | CGACCATCACATACTG<br>TGCC      | TTGAAATATTGGGCTCA<br>GGC | 60.0                             | 700                                           | DRR                                               | Ca_13992                            | --                    | --    |
| Ca4_P4_19276409  | Ca4                                     | 19276409                      | AC/A                                                                        | CAATGACGTAGGGAAA<br>TCGAA     | CCTTGAGTTCGACACT<br>CGGT | 59.9                             | 296                                           | DRR                                               | Ca_14024                            | --                    | --    |
| Ca4_P4_19680920  | Ca4                                     | 19680920                      | AATATATATATATATATATAT/AAAT<br>ATATATATATATATATAT                            | TTTGTTCACTTTTATGA<br>TGTTGGTG | TTATATAGCCCCAGCC<br>GTTG | 59.0                             | 610                                           | DRR                                               | Ca_14054                            | S                     | --    |
| Ca4_P4_19708013  | Ca4                                     | 19708013                      | TAAAAAAAAA/TAAAAAAAAA                                                       | CAATTGCCAGAAGTTG<br>TTGG      | GATTGCTGGATTGGA<br>AGGA  | 59.2                             | 842                                           | DRR                                               | Ca_14058                            | J                     | NF-YB |
| Ca4_P4_19757541  | Ca4                                     | 19757541                      | GAAAAAAAAA/GAAAAAAAAA<br>AAA                                                | TATGAGGAAAAATGGG<br>CCAG      | AACCTATTGCGAACGT<br>CGTC | 59.9                             | 163                                           | DRR                                               | Ca_14064                            | U                     | GATA  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                    | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                  |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca4_P4_20213739  | Ca4                                     | 20213739                      | TCGTTAC/TC                                                                       | TCAGCTTTTGGCTGA<br>TGTG  | GCGTGAATTTGAACAC<br>GAGA | 60.0                             | 698                                           | DRR                                               | Ca_17141                            | PT                    | FAR1     |
| Ca4_P4_2035697   | Ca4                                     | 2035697                       | ATTT/AT                                                                          | AGTCCAGTCTAAGCTG<br>CCCA | TGGAATCATGCCATGC<br>TAGA | 60.0                             | 436                                           | DRR                                               | Ca_07823                            | R                     | MYB      |
| Ca4_P4_2035798   | Ca4                                     | 2035798                       | A/AGTGT                                                                          | AGTCCAGTCTAAGCTG<br>CCCA | TGGAATCATGCCATGC<br>TAGA | 60.0                             | 436                                           | DRR                                               | Ca_07823                            | R                     | MYB      |
| Ca4_P4_20870966  | Ca4                                     | 20870966                      | ATTTTTTTT/ATTTTTTT                                                               | ACTCATTGTGTTGGCT<br>TTCG | GTGGATGAAGGGGTA<br>GGTT  | 58.8                             | 776                                           | DRR                                               | Ca_19043                            | --                    | --       |
| Ca4_P4_21175270  | Ca4                                     | 21175270                      | ATTTTT/ATTTTTT                                                                   | GACACCAGGAGGCATG<br>TTTT | GGAAGGCTTGTCAGCT<br>TGAG | 60.0                             | 386                                           | DRR                                               | Ca_19056                            | --                    | --       |
| Ca4_P4_21230030  | Ca4                                     | 21230030                      | CTTTTT/CTTTTTT                                                                   | TCACTTTGATTGGTTG<br>CTGG | TGAAATTATGGGTGGG<br>CATT | 59.7                             | 371                                           | DRR                                               | Ca_19058                            | --                    | Trihelix |
| Ca4_P4_21774546  | Ca4                                     | 21774546                      | AATATATATATATATATATATATAT<br>ATATATATAAATATATATATATATAT<br>ATATATATATATATATATATA | TCAACCAATATGAATCC<br>GCA | AAAAGGAATGATTGAT<br>GCCG | 59.9                             | 557                                           | DRR                                               | Ca_19080                            | --                    | --       |
| Ca4_P4_21933188  | Ca4                                     | 21933188                      | GAAAAAAAAA/GAAAAAAAAA                                                            | GTTGGGCAATGGATCT<br>GAAT | TGCTCACCGTTTGATCT<br>TTG | 59.8                             | 862                                           | DRR                                               | Ca_20146                            | --                    | --       |
| Ca4_P4_22134995  | Ca4                                     | 22134995                      | CATAT/CAT                                                                        | GCACCTATGGTGGCAA<br>AAAC | TTTGATGCCACATTGA<br>AGA  | 60.4                             | 506                                           | DRR                                               | Ca_20134                            | J                     | --       |
| Ca4_P4_22237363  | Ca4                                     | 22237363                      | TAG/T                                                                            | CCCTCTTGATTGGCA<br>TGAT  | AATAAACAGCATGGCG<br>GAAG | 59.9                             | 568                                           | DRR                                               | Ca_20127                            | --                    | ERF      |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_22288876  | Ca4                                     | 22288876                      | TTTCTACAAAATCAGTTCTACAAAAT<br>CAGT/TTTCTACAAAATCAGT           | TGCACTCCACACCCTA<br>CAAA   | CCATGCAAAACTCCAT<br>GTTG    | 60.2                             | 685                                           | DRR                                               | Ca_20125                            | TR                    | --  |
| Ca4_P4_22649708  | Ca4                                     | 22649708                      | TTAATAATAATAATAATAATAATAAT<br>AA/TTAATAATAATAATAATAATAA       | CGTACAACCTGGGGCT<br>TGAT   | CATTACCATGTGCTTT<br>TTATGC  | 60.0                             | 725                                           | DRR                                               | Ca_14478                            | --                    | --  |
| Ca4_P4_22792153  | Ca4                                     | 22792153                      | GAAAAAAAA/GAAAAAAAAA                                          | CTCATTTTCATTCACCG<br>GCT   | ACGAAGCATTAGGCAT<br>GGAT    | 60.1                             | 931                                           | DRR                                               | Ca_14472                            | --                    | --  |
| Ca4_P4_22808161  | Ca4                                     | 22808161                      | A/AC                                                          | CATGGTTTTCGCTTAC<br>CGTT   | TTGGGTGATGTGGCAA<br>AATA    | 60.0                             | 559                                           | DRR                                               | Ca_14470                            | H                     | --  |
| Ca4_P4_22837725  | Ca4                                     | 22837725                      | AAATAATAA/AAATAA                                              | TTGAAATGGCAAAGAG<br>GGTC   | ATGCATGGGTGAAAT<br>ACCC     | 60.1                             | 556                                           | DRR                                               | Ca_14468                            | --                    | --  |
| Ca4_P4_22973152  | Ca4                                     | 22973152                      | TTAAATGTAAATGTA/TTAAATG<br>TAAATGTAAATGTA                     | ATTTTATTGGCATCGG<br>CATT   | TGCGAATGTGCTTTCT<br>GTCT    | 59.3                             | 672                                           | DRR                                               | Ca_14460                            | --                    | --  |
| Ca4_P4_22974338  | Ca4                                     | 22974338                      | A/AAT                                                         | ATTTTGGGCGAAATCC<br>TTTT   | GAACCACTCATCCTCC<br>CAAA    | 59.8                             | 442                                           | DRR                                               | Ca_14460                            | --                    | --  |
| Ca4_P4_23055017  | Ca4                                     | 23055017                      | T/TG                                                          | GTGTGCTTGGAAGTC<br>GTTG    | TTTGATGTTGTTGGAG<br>ATGAAAA | 59.3                             | 485                                           | DRR                                               | Ca_14459                            | --                    | --  |
| Ca4_P4_23055098  | Ca4                                     | 23055098                      | CTTTATTTTATTTTATTTTATTT/CT<br>TTATTTTATTTTATTTT               | GTGTGCTTGGAAGTC<br>GTTG    | TTTGATGTTGTTGGAG<br>ATGAAAA | 59.3                             | 485                                           | DRR                                               | Ca_14459                            | --                    | --  |
| Ca4_P4_23055622  | Ca4                                     | 23055622                      | TAAGAA/TAAGAAAGAA                                             | TGAATTAAGGATTGC<br>ATGAACA | CCGTTGAATGAAAAAT<br>CACC    | 59.5                             | 530                                           | DRR                                               | Ca_14459                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca4_P4_23098190  | Ca4                                     | 23098190                      | TC/T                                                          | GGCGGTCGAGAGTTTA<br>TGTG | TGAGTGCCAACAAGCT<br>GAAC | 60.7                             | 495                                           | DRR                                               | Ca_14457                            | R                     | MYB      |
| Ca4_P4_23098234  | Ca4                                     | 23098234                      | GTTTT/GTTTTT                                                  | GGCGGTCGAGAGTTTA<br>TGTG | TGAGTGCCAACAAGCT<br>GAAC | 60.7                             | 495                                           | DRR                                               | Ca_14457                            | R                     | MYB      |
| Ca4_P4_23108687  | Ca4                                     | 23108687                      | C/CT                                                          | GTGGGTGGAATGAAAA<br>TACG | GCATCGGGAGATACGT<br>AGGA | 60.1                             | 659                                           | DRR                                               | Ca_14456                            | --                    | --       |
| Ca4_P4_23340817  | Ca4                                     | 23340817                      | TTGTGTGT/TTGTGT                                               | TGTTTGGCAGCTAAGC<br>AATG | AAGTTCCTTACGGTC<br>CTTG  | 60.0                             | 396                                           | DRR                                               | Ca_14446                            | S                     | --       |
| Ca4_P4_24438141  | Ca4                                     | 24438141                      | CAAAAA/CAAAAA                                                 | CCGCTCTGGAATCAT<br>TCAT  | AAGACTCGGGATAATG<br>GCCT | 60.0                             | 551                                           | DRR                                               | Ca_20867                            | --                    | --       |
| Ca4_P4_24608867  | Ca4                                     | 24608867                      | GTTTTTTTTT/GTTTTTTTTT                                         | AGTGGATGGGTCGCAT<br>TTAG | GCTTTGCCACGTCAGT<br>GTAA | 60.0                             | 570                                           | DRR                                               | Ca_20856                            | GE                    | HB-other |
| Ca4_P4_24786141  | Ca4                                     | 24786141                      | CTTTTTTTTT/CTTTTTTTTT                                         | CTTCACTGCGTCCCTT<br>CTTC | GGGGTTGCAGATGATG<br>TTGT | 60.0                             | 415                                           | DRR                                               | Ca_20850                            | --                    | --       |
| Ca4_P4_24865397  | Ca4                                     | 24865397                      | ATTTTTT/ATTTTTT                                               | TTCGGTCGCTTATTCT<br>CTCC | CCAGCTAGAACAAAAT<br>GGCG | 59.4                             | 534                                           | DRR                                               | Ca_20847                            | T                     | bZIP     |
| Ca4_P4_25252210  | Ca4                                     | 25252210                      | GTT/GT                                                        | AAGGGGGCCCTAATAA<br>GGTT | GATGTGCCTGGTTGGA<br>AAGT | 60.0                             | 855                                           | DRR                                               | Ca_16567                            | CD                    | --       |
| Ca4_P4_25282410  | Ca4                                     | 25282410                      | CTTA/CTTATTA                                                  | AGCTTTAGCTTGAGGG<br>GGAG | TGGTCACTGGTGCTTC<br>TCTG | 60.0                             | 965                                           | DRR                                               | Ca_16569                            | B                     | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')      | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                   |                              |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca4_P4_25457334  | Ca4                                     | 25457334                      | ATTTTTTT/ATTTTTTTT                                                | CATTTTACTCATCGATC<br>TTTGTTG | TGGACAAAATCATGTCT<br>CTTTGA   | 59.9                             | 336                                           | DRR                                               | Ca_16577                            | --                    | --       |
| Ca4_P4_25457701  | Ca4                                     | 25457701                      | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>ATATATA | TCAAAGAGACATGATT<br>TGTCCA   | TCACTTTGCTTTGTGTG<br>TCTCA    | 59.6                             | 524                                           | DRR                                               | Ca_16577                            | --                    | --       |
| Ca4_P4_25526065  | Ca4                                     | 25526065                      | ATG/ATGTG                                                         | ATTGCGACCAAACAAC<br>AACA     | CTTCCCAACTGAACTC<br>CGAA      | 60.0                             | 689                                           | DRR                                               | Ca_16580                            | --                    | --       |
| Ca4_P4_25527044  | Ca4                                     | 25527044                      | TAAAAAAA/TAAAAAAA                                                 | ATTGAAGCGGCACCTA<br>TTGA     | GCAAATTGTAAAGTAG<br>TCTTTGAGC | 60.6                             | 706                                           | DRR                                               | Ca_16580                            | --                    | --       |
| Ca4_P4_25596215  | Ca4                                     | 25596215                      | ATGTGTGTGTGTGT/ATGTGTGTGT<br>GT                                   | TTCTCACGAAAGCGCT<br>GTAA     | GGGCAAGGGGATCTGA<br>ATA       | 59.8                             | 585                                           | DRR                                               | Ca_16586                            | --                    | Trihelix |
| Ca4_P4_25779217  | Ca4                                     | 25779217                      | CTTAATTAATTAATTAATTAATTA/CT<br>TAATTAATTAATTAATTA                 | ATACCGAGATGGACAC<br>CACC     | TAACCCCTCAACATCTG<br>GGC      | 59.7                             | 367                                           | DRR                                               | Ca_16597                            | R                     | NAC      |
| Ca4_P4_25779465  | Ca4                                     | 25779465                      | AATA/AA                                                           | GCCAGATGTTGAAGG<br>GTTA      | TTTGTCATCTCATAGGC<br>CCC      | 59.9                             | 209                                           | DRR                                               | Ca_16597                            | R                     | NAC      |
| Ca4_P4_25916811  | Ca4                                     | 25916811                      | CTTTTTTTTT/CTTTTTTTTTTTT                                          | ATGGTAACAGATATCG<br>CCGC     | ATTGTAGCATTGCCCA<br>AAGG      | 60.0                             | 627                                           | DRR                                               | Ca_16606                            | I                     | --       |
| Ca4_P4_25962811  | Ca4                                     | 25962811                      | GTATATATAT/GTATATATATAT                                           | TGGTTGGAAGCTCCAG<br>AAGT     | GAAAAGGTGAGGAATC<br>GCTG      | 59.8                             | 275                                           | DRR                                               | Ca_16607                            | --                    | B3       |
| Ca4_P4_25974119  | Ca4                                     | 25974119                      | AG/A                                                              | AGCTCCGTGACCTTCT<br>CAAA     | TCTTTCTGATCAATGG<br>CCC       | 60.0                             | 934                                           | DRR                                               | Ca_16608                            | --                    | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca4_P4_26011159  | Ca4                                     | 26011159                      | AT/AACAGAACTCCT                                               | GAAACCCCAACA<br>ATGG      | AGCATCATGGATTCTT<br>CCG     | 60.1                             | 438                                           | DRR                                               | Ca_16611                            | C                     | --     |
| Ca4_P4_2609181   | Ca4                                     | 2609181                       | T/TGTGCTATA                                                   | GCTTCTGCTAGGCATC<br>CATC  | ATGCATGTGCTGATGC<br>TTGT    | 59.9                             | 907                                           | DRR                                               | Ca_12062                            | --                    | --     |
| Ca4_P4_26173966  | Ca4                                     | 26173966                      | CATAT/CAT                                                     | AGAGTGCATGTGGGAT<br>AGGG  | TTCCATGATGCTCTTTT<br>GGG    | 60.0                             | 563                                           | DRR                                               | Ca_16612                            | --                    | HD-ZIP |
| Ca4_P4_26326139  | Ca4                                     | 26326139                      | GAAAAAAA/GAAAAAAA                                             | CTCCAACAGCATCAAT<br>TCCA  | GATCCTGGGATTGTGA<br>GCAT    | 59.6                             | 724                                           | DRR                                               | Ca_25306                            | R                     | --     |
| Ca4_P4_26337485  | Ca4                                     | 26337485                      | GTTTTTT/GTTTTTTT                                              | CCTTTCCACCCAGAAA<br>GGAG  | TGGCAGAGCACTACCA<br>ACAA    | 61.0                             | 362                                           | DRR                                               | Ca_25305                            | --                    | FAR1   |
| Ca4_P4_26418036  | Ca4                                     | 26418036                      | TCACACACACACACA/TCACACA<br>CACACACACACA                       | CCAAAATTCAAACACCA<br>CCC  | AACCCTGATTGACGGT<br>GAAG    | 60.1                             | 542                                           | DRR                                               | Ca_25299                            | --                    | --     |
| Ca4_P4_26519771  | Ca4                                     | 26519771                      | CAAA/CAAAAAA                                                  | AAACCTCTTCGCCTTTT<br>TGC  | TATTTTACGTACCCGCT<br>GCC    | 60.7                             | 351                                           | DRR                                               | Ca_25005                            | R                     | NAC    |
| Ca4_P4_26524092  | Ca4                                     | 26524092                      | GAA/GAAAA                                                     | TGAAATAGAGGGCCAG<br>GTTG  | TTCGTCCTTTGTCATCA<br>AACA   | 60.1                             | 317                                           | DRR                                               | Ca_25004                            | P                     | --     |
| Ca4_P4_26524408  | Ca4                                     | 26524408                      | C/CCTTAA                                                      | TGTTTGATGACAAAGG<br>ACGAA | AGAGGCACATTGAGAG<br>CGTA    | 59.2                             | 421                                           | DRR                                               | Ca_25004                            | P                     | --     |
| Ca4_P4_26766370  | Ca4                                     | 26766370                      | ATT/ATTT                                                      | AGTTTTGGCCCTTTT<br>GATT   | TTGAGATGTTTCATGTT<br>TCCATT | 59.8                             | 678                                           | DRR                                               | Ca_20437                            | K                     | MYB    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_26970354  | Ca4                                     | 26970354                      | TAAAAAAA/TAAAA                                                | ATTGTTTGCAGTTG<br>AGGC       | TTCTCGTTACAAAATT<br>TCCAAAA | 60.3                             | 696                                           | DRR                                               | Ca_20452                            | A                     | --    |
| Ca4_P4_26970810  | Ca4                                     | 26970810                      | TAAAAAAA/TAAAAAA                                              | GAAAAGCTGAACTGT<br>ATTTTGGAA | AACAGTGCCGATGAAT<br>AGTTTT  | 60.1                             | 306                                           | DRR                                               | Ca_20452                            | A                     | --    |
| Ca4_P4_27197342  | Ca4                                     | 27197342                      | ATTTTT/ATTTTTTT                                               | CCTCAGACATCTTGC<br>CCAT      | AAGTGTTGGACGGACC<br>CTTA    | 60.1                             | 656                                           | DRR                                               | Ca_20458                            | --                    | NF-YB |
| Ca4_P4_27197635  | Ca4                                     | 27197635                      | TAAAAAAAAA/TAAAAAAAAA                                         | TTCAGGTTGCACCACA<br>AAAC     | TCAAATGCTACCGTTG<br>GACA    | 59.6                             | 691                                           | DRR                                               | Ca_20458                            | --                    | NF-YB |
| Ca4_P4_27267123  | Ca4                                     | 27267123                      | TAAAAA/TAAAA                                                  | CCCTCAACTCAACTGA<br>GATCC    | TGCATTGGTTTGAATT<br>GGA     | 58.7                             | 568                                           | DRR                                               | Ca_20461                            | R                     | --    |
| Ca4_P4_27283830  | Ca4                                     | 27283830                      | GTTT/GTTTT                                                    | TATTGGTCGTCAAGCA<br>GCAG     | TTTCCAATCGATTTC<br>TTC      | 60.0                             | 681                                           | DRR                                               | Ca_20463                            | --                    | --    |
| Ca4_P4_27378491  | Ca4                                     | 27378491                      | TAAAAAAAAA/TAAAAAAAAA                                         | GGATCCGTCCTCGCA<br>TAAA      | TTGCACAGGTTGTTT<br>GTTG     | 60.0                             | 585                                           | DRR                                               | Ca_21323                            | --                    | --    |
| Ca4_P4_27627265  | Ca4                                     | 27627265                      | A/AGAAGAG                                                     | TTCTGCACCTGTGGTG<br>AAGG     | ATGCCATCGCTTTCCTC<br>AAT    | 59.9                             | 526                                           | DRR                                               | Ca_21312                            | --                    | --    |
| Ca4_P4_27637047  | Ca4                                     | 27637047                      | TAAAAAAA/TAAAAAA                                              | CAACAAAGCGTCCACC<br>TGTA     | CCAATGATTTTCATGCC<br>ACA    | 59.8                             | 810                                           | DRR                                               | Ca_21310                            | --                    | --    |
| Ca4_P4_27637430  | Ca4                                     | 27637430                      | TG/TGG                                                        | TTGGAGTGGTGGTTC<br>TCAA      | CCAATGATTTTCATGCC<br>ACA    | 59.1                             | 482                                           | DRR                                               | Ca_21310                            | --                    | --    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_27638049  | Ca4                                     | 27638049                      | CAAAAAAAAA/CAAAAAAAAA                                         | TTGTTTGATTGAGCATGT      | TTCAATTGGATTGGATTGAT    | 59.3                             | 510                                           | DRR                                               | Ca_21310                            | --                    | --    |
| Ca4_P4_28060298  | Ca4                                     | 28060298                      | GATATATATATATATATAT/GATATATATATATATAT                         | TGCTGCACCCAAATTAACAA    | TGTCAGCCGACAACAAA       | 60.1                             | 318                                           | DRR                                               | Ca_23178                            | --                    | --    |
| Ca4_P4_28234444  | Ca4                                     | 28234444                      | AAAA/AAAAATAAAA                                               | GTTCCATCTGTTGCTGCTGA    | CCTTCTTTTGCCATCTTGC     | 60.0                             | 818                                           | DRR                                               | Ca_23168                            | --                    | --    |
| Ca4_P4_28282247  | Ca4                                     | 28282247                      | ATTTTT/ATTTTTT                                                | TCCAGAAGGCATTCTTGGT     | AGGTTAGTTGGAGCGTTTGAA   | 59.7                             | 430                                           | DRR                                               | Ca_23166                            | TR                    | FAR1  |
| Ca4_P4_28788052  | Ca4                                     | 28788052                      | GTTTTTTTTTT/GTTTTTTTTTT                                       | AAGCATGAAGAGCCTCGGTA    | GGCTCAAGTTGCTGTGATT     | 60.0                             | 923                                           | DRR                                               | Ca_23697                            | E                     | TALE  |
| Ca4_P4_28949557  | Ca4                                     | 28949557                      | CAAAAAAAAA/CAAAAAAAAA                                         | TTTCATCATTTCTGGAGGCA    | GTGAGGATGAGCTGACACGA    | 59.2                             | 528                                           | DRR                                               | Ca_23705                            | J                     | --    |
| Ca4_P4_28996068  | Ca4                                     | 28996068                      | CTTTTTTTTTT/CTTTTTTTTTT                                       | TAACAGCATTGCATTGGAA     | TTCCAACACTAAAGGGGTGC    | 60.1                             | 243                                           | DRR                                               | Ca_23706                            | --                    | NF-YB |
| Ca4_P4_29156546  | Ca4                                     | 29156546                      | CTATA/CTA                                                     | AGTTGGTTTGGTGGTAAGG     | GCATGGTAAAGGCTGTGGT     | 59.9                             | 841                                           | DRR                                               | Ca_23711                            | --                    | --    |
| Ca4_P4_29211121  | Ca4                                     | 29211121                      | AT/A                                                          | GATGTTTAAGGTCTGTTGGCA   | AACTTCAGCCGTCATTGGTT    | 59.1                             | 641                                           | DRR                                               | Ca_14151                            | --                    | --    |
| Ca4_P4_29367942  | Ca4                                     | 29367942                      | TTA/TTATATA                                                   | ATTTTGGCAACACATCCCA     | TGGATCAAGTTGTTGTACAG    | 59.8                             | 634                                           | DRR                                               | Ca_14154                            | --                    | --    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |           |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----------|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs       |
| Ca4_P4_29368197  | Ca4                                     | 29368197                      | TTA/TTAGTA                                                    | ATTTTGGCAACACATCA<br>CCA | CCTTGGCATATTTTTC<br>TGG     | 59.8                             | 737                                           | DRR                                               | Ca_14154                            | --                    | --        |
| Ca4_P4_29646991  | Ca4                                     | 29646991                      | GGATCG/GG                                                     | AGGATTCGGTCTGTGT<br>TTGG | TCAGGACTGCAAATAA<br>CCCA    | 60.0                             | 555                                           | DRR                                               | Ca_14165                            | S                     | --        |
| Ca4_P4_29721716  | Ca4                                     | 29721716                      | G/GA                                                          | CCTCACCTTCCCTTTCA<br>ACA | CGGTGCGACGTGTGATA<br>TGAA   | 60.1                             | 259                                           | DRR                                               | Ca_14167                            | --                    | --        |
| Ca4_P4_29722401  | Ca4                                     | 29722401                      | AAT/AATAT                                                     | TTCGCAGTGGAGTTTG<br>AATG | CGATAAAAACAAATTG<br>TACACCG | 59.8                             | 550                                           | DRR                                               | Ca_14167                            | --                    | --        |
| Ca4_P4_29904472  | Ca4                                     | 29904472                      | T/TA                                                          | CCAAGTGTGCAAACT<br>TCAA  | ATGTTTGACGAAGAGG<br>GCAC    | 59.9                             | 731                                           | DRR                                               | Ca_14176                            | --                    | M-type    |
| Ca4_P4_30045432  | Ca4                                     | 30045432                      | CATATAT/CATATATAT                                             | GCGTGCATAAGTGGTT<br>GATG | ACTCACGGTGATGAGT<br>GTGG    | 60.1                             | 345                                           | DRR                                               | Ca_14181                            | --                    | S1Fa-like |
| Ca4_P4_30206461  | Ca4                                     | 30206461                      | TAAAAAAAAA/TAAAAAAAAA                                         | TCCCTCGAGCTATAGG<br>ATGC | ATGCAATGGTTTATTCC<br>CCA    | 59.4                             | 643                                           | DRR                                               | Ca_14187                            | --                    | --        |
| Ca4_P4_30230521  | Ca4                                     | 30230521                      | A/AAAG                                                        | GGTATGCTGTTTCGGT<br>TCGT | TTGCTAATTTTGCAA<br>ACC      | 60.0                             | 406                                           | DRR                                               | Ca_14188                            | --                    | --        |
| Ca4_P4_30230800  | Ca4                                     | 30230800                      | ATTT/ATT                                                      | CCGTGAACCACTACTC<br>ACGA | CATGACCATTTTGAT<br>GTCG     | 59.7                             | 397                                           | DRR                                               | Ca_14188                            | --                    | --        |
| Ca4_P4_30543529  | Ca4                                     | 30543529                      | T/TC                                                          | CACGAGATTCGTCGAG<br>AACA | TGATGGGTCATTTAGT<br>GCCA    | 60.0                             | 196                                           | DRR                                               | Ca_14205                            | --                    | --        |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca4_P4_30575118  | Ca4                                     | 30575118                      | ATT/ATTT                                                      | TGTTCAACCATCAATTG<br>TTTCC | GGCGGAATTTTTCATA<br>GCAA     | 59.7                             | 222                                           | DRR                                               | Ca_14206                            | A                     | --          |
| Ca4_P4_30856676  | Ca4                                     | 30856676                      | A/AT                                                          | TGCACTGTATTGGAAT<br>TGTGTA | GAAATGACTGAAAAATT<br>TTGGACC | 59.1                             | 482                                           | DRR                                               | Ca_14212                            | --                    | bZIP        |
| Ca4_P4_31029219  | Ca4                                     | 31029219                      | GA/GATAA                                                      | TGCATCGTGAGTTTGA<br>GGAG   | GCCATTTGGAAGTGA<br>AGAA      | 60.0                             | 714                                           | DRR                                               | Ca_14217                            | Q                     | --          |
| Ca4_P4_31195751  | Ca4                                     | 31195751                      | GAAAAAAAA/GAAAAAAAAA                                          | CAACACCATTCAAACC<br>ACCA   | GCGGCAGAATTCAAAT<br>CAGT     | 60.3                             | 500                                           | DRR                                               | Ca_14224                            | --                    | S1Fa-like   |
| Ca4_P4_31248634  | Ca4                                     | 31248634                      | ACC/AC                                                        | TGGGTCATTTCTCATTA<br>TGTCG | TGCTATGCCTTTTGATC<br>GC      | 59.8                             | 645                                           | DRR                                               | Ca_14228                            | --                    | Trihelix    |
| Ca4_P4_31255409  | Ca4                                     | 31255409                      | CA/CAA                                                        | CGCTTACCAGAGCAGT<br>TTCC   | GAGAGAAGTGCTTTG<br>CGGG      | 60.0                             | 681                                           | DRR                                               | Ca_14229                            | R                     | bHLH        |
| Ca4_P4_31261325  | Ca4                                     | 31261325                      | AAAATAAA/AAAA                                                 | TTGAAGTTTGAGAGGA<br>CGGG   | AATTCCAATTGTGCCAC<br>CTC     | 60.2                             | 323                                           | DRR                                               | Ca_14230                            | R                     | MYB_related |
| Ca4_P4_31360317  | Ca4                                     | 31360317                      | TAAAAAA/TAAAAAAA                                              | ACTCATATGACGGGGT<br>GCAT   | GGCAGACGTTGGAAG<br>CTAA      | 60.2                             | 715                                           | DRR                                               | Ca_14232                            | --                    | Trihelix    |
| Ca4_P4_31653241  | Ca4                                     | 31653241                      | GATAAA/GATAAAAAATAA                                           | TTCAAACGATGGCAAC<br>AAAA   | TCATGGGATTAAGCCT<br>CCAC     | 60.1                             | 268                                           | DRR                                               | Ca_15442                            | U                     | EIL         |
| Ca4_P4_31754313  | Ca4                                     | 31754313                      | CTTTTTTTTT/CTTTTTTTTT                                         | GGTTGGTGCAGATTTT<br>TGCT   | AGCACAAAGGCAGAGA<br>AGGA     | 60.1                             | 266                                           | DRR                                               | Ca_15446                            | --                    | --          |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_31866813  | Ca4                                     | 31866813                      | GAGAAAA/G                                                     | TCGCACAATAGTGCAA<br>ACTCA   | TGGTAAGGCGACAAAC<br>AACA | 60.5                             | 512                                           | DRR                                               | Ca_15450                            | --                    | C2H2  |
| Ca4_P4_31978850  | Ca4                                     | 31978850                      | CAA/CAAA                                                      | ACATTCTTATGTCGGG<br>GCAG    | ACAGCCTTTTCTCCATC<br>CCT | 60.0                             | 605                                           | DRR                                               | Ca_15457                            | S                     | --    |
| Ca4_P4_31994404  | Ca4                                     | 31994404                      | TAAAA/TAAAAA                                                  | ATCAGCGAGGATGCAG<br>AACT    | CATCGCTCAGTTTGGA<br>CTCA | 60.0                             | 796                                           | DRR                                               | Ca_15458                            | --                    | --    |
| Ca4_P4_32045859  | Ca4                                     | 32045859                      | T/TA                                                          | TGGGGTTTTGATCCAT<br>TTGT    | TGATGTCTTTCGATCCA<br>CCT | 60.0                             | 607                                           | DRR                                               | Ca_15459                            | --                    | --    |
| Ca4_P4_32046303  | Ca4                                     | 32046303                      | GTTTTT/GTTTTTTT                                               | TTTGGGCTTTTCTTGAT<br>TGG    | AGTCGGCTTCAAAGGC<br>ACTA | 60.0                             | 646                                           | DRR                                               | Ca_15459                            | --                    | --    |
| Ca4_P4_32069410  | Ca4                                     | 32069410                      | A/AC                                                          | CCAGTGGTGTCCCTCT<br>TGAT    | GAGACGGAATTTGGGA<br>CAGA | 60.0                             | 767                                           | DRR                                               | Ca_15461                            | R                     | --    |
| Ca4_P4_32565833  | Ca4                                     | 32565833                      | TAAAAAAA/TAAAAAAA                                             | CCGTTGACTAGACGTA<br>AACAACA | ACCAACAAACCATGCA<br>CAAA | 59.3                             | 879                                           | DRR                                               | Ca_15483                            | T                     | YABBY |
| Ca4_P4_32602184  | Ca4                                     | 32602184                      | CA/C                                                          | TGGGGATCAACAGACT<br>CTAAAA  | GTGAAAATCGAAGTGC<br>GACA | 58.7                             | 456                                           | DRR                                               | Ca_15484                            | R                     | AP2   |
| Ca4_P4_32603125  | Ca4                                     | 32603125                      | TCC/TC                                                        | GTCAAAACATGTTCCC<br>ACCC    | GCCCAACCACTAGGTT<br>GAAA | 60.1                             | 219                                           | DRR                                               | Ca_15484                            | R                     | AP2   |
| Ca4_P4_32635688  | Ca4                                     | 32635688                      | TAAAAAAAAA/TAAAAAAAAA                                         | TATGTGTGTGGCAGCA<br>TGAA    | TGCATTTGCCTGCTCT<br>ATG  | 59.7                             | 639                                           | DRR                                               | Ca_15486                            | R                     | NAC   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca4_P4_32650019  | Ca4                                     | 32650019                      | ATTTTT/ATTTTT                                                 | TTGTGTTTTGGTTGGG<br>ATCA | TTTCATGGGTTTGTGT<br>GAAAT | 59.8                             | 451                                           | DRR                                               | Ca_15487                            | --                    | --      |
| Ca4_P4_33308913  | Ca4                                     | 33308913                      | GAAAA/GAAA                                                    | TCATTTTCCCTCGTT<br>CTG   | TTGGCCAAAACCTTTTG<br>ATG  | 60.0                             | 183                                           | DRR                                               | Ca_24021                            | R                     | C2H2    |
| Ca4_P4_33397720  | Ca4                                     | 33397720                      | ATTTTTTTTT/ATTTTTTTTT                                         | CTCCATTTTGTGGGG<br>CTTA  | GCCAACAAACAACCAT<br>GCTA  | 59.9                             | 584                                           | DRR                                               | Ca_24022                            | --                    | --      |
| Ca4_P4_3365913   | Ca4                                     | 3365913                       | AATATATATATATATATATATAT<br>/AATATATATATATATATATATAT           | AAAGAGGGCATGACAC<br>CAAT | TCGGATCGGACACTAT<br>GACA  | 59.4                             | 466                                           | DRR                                               | Ca_12139                            | --                    | --      |
| Ca4_P4_3413984   | Ca4                                     | 3413984                       | A/ACTTGG                                                      | CGTCATTGCCACATCA<br>TTTC | TTCAGAGAATCTGCAT<br>CCCA  | 59.9                             | 508                                           | DRR                                               | Ca_12143                            | J                     | --      |
| Ca4_P4_34458862  | Ca4                                     | 34458862                      | CAAAA/CAAAA                                                   | CCAAACGTTCTCCAC<br>AACT  | GAGGATGCCAAAATGC<br>CTAA  | 60.0                             | 744                                           | DRR                                               | Ca_20351                            | --                    | --      |
| Ca4_P4_34492879  | Ca4                                     | 34492879                      | TAAAAAAAA/TAAAAAAAA                                           | CTGATCAGTCGTTGGG<br>AGGT | TGAGTTGATCGTTCCA<br>CCA   | 60.1                             | 538                                           | DRR                                               | Ca_20350                            | R                     | G2-like |
| Ca4_P4_35292340  | Ca4                                     | 35292340                      | C/CTAAGATTGTTTTGA                                             | TGGCCAAAGGAGTCAT<br>GTTT | GTGTTGATGTCCGACA<br>ATGC  | 60.5                             | 496                                           | DRR                                               | Ca_20016                            | DZ                    | --      |
| Ca4_P4_35681392  | Ca4                                     | 35681392                      | TAAAAAAAA/TAAAAAAAAA<br>A                                     | TGGTCCCGAGTACGTA<br>GGAG | GCAGGTTCCACCTAGA<br>CCAA  | 60.1                             | 548                                           | DRR                                               | Ca_22446                            | QI                    | B3      |
| Ca4_P4_36245892  | Ca4                                     | 36245892                      | TTATATATATATATATATATAT/<br>TTATATATATATATATATAT               | TACATGCAAGCGAAAT<br>GGAA | AGGCATGGTGTGGAG<br>TCAT   | 60.2                             | 287                                           | DRR                                               | Ca_14846                            | O                     | --      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_36377514  | Ca4                                     | 36377514                      | TCACACA/TCACA                                                 | AGCACGTGGTATCATG<br>TCTCC | CGGCTTCATAATTGGG<br>CTTA  | 60.0                             | 792                                           | DRR                                               | Ca_14838                            | TU                    | C2H2  |
| Ca4_P4_36404496  | Ca4                                     | 36404496                      | TAAA/TAA                                                      | GGAATGGTATTGTCAA<br>CCGC  | AGGCTCAATGACGCAG<br>AACT  | 60.2                             | 701                                           | DRR                                               | Ca_14836                            | R                     | NAC   |
| Ca4_P4_36450503  | Ca4                                     | 36450503                      | TTAT/TT                                                       | GACACCAAATTGGGAA<br>AGGA  | GCGGTGACATGTACGA<br>TTTG  | 59.8                             | 710                                           | DRR                                               | Ca_14833                            | S                     | --    |
| Ca4_P4_36458353  | Ca4                                     | 36458353                      | ATTT/ATTTTT                                                   | AATCCGATTCAACCCA<br>CAAA  | CAAGGTCCATATTCAA<br>TGCG  | 60.2                             | 438                                           | DRR                                               | Ca_14832                            | T                     | YABBY |
| Ca4_P4_36483891  | Ca4                                     | 36483891                      | GTTTTTTTTTTT/GTTTTTTTTT                                       | AATATGTTGGAGTGGC<br>CCTG  | CGGACCACAAAATTGT<br>AAACG | 59.8                             | 552                                           | DRR                                               | Ca_14829                            | QR                    | B3    |
| Ca4_P4_36487114  | Ca4                                     | 36487114                      | TAAAATCTAACATAAAAAAT/TAAAAT                                   | AACAGCCATGGAATTT<br>GTCA  | GCCTTCTTCTCATGAG<br>CCAC  | 59.0                             | 713                                           | DRR                                               | Ca_14828                            | --                    | --    |
| Ca4_P4_36487202  | Ca4                                     | 36487202                      | CA/CAA                                                        | TCCTCCATTGTTCCCT<br>AAGAA | CGTCCCAGACCATCTT<br>TTGT  | 59.9                             | 947                                           | DRR                                               | Ca_14828                            | --                    | --    |
| Ca4_P4_36565480  | Ca4                                     | 36565480                      | T/TAAACCCC                                                    | CACGCTTTCTCCCAA<br>ACAT   | GGCACTGAGATCAACA<br>TGAGG | 60.1                             | 603                                           | DRR                                               | Ca_14822                            | --                    | --    |
| Ca4_P4_36566713  | Ca4                                     | 36566713                      | TAAAAA/TAAAAA                                                 | TGATTTATAATGCCAC<br>CAAAA | GAGATGCAGAAAGGG<br>ATGA   | 59.2                             | 686                                           | DRR                                               | Ca_14822                            | --                    | --    |
| Ca4_P4_36601135  | Ca4                                     | 36601135                      | ATT/ATTT                                                      | ATTGATCCCCATTGTT<br>GGA   | TGAAGTGGAATTGGG<br>GTAG   | 60.0                             | 341                                           | DRR                                               | Ca_14819                            | --                    | MYB   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                                       |                              |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_36602493  | Ca4                                     | 36602493                      | TTA/TTAATA                                                            | CGGTTTCAACGTTGTT<br>GTTG     | GCCTTTTATGCTGATT<br>TCTTTG | 60.0                             | 866                                           | DRR                                               | Ca_14819                            | --                    | MYB   |
| Ca4_P4_36638657  | Ca4                                     | 36638657                      | GAAAA/GAAAAA                                                          | CTGGGATTATGGGGTC<br>ATTG     | ATTCAGCTTAGTGGA<br>AGGC    | 60.0                             | 446                                           | DRR                                               | Ca_14816                            | H                     | --    |
| Ca4_P4_36928403  | Ca4                                     | 36928403                      | TAAAAAAAAA/TAAAAAAAAA                                                 | TTCAAAAATTGAAACA<br>ATACCCA  | TTGGAAAGCTTATTCTC<br>GCA   | 59.7                             | 548                                           | DRR                                               | Ca_14798                            | --                    | --    |
| Ca4_P4_37096660  | Ca4                                     | 37096660                      | ATTTTTTTTTTT/ATTTTTTTTT                                               | GCGACCAATTCTATGA<br>TGAATAAA | GGGAGTGGTGATTTC<br>TTTTTC  | 59.4                             | 504                                           | DRR                                               | Ca_14791                            | --                    | B3    |
| Ca4_P4_37155367  | Ca4                                     | 37155367                      | ACCCC/ACCCCC                                                          | TGGTCTATCGTACGGT<br>GACATAC  | ATGTAAGAGTTGGAAC<br>GCCG   | 58.9                             | 634                                           | DRR                                               | Ca_15155                            | G                     | --    |
| Ca4_P4_3716263   | Ca4                                     | 3716263                       | TTAATAATAATAATAATAATAAT<br>AATAATAA/TTAATAATAATAATAA<br>ATAATAATAATAA | TGCTTTGGCCTGAAAG<br>AAGT     | GCACGATTTCTCCCTC<br>TCTG   | 60.0                             | 824                                           | DRR                                               | Ca_12170                            | R                     | --    |
| Ca4_P4_37174812  | Ca4                                     | 37174812                      | GAAAAA/GAAAAAA                                                        | AAATGGACCCCACATT<br>CAAA     | TCCCTCTCTCTCTGCC<br>ACAT   | 60.0                             | 532                                           | DRR                                               | Ca_15153                            | A                     | bHLH  |
| Ca4_P4_37187797  | Ca4                                     | 37187797                      | TT/TTCT                                                               | AAAAATGCATGGTGGC<br>ATCT     | TTTCATTAGTTTGCA<br>TCG     | 60.3                             | 567                                           | DRR                                               | Ca_15152                            | I                     | bHLH  |
| Ca4_P4_3734203   | Ca4                                     | 3734203                       | ATTTTTTTTTTTTTTT/ATTTTTTTTTTT<br>TT                                   | GAAAATGTTGACCGTA<br>TGCAA    | TGCTTTTAATTCTCAA<br>ACCCAA | 58.5                             | 183                                           | DRR                                               | Ca_12174                            | R                     | --    |
| Ca4_P4_37366698  | Ca4                                     | 37366698                      | AAA/AAACCAA                                                           | TTACCCTCTGTTGCTTT<br>GCC     | ACCATGGACACCGTTT<br>GTTT   | 60.2                             | 430                                           | DRR                                               | Ca_15139                            | R                     | NF-YA |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                  |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_37367041  | Ca4                                     | 37367041                      | TC/T                                                             | CCACCTTTGTCATTGC<br>TTCA | GATCAACACCTTCGAC<br>CGTT  | 59.7                             | 520                                           | DRR                                               | Ca_15140                            | S                     | --  |
| Ca4_P4_37367413  | Ca4                                     | 37367413                      | TCCC/TCC                                                         | CCACCTTTGTCATTGC<br>TTCA | GATCAACACCTTCGAC<br>CGTT  | 59.7                             | 520                                           | DRR                                               | Ca_15140                            | S                     | --  |
| Ca4_P4_373755    | Ca4                                     | 373755                        | AATATATATATATATATATATATATATATATAT/AAATATATATATATATATATATATATATAT | ATTATGGGGCAACATG<br>GAAA | GAACTCGATTGGATT<br>CGGA   | 60.0                             | 227                                           | DRR                                               | Ca_07670                            | --                    | --  |
| Ca4_P4_37385994  | Ca4                                     | 37385994                      | TTACTA/TTA                                                       | TGTGCTTGCATAGTGC<br>ATTG | TGAATAATTCCTGCTC<br>CGC   | 59.5                             | 221                                           | DRR                                               | Ca_15138                            | T                     | HSF |
| Ca4_P4_37396824  | Ca4                                     | 37396824                      | TATTAATAATTAA/TATTAATAATAAA<br>TTAA                              | TGTCATCAAAACGGAT<br>CCAA | TACATTGCACCCACCAT<br>GAC  | 59.9                             | 222                                           | DRR                                               | Ca_15137                            | R                     | MYB |
| Ca4_P4_37397137  | Ca4                                     | 37397137                      | TA/T                                                             | CGGATCCAAAATGTTA<br>ACGG | TCCACCATTGGTTCCT<br>CATT  | 60.2                             | 884                                           | DRR                                               | Ca_15137                            | R                     | MYB |
| Ca4_P4_37408226  | Ca4                                     | 37408226                      | TTTAAG/T                                                         | CAGAGCCAGTGTCTAT<br>GCCA | AGCCAAAGCTGTCTCT<br>TGAA  | 60.0                             | 534                                           | DRR                                               | Ca_15136                            | --                    | --  |
| Ca4_P4_37544414  | Ca4                                     | 37544414                      | TG/TGG                                                           | AAGAAATGTTGATGGA<br>GGCG | TAATGTGTGCTCCATTC<br>CCA  | 60.1                             | 296                                           | DRR                                               | Ca_15126                            | --                    | --  |
| Ca4_P4_37615197  | Ca4                                     | 37615197                      | T/TAG                                                            | TATTGCACTCCAGCAA<br>CAGG | AACCTGAGCCAATCATT<br>TCA  | 59.9                             | 655                                           | DRR                                               | Ca_15120                            | --                    | --  |
| Ca4_P4_37648089  | Ca4                                     | 37648089                      | CA/CATA                                                          | GCTCATGCAATGCTA<br>GCTG  | ACCCGTGCAAAACACAT<br>AACA | 59.7                             | 617                                           | DRR                                               | Ca_15116                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_37691102  | Ca4                                     | 37691102                      | ATACAATTACAA/ATACAA                                           | ATGCCCAAAAACAAA<br>GCAA   | ATGAACTGCGATGTG<br>ACAA     | 60.5                             | 604                                           | DRR                                               | Ca_15112                            | --                    | --  |
| Ca4_P4_37701400  | Ca4                                     | 37701400                      | ATTTTTTTTT/ATTTTTTTTTT                                        | TGAACACCGCATTAAAT<br>GGA  | GGGTTTTGTTCGAAG<br>ATTTTG   | 59.9                             | 262                                           | DRR                                               | Ca_15111                            | F                     | --  |
| Ca4_P4_37705943  | Ca4                                     | 37705943                      | GA/GATAA                                                      | GCCGGGATGTTCTTT<br>TGTA   | TTTACTGAATGCCATGC<br>TGC    | 59.9                             | 679                                           | DRR                                               | Ca_15110                            | C                     | MYB |
| Ca4_P4_37706091  | Ca4                                     | 37706091                      | TTCT/TT                                                       | GCCGGGATGTTCTTT<br>TGTA   | GAGGGGAGGCCTTCTC<br>ATAC    | 59.9                             | 818                                           | DRR                                               | Ca_15110                            | C                     | MYB |
| Ca4_P4_37706158  | Ca4                                     | 37706158                      | G/GA                                                          | GCCGGGATGTTCTTT<br>TGTA   | GAGGGGAGGCCTTCTC<br>ATAC    | 59.9                             | 818                                           | DRR                                               | Ca_15110                            | C                     | MYB |
| Ca4_P4_37744026  | Ca4                                     | 37744026                      | ATAGAAAATTTATTTA/ATA                                          | TCGATTCTCTTGTTG<br>TGGA   | ACTTATGTTGCGGTTG<br>GAGG    | 59.2                             | 698                                           | DRR                                               | Ca_15105                            | --                    | --  |
| Ca4_P4_37980075  | Ca4                                     | 37980075                      | TCC/TC                                                        | AGGGAGAGGGATAAG<br>GCGTA  | TTGTGGCGACATAGCA<br>CAAT    | 60.1                             | 588                                           | DRR                                               | Ca_13148                            | --                    | --  |
| Ca4_P4_37981676  | Ca4                                     | 37981676                      | AATATATATATATATA/AATATATA<br>TATATATATATA                     | AAATGGCAACTTCCCA<br>CAAG  | GGCATTTCGAACTTGG<br>ACTT    | 60.0                             | 489                                           | DRR                                               | Ca_13148                            | --                    | --  |
| Ca4_P4_38018994  | Ca4                                     | 38018994                      | T/TG                                                          | TGGGCTAAAGCATCTC<br>CATC  | AATCGGCATTGGATT<br>TTG      | 60.2                             | 998                                           | DRR                                               | Ca_13143                            | E                     | --  |
| Ca4_P4_38026240  | Ca4                                     | 38026240                      | CTTTTTT/CTTTT                                                 | GGATTCTGAAGTCGGAA<br>CAAA | CAATGTGTTTTCACTCC<br>ATTTTT | 60.1                             | 277                                           | DRR                                               | Ca_13142                            | O                     | ERF |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                            | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                                                                                                          |                           |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca4_P4_38035645  | Ca4                                     | 38035645                      | CTTA/CTTATTA                                                                                                                                             | TTCTTGCCAAGCTTTC<br>ACTT  | TCCACCAAGGAAGAA<br>AATG       | 60.0                             | 652                                           | DRR                                               | Ca_13141                            | --                    | MYB_related |
| Ca4_P4_38051216  | Ca4                                     | 38051216                      | AT/ATGT                                                                                                                                                  | GGAAATTAATGGTGC<br>CCCT   | TTTCTTCTAACCACATT<br>TTTCAACC | 60.0                             | 807                                           | DRR                                               | Ca_13140                            | P                     | --          |
| Ca4_P4_38051360  | Ca4                                     | 38051360                      | GAAAA/GAAAAAA                                                                                                                                            | GGAAATTAATGGTGC<br>CCCT   | TTTCTTCTAACCACATT<br>TTTCAACC | 60.0                             | 807                                           | DRR                                               | Ca_13140                            | P                     | --          |
| Ca4_P4_38175024  | Ca4                                     | 38175024                      | CTATTATTATTATTATTATTATTA<br>TTACTATTATTATTATTGTTATTATTA<br>TTATTATTATTATTAT/CTATTATTAT<br>TATTATTATTATTACTATTATTAT<br>TATTGTTATTATTATTATTATTATTAT<br>TAT | GTGGACAACATATCCG<br>GACC  | AGGCTAGGGTGAGACA<br>GCAA      | 60.1                             | 558                                           | DRR                                               | Ca_13136                            | --                    | --          |
| Ca4_P4_38367094  | Ca4                                     | 38367094                      | T/TAGATTGGAA                                                                                                                                             | TCGTTTAGCGGTGAAA<br>CTCA  | CAAGCTCTTGCCATGT<br>TTGA      | 59.5                             | 158                                           | DRR                                               | Ca_13120                            | S                     | --          |
| Ca4_P4_38414507  | Ca4                                     | 38414507                      | CA/CAAAA                                                                                                                                                 | GGTTGAACGTCTTGTC<br>TCGAA | TGATCAACTTCATGGC<br>CAAA      | 60.3                             | 407                                           | DRR                                               | Ca_13116                            | R                     | --          |
| Ca4_P4_38446174  | Ca4                                     | 38446174                      | AATTAT/AATTATTAT                                                                                                                                         | CTCCTTGATTCACGTG<br>GGTT  | TTAAAAACACTGTTGGC<br>GTGA     | 60.0                             | 230                                           | DRR                                               | Ca_13113                            | O                     | --          |
| Ca4_P4_38446443  | Ca4                                     | 38446443                      | TAA/TAAGAA                                                                                                                                               | CTCCTTGATTCACGTG<br>GGTT  | TGATCGAAATTTTATGG<br>GGA      | 60.0                             | 484                                           | DRR                                               | Ca_13113                            | O                     | --          |
| Ca4_P4_38536722  | Ca4                                     | 38536722                      | TTATATATAT/TTATATATATAT                                                                                                                                  | GAAGGCGTGTTCACCT<br>TGAT  | TTCCAATCCATCCTCAC<br>ACA      | 60.1                             | 260                                           | DRR                                               | Ca_13110                            | G                     | --          |
| Ca4_P4_38537057  | Ca4                                     | 38537057                      | TTTAATT/TTT                                                                                                                                              | TGTGTGAGGATGGATT<br>GGAA  | TCTAGCGGTATCAGCT<br>TGGG      | 59.9                             | 595                                           | DRR                                               | Ca_13110                            | G                     | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca4_P4_38537586  | Ca4                                     | 38537586                      | ACGT/ACGTCGT                                                  | TTCGCAACATGGGAAC<br>ATAA  | TTGGTTTGAATTGG<br>AAGG       | 59.9                             | 257                                           | DRR                                               | Ca_13110                            | G                     | --          |
| Ca4_P4_38547921  | Ca4                                     | 38547921                      | CATT/CATTAAATT                                                | TCTGAAAAGAGGGGGT<br>GAAA  | CCGGAAAAGCTGACCA<br>AATA     | 59.6                             | 326                                           | DRR                                               | Ca_13108                            | T                     | bHLH        |
| Ca4_P4_38620126  | Ca4                                     | 38620126                      | TAAAAATAAAATAAAAA/TAAAAA                                      | CCCACCCAATCACCAT<br>TTAC  | CCCCATTGCTTGTTGA<br>CTT      | 59.9                             | 434                                           | DRR                                               | Ca_13103                            | L                     | --          |
| Ca4_P4_38620449  | Ca4                                     | 38620449                      | CCTTCTT/CCTT                                                  | AAGTCAAACAAGCAAT<br>GGGG  | GTTGCTGCCCTTGAGA<br>CTTC     | 60.0                             | 461                                           | DRR                                               | Ca_13103                            | L                     | --          |
| Ca4_P4_38816584  | Ca4                                     | 38816584                      | AATTTATATTTA/AATTTATATTTATA<br>TTTA                           | ATGCCTTTACATGCAC<br>AAAAT | GCAAATATTGTCTGCC<br>AAAAGTG  | 57.2                             | 724                                           | DRR                                               | Ca_13093                            | K                     | NF-YB       |
| Ca4_P4_38837626  | Ca4                                     | 38837626                      | CTTTTT/CTTTT                                                  | TCATTGGATCGCGGTT<br>TT    | TGAAGGATTTAGGAGC<br>TGACAA   | 60.0                             | 814                                           | DRR                                               | Ca_13090                            | --                    | --          |
| Ca4_P4_38891821  | Ca4                                     | 38891821                      | CA/CAA                                                        | TTATTGCTTTTGCATGG<br>TGA  | TTGGACAAATTAGCCTA<br>TGAAACA | 57.8                             | 516                                           | DRR                                               | Ca_13087                            | --                    | ERF         |
| Ca4_P4_38959403  | Ca4                                     | 38959403                      | CGTGT/CGT                                                     | TCTGAAACGGAGGAAG<br>TAGCA | ATCCTTTGGTTCCCGA<br>AATC     | 60.0                             | 879                                           | DRR                                               | Ca_13083                            | O                     | MYB_related |
| Ca4_P4_38963393  | Ca4                                     | 38963393                      | AT/A                                                          | TGGTGCGTATTTGGAA<br>TTGA  | TGATTGACGACCAACT<br>AGCAA    | 59.9                             | 513                                           | DRR                                               | Ca_13082                            | O                     | MYB_related |
| Ca4_P4_38963586  | Ca4                                     | 38963586                      | TA/TAA                                                        | GGGGAGAGACAAATGC<br>GTTA  | TGTCTATTTGCGCCGT<br>ATGTT    | 60.1                             | 770                                           | DRR                                               | Ca_13082                            | O                     | MYB_related |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                          | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                                        |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_38983278  | Ca4                                     | 38983278                      | TAAAA/TAAA                                                                             | GAGGTGGGGAAGTA<br>GCCTC  | TTGTTGGTGTGTCGTG<br>GTTT  | 60.1                             | 814                                           | DRR                                               | Ca_13081                            | H                     | --   |
| Ca4_P4_38993838  | Ca4                                     | 38993838                      | AAAAATTC/AAAAATTCCTACATAC<br>GAAAAATTC                                                 | CCAAAAATTCGAAAC<br>TCGAC | AAGACCGGAAAAGGGT<br>ATGC  | 60.0                             | 643                                           | DRR                                               | Ca_13080                            | --                    | bHLH |
| Ca4_P4_39038460  | Ca4                                     | 39038460                      | ACTTGCTTG/ACTTG                                                                        | CCGGTCACATTCAATA<br>GCCT | ATTGCGTTGTTCTTCC<br>AGG   | 60.0                             | 411                                           | DRR                                               | Ca_13078                            | A                     | --   |
| Ca4_P4_39051123  | Ca4                                     | 39051123                      | T/TC                                                                                   | TGTTTGCAATTAGCGG<br>TTCA | CCCAAAGCAGAAAACC<br>AAAA  | 60.3                             | 285                                           | DRR                                               | Ca_13076                            | --                    | --   |
| Ca4_P4_40348298  | Ca4                                     | 40348298                      | AATATATATATATATATATATATATAT<br>ATATATATAAATATATATATATATATAT<br>ATATATATATATATATATATATA | CCATCCTTCGAATTTG<br>GCTA | TGGTTAAAGGCCAGGA<br>TTTC  | 60.0                             | 668                                           | DRR                                               | Ca_14889                            | PET                   | NAC  |
| Ca4_P4_40354186  | Ca4                                     | 40354186                      | TAAAAAAAA/TAAAAAAAA                                                                    | TAGCCTAAACCCGATG<br>GATG | ATTGTTCCATCACTTGC<br>GTG  | 59.9                             | 424                                           | DRR                                               | Ca_14888                            | J                     | --   |
| Ca4_P4_40483531  | Ca4                                     | 40483531                      | ATT/ATTAGCGGTCTT                                                                       | TCCACATTGGTAGTT<br>CCGT  | AGCTGAACCCCTTGCTG<br>TGAT | 60.2                             | 500                                           | DRR                                               | Ca_14877                            | I                     | --   |
| Ca4_P4_40534591  | Ca4                                     | 40534591                      | TGG/TGGG                                                                               | TAGGAGACTGCTCCG<br>CAAT  | GGTGCTCTTGACAGCA<br>CAAA  | 60.0                             | 109                                           | DRR                                               | Ca_14873                            | --                    | --   |
| Ca4_P4_40559341  | Ca4                                     | 40559341                      | TAA/TA                                                                                 | TCAGGCCATTAGGGT<br>TCTG  | ATTGAATGCGGTCTCA<br>GTGC  | 60.1                             | 410                                           | DRR                                               | Ca_14870                            | --                    | --   |
| Ca4_P4_40588010  | Ca4                                     | 40588010                      | TAAA/TAAAA                                                                             | CTTGACACAATGCGA<br>TCAT  | GGTCCGAAACTGACAA<br>AAGC  | 60.7                             | 641                                           | DRR                                               | Ca_14868                            | K                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                               |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca4_P4_40588106  | Ca4                                     | 40588106                      | ATTTTT/ATTTTTTT                                               | CTTGACACAATGCGA<br>TCAT       | GGTCCGAACTGACAA<br>AAGC  | 60.7                             | 641                                           | DRR                                               | Ca_14868                            | K                     | --      |
| Ca4_P4_40647015  | Ca4                                     | 40647015                      | GTTTTTTT/GTTTTTTTT                                            | CCAAGCATCATTCCAA<br>ATCC      | CACCACAAGCCAGAGC<br>AATA | 60.3                             | 553                                           | DRR                                               | Ca_14865                            | --                    | --      |
| Ca4_P4_40720882  | Ca4                                     | 40720882                      | CTTTTT/CTTTTTTT                                               | TCATCAATGGGAACCT<br>CACA      | TGATGACTGTCAAAGA<br>GCCG | 59.9                             | 143                                           | DRR                                               | Ca_23910                            | S                     | C2H2    |
| Ca4_P4_40738323  | Ca4                                     | 40738323                      | TAAAAAAAA/TAAAAAAAA                                           | TTTACCGAGCCAATTT<br>CAG       | TCAAGGTCAGCAGCAT<br>GGTA | 60.1                             | 920                                           | DRR                                               | Ca_23908                            | R                     | NAC     |
| Ca4_P4_40799742  | Ca4                                     | 40799742                      | TCCCCC/TCCCCC                                                 | ACAAACCCATTGGTG<br>ACAT       | TGGCTTGTAAGGCTGT<br>GTTG | 60.0                             | 740                                           | DRR                                               | Ca_23902                            | R                     | --      |
| Ca4_P4_40811635  | Ca4                                     | 40811635                      | GAAAA/GAA                                                     | TTACCACCAAGGTCAG<br>CTCC      | CGGGAAGATCATTAC<br>GAAG  | 60.1                             | 704                                           | DRR                                               | Ca_23901                            | R                     | MYB     |
| Ca4_P4_40853669  | Ca4                                     | 40853669                      | AA/AAGA                                                       | TTCAATTTTATGGATTT<br>TGTTTGAA | CGTGGGTACTTTCTGG<br>GTGT | 58.9                             | 411                                           | DRR                                               | Ca_23897                            | --                    | --      |
| Ca4_P4_40854093  | Ca4                                     | 40854093                      | TAAAAA/TAAAAA                                                 | ACACCCAGAAAGTACC<br>CACG      | TGAAATGCATTCTGCA<br>CACA | 59.9                             | 610                                           | DRR                                               | Ca_23897                            | --                    | --      |
| Ca4_P4_40893508  | Ca4                                     | 40893508                      | AG/A                                                          | TGAACCTCGGCTAGGAG<br>GAAA     | CGCAAGTGTGGACAA<br>TGAT  | 59.9                             | 703                                           | DRR                                               | Ca_11020                            | R                     | G2-like |
| Ca4_P4_40924286  | Ca4                                     | 40924286                      | ACAATATG/ACAATATGTAGCTTCAA<br>TATG                            | GTGATCTACGTGGTGC<br>CCTT      | ACCCAAAATGAGGTGG<br>TTCA | 60.0                             | 548                                           | DRR                                               | Ca_11015                            | --                    | bZIP    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_40940117  | Ca4                                     | 40940117                      | TAAAAAAAAAAAAA/TAAAAAAAAA                                     | TCCAAGTTCTCATCAG<br>GCAG  | GATCATGTGGAGCGGA<br>AGAT   | 60.0                             | 635                                           | DRR                                               | Ca_11014                            | O                     | MYB  |
| Ca4_P4_40948599  | Ca4                                     | 40948599                      | CAAAAAAAAA/CAAAAAAAAA                                         | AGGGTTGGGTTTGAGA<br>GAAA  | GGGAAGGGAAAAATGG<br>ATGT   | 58.6                             | 702                                           | DRR                                               | Ca_11013                            | --                    | --   |
| Ca4_P4_40996538  | Ca4                                     | 40996538                      | GTTT/GTT                                                      | CGGTGTTAAAAATTGG<br>GGTG  | AAACGTGGAGGTGATT<br>TTGC   | 60.1                             | 445                                           | DRR                                               | Ca_11010                            | --                    | --   |
| Ca4_P4_41010880  | Ca4                                     | 41010880                      | CATTATATTATATT/CATTATATT                                      | CTTCTCCCTGTTAGT<br>CCCC   | AGGTCAAACCGTCAAA<br>GTGC   | 59.9                             | 730                                           | DRR                                               | Ca_11009                            | --                    | bHLH |
| Ca4_P4_41012180  | Ca4                                     | 41012180                      | TAAAAA/TAAAA                                                  | GCTTGATGGGAGAGCA<br>AAAA  | TTTGGCAGCACTTCTAT<br>TG TG | 60.3                             | 738                                           | DRR                                               | Ca_11009                            | --                    | bHLH |
| Ca4_P4_41012767  | Ca4                                     | 41012767                      | AAA/AAACAA                                                    | TTCCCAAATGGGTTTTT<br>CTT  | GGAGGAGGAGGAGGA<br>TCAAC   | 58.4                             | 540                                           | DRR                                               | Ca_11009                            | --                    | bHLH |
| Ca4_P4_4103051   | Ca4                                     | 4103051                       | CA/CAAA                                                       | AACATGGCAATTGATT<br>GAAGG | AGTCCAACCTCATTGC<br>CTGC   | 59.8                             | 496                                           | DRR                                               | Ca_03844                            | --                    | --   |
| Ca4_P4_4143078   | Ca4                                     | 4143078                       | CTT/CTTCTGTT                                                  | ATCCATCCAATGATTCC<br>CAA  | TGCTGATCTGACTTTG<br>CCAC   | 60.0                             | 746                                           | DRR                                               | Ca_03842                            | --                    | --   |
| Ca4_P4_41808321  | Ca4                                     | 41808321                      | ATTT/ATTTT                                                    | TGCAAACTAGCCGAG<br>TGAA   | GGGTCAGTGCCATTAT<br>TGCT   | 59.6                             | 908                                           | DRR                                               | Ca_10934                            | QR                    | B3   |
| Ca4_P4_41808826  | Ca4                                     | 41808826                      | CAAAAA/CAAAAA                                                 | TCCAACCAAATTGTGC<br>AAGA  | AAGGAGTTGAAAGTGT<br>CATCCA | 60.1                             | 153                                           | DRR                                               | Ca_10934                            | QR                    | B3   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                   |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca4_P4_4196538   | Ca4                                     | 4196538                       | ATTTT/ATTT                                                                        | ATTGGCCGGAAATTGT<br>ACTG     | TAACCCAAGGCCATAT<br>CCTG   | 59.8                             | 841                                           | DRR                                               | Ca_03838                            | R                     | --       |
| Ca4_P4_4196827   | Ca4                                     | 4196827                       | AT/A                                                                              | TGCACGTGATCACAAA<br>ACCT     | AATGTGTGGGCACTGA<br>TTGA   | 60.2                             | 349                                           | DRR                                               | Ca_03838                            | R                     | --       |
| Ca4_P4_41984896  | Ca4                                     | 41984896                      | ACTCT/ACTCTCT                                                                     | TCCGCTTTCTTTTGGG<br>TATG     | AATCCTCACACCCTAC<br>GTGC   | 60.1                             | 845                                           | DRR                                               | Ca_10923                            | B                     | NF-YC    |
| Ca4_P4_42118929  | Ca4                                     | 42118929                      | GTAT/GTATAT                                                                       | GCAGAAGTTGGCTTCT<br>TTGG     | TCACGGCATAAGGTTT<br>GTCA   | 60.0                             | 677                                           | DRR                                               | Ca_10911                            | R                     | Nin-like |
| Ca4_P4_42159815  | Ca4                                     | 42159815                      | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATAT                             | CGGGCATCGATTTGTC<br>TATT     | GCAAATTCAAAATCTA<br>AAAGCC | 59.9                             | 413                                           | DRR                                               | Ca_10909                            | L                     | --       |
| Ca4_P4_4242821   | Ca4                                     | 4242821                       | A/ATCTG                                                                           | TCCGTTTCAATCATCGT<br>TCA     | CACAAATAAGCACCTC<br>CCAAA  | 60.0                             | 765                                           | DRR                                               | Ca_03833                            | I                     | --       |
| Ca4_P4_42772443  | Ca4                                     | 42772443                      | TATAATAATAATAATAATAATAA<br>TAATAATAATAATA/TATAATAATAAT<br>AATAATAATAATAATAATAATAA | CGAGCAGTGCACCAAT<br>TCTA     | GCCAAGCCAACCACTA<br>TCAT   | 60.0                             | 753                                           | DRR                                               | Ca_10886                            | --                    | SRS      |
| Ca4_P4_4324103   | Ca4                                     | 4324103                       | TTTTAAATTTAAATTTAAAT/TTT<br>TAAATTTAAAT                                           | CCAATGGCATCACTCT<br>TTCA     | ATCGGATCCCATTITGA<br>GGT   | 59.6                             | 631                                           | DRR                                               | Ca_03827                            | K                     | --       |
| Ca4_P4_43320740  | Ca4                                     | 43320740                      | TCA/T                                                                             | CCTGGAATGGTTGTTA<br>CGCT     | TCCCTTGTTGGGTTTC<br>AAAG   | 60.0                             | 279                                           | DRR                                               | Ca_23683                            | D                     | M-type   |
| Ca4_P4_43323630  | Ca4                                     | 43323630                      | TATAA/TA                                                                          | GCAACAACATTTTGTCT<br>TGTGTGC | CAATGATTGTCACGAA<br>AGAGTT | 61.0                             | 326                                           | DRR                                               | Ca_23684                            | --                    | bHLH     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |           |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----------|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs       |
| Ca4_P4_43346458  | Ca4                                     | 43346458                      | CA/CAAACTATAA                                                 | GGGCAAGAGTCCCCAT<br>TATT | CTACATTGCGCCTCT<br>GTCA     | 60.2                             | 657                                           | DRR                                               | Ca_23685                            | --                    | S1Fa-like |
| Ca4_P4_43450204  | Ca4                                     | 43450204                      | A/AT                                                          | TTCGTGTCAGCAAGAC<br>CAAG | AGGGAGATTCTTGGAG<br>AGAGC   | 60.0                             | 194                                           | DRR                                               | Ca_23690                            | --                    | --        |
| Ca4_P4_44522624  | Ca4                                     | 44522624                      | GAAAAAA/GAAAAAAA                                              | GAAGTTGCTTGCTCCG<br>ATTC | CCCTAGCAAGTGCTAA<br>CCCA    | 60.0                             | 675                                           | DRR                                               | Ca_09124                            | --                    | ERF       |
| Ca4_P4_44522868  | Ca4                                     | 44522868                      | A/AG                                                          | ACAATCCCTTCGTTCC<br>CTCT | CCCTAGCAAGTGCTAA<br>CCCA    | 59.9                             | 516                                           | DRR                                               | Ca_09124                            | --                    | ERF       |
| Ca4_P4_44532358  | Ca4                                     | 44532358                      | TAAAAAAA/TAAAAAAA                                             | CTTCATGGCTGATGAG<br>TGGA | CCGATGAACATTCACC<br>GATT    | 59.8                             | 143                                           | DRR                                               | Ca_09125                            | L                     | --        |
| Ca4_P4_44568994  | Ca4                                     | 44568994                      | ATTACTCTCA/ATTACTCTCACGTTT<br>TTTTTTACTCTCA                   | CGGAATTGGGATGAGA<br>AAGA | AGACTGCAGTTCCTGG<br>GCTA    | 60.0                             | 411                                           | DRR                                               | Ca_09127                            | P                     | --        |
| Ca4_P4_4458327   | Ca4                                     | 4458327                       | CAAAAAAAAA/CAAAAAAAAA                                         | GGAGTGATCGGATGTG<br>TGTG | AATAGTGGGGAGGGAA<br>CCAG    | 60.0                             | 709                                           | DRR                                               | Ca_03811                            | --                    | --        |
| Ca4_P4_4459373   | Ca4                                     | 4459373                       | TAA/TA                                                        | AGCGAAGGCCTCTGTA<br>GTCA | GGCCAAGCATTGTCGT<br>TATT    | 60.2                             | 439                                           | DRR                                               | Ca_03811                            | --                    | --        |
| Ca4_P4_44629912  | Ca4                                     | 44629912                      | A/ACGTTAAG                                                    | TTGGATTGGGACTGTC<br>CTTC | ATCACAGCCACATAGA<br>GGGG    | 59.9                             | 613                                           | DRR                                               | Ca_09133                            | --                    | WRKY      |
| Ca4_P4_44638085  | Ca4                                     | 44638085                      | TC/T                                                          | CAATGATGGCACACAT<br>CACA | TTCTTGATCATTGTTTA<br>TGACGC | 60.0                             | 377                                           | DRR                                               | Ca_09135                            | R                     | MYB       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')         | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |           |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----------|
|                  |                                         |                               |                                                               |                                 |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs       |
| Ca4_P4_44654366  | Ca4                                     | 44654366                      | G/GGA                                                         | CCCGTACACACCATGT<br>ATTCC       | ATGGTGCTGGCTTTGG<br>TTAT        | 60.0                             | 813                                           | DRR                                               | Ca_09137                            | R                     | NF-YA     |
| Ca4_P4_4465836   | Ca4                                     | 4465836                       | CAAAAAAAAA/CAAAAAAAAAA                                        | TAGATTTTCGAGGAGGG<br>AGGG       | GTCATACGTGTACAT<br>CGCC         | 60.5                             | 491                                           | DRR                                               | Ca_03810                            | GOT                   | --        |
| Ca4_P4_44670060  | Ca4                                     | 44670060                      | AC/ACC                                                        | TGCCTAAGACCCCAA<br>TCAA         | GCCACTTCTGGAATCA<br>CCAT        | 60.4                             | 682                                           | DRR                                               | Ca_09140                            | E                     | --        |
| Ca4_P4_4480380   | Ca4                                     | 4480380                       | TC/TCC                                                        | TGGTCACATGGAGGAT<br>GAAA        | TTTAATACCTCGTATTT<br>CCTATCAAGA | 59.9                             | 609                                           | DRR                                               | Ca_03809                            | --                    | S1Fa-like |
| Ca4_P4_4480858   | Ca4                                     | 4480858                       | AATGAAAGT/A                                                   | TTGGTTAAACAAAATTG<br>ACTTACTTGA | GGCCTTGAGAAAATTT<br>GATTTC      | 59.5                             | 574                                           | DRR                                               | Ca_03809                            | --                    | S1Fa-like |
| Ca4_P4_4481135   | Ca4                                     | 4481135                       | TAA/TAAA                                                      | TGAAATCAAAATTTCTC<br>AAGGC      | AAACGACATTACGTTAT<br>TTCTTCATT  | 58.4                             | 120                                           | DRR                                               | Ca_03809                            | --                    | S1Fa-like |
| Ca4_P4_4481876   | Ca4                                     | 4481876                       | A/ATAT                                                        | GGAGGTAGAAGAGGC<br>GGAAC        | AGCAAACGGAAAGAGC<br>AATC        | 60.2                             | 520                                           | DRR                                               | Ca_03809                            | --                    | S1Fa-like |
| Ca4_P4_44830692  | Ca4                                     | 44830692                      | TAGAAGAAG/TAGAAG                                              | AAGACGCCAAAGTTCTG<br>AAGA       | CCACACTGCTGAAGGT<br>CAAA        | 60.0                             | 311                                           | DRR                                               | Ca_09148                            | K                     | --        |
| Ca4_P4_44856654  | Ca4                                     | 44856654                      | GTGTTACAT/GTGTTACATCTCTGTT<br>ACAT                            | CGTTGTGGCCATAATG<br>TTGA        | CTGTCTCTGAAAAGAC<br>CGCC        | 60.4                             | 491                                           | DRR                                               | Ca_09150                            | DT                    | --        |
| Ca4_P4_44856846  | Ca4                                     | 44856846                      | AT/ATGTTT                                                     | TCTAGCAGCTCCTTCC<br>TTGC        | TCATCTCAATTTGGTTG<br>GCA        | 59.9                             | 616                                           | DRR                                               | Ca_09150                            | DT                    | --        |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_4487000   | Ca4                                     | 4487000                       | TAAA/TAAAA                                                    | GGCCAAATGAAGGACT<br>CAAA | GAATCGTTCGGGAGAG<br>TCTG  | 60.1                             | 672                                           | DRR                                               | Ca_03808                            | --                    | --   |
| Ca4_P4_4487086   | Ca4                                     | 4487086                       | AT/ACAGAAATATATT                                              | GGCCAAATGAAGGACT<br>CAAA | CGTACGACGTCTTTTCG<br>TCAA | 60.1                             | 932                                           | DRR                                               | Ca_03808                            | --                    | --   |
| Ca4_P4_4487144   | Ca4                                     | 4487144                       | CAAAAA/CAAAAAA                                                | GAAGTTCAACTGGCAC<br>CACA | CGTACGACGTCTTTTCG<br>TCAA | 59.7                             | 647                                           | DRR                                               | Ca_03808                            | --                    | --   |
| Ca4_P4_4487412   | Ca4                                     | 4487412                       | AT/ATTAATAAAGT                                                | TCAGACTCTCCGAAC<br>GATT  | CGTACGACGTCTTTTCG<br>TCAA | 59.8                             | 281                                           | DRR                                               | Ca_03808                            | --                    | --   |
| Ca4_P4_44901004  | Ca4                                     | 44901004                      | GT/GTGTAT                                                     | AGCTTCAAGTGGCTGA<br>AGGA | ATGAACACGGGCGTAT<br>CTTC  | 60.1                             | 527                                           | DRR                                               | Ca_09152                            | --                    | C2H2 |
| Ca4_P4_44902306  | Ca4                                     | 44902306                      | ATTTTT/ATTTTTTT                                               | TTGGGCAATTTTAAGC<br>CAAA | TTATTTGTGTGTTGCAG<br>CGTC | 60.4                             | 765                                           | DRR                                               | Ca_09152                            | --                    | C2H2 |
| Ca4_P4_44917117  | Ca4                                     | 44917117                      | A/ACAACAACAACAC                                               | TTCCACCTTCAATGCAA<br>CAA | TCAGGCACACATTTTTC<br>ACC  | 60.1                             | 235                                           | DRR                                               | Ca_09155                            | Q                     | --   |
| Ca4_P4_44917486  | Ca4                                     | 44917486                      | AATATATATATA/AATATATATATATA                                   | TTCCACCTTCAATGCAA<br>CAA | TTTGAATTGGTCCAA<br>GAGC   | 60.1                             | 899                                           | DRR                                               | Ca_09155                            | Q                     | --   |
| Ca4_P4_44944900  | Ca4                                     | 44944900                      | TAAAA/TAAA                                                    | GGGAAACAAATTCGTG<br>GAAA | ACATGCCAAATGCAAT<br>GTGT  | 59.8                             | 388                                           | DRR                                               | Ca_09157                            | G                     | --   |
| Ca4_P4_4500366   | Ca4                                     | 4500366                       | ATTTTTTTT/ATTTTTTTTTT                                         | CTCGAGTGCACTGTCG<br>TCAT | CGGCCAAGTCTTCATA<br>TCGT  | 60.1                             | 783                                           | DRR                                               | Ca_03807                            | --                    | FAR1 |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                       | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                                     |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca4_P4_4500439   | Ca4                                     | 4500439                       | AC/ACC                                                                              | CTCGAGTGCACGTGCTG<br>TCAT | CGGCCAAGTCTTCATA<br>TCGT  | 60.1                             | 783                                           | DRR                                               | Ca_03807                            | --                    | FAR1        |
| Ca4_P4_4501473   | Ca4                                     | 4501473                       | CT/CTT                                                                              | TGTACGGAGCCTCCAA<br>AAAT  | TGTCGGAAAACATTGG<br>TGAA  | 59.6                             | 576                                           | DRR                                               | Ca_03807                            | --                    | FAR1        |
| Ca4_P4_45024273  | Ca4                                     | 45024273                      | AATTATTATTATTATTATTATTAT<br>TATTATTATTATT/AATTATTATTATT<br>ATTATTATTATTATTATTATTATT | CATGCACCTTGGTGAC<br>AACT  | CGACACCTCCTTTTCC<br>AATTT | 59.6                             | 373                                           | DRR                                               | Ca_09165                            | D                     | bHLH        |
| Ca4_P4_45051417  | Ca4                                     | 45051417                      | TAAAAAAA/TAAAAAAA                                                                   | CGTTCGAAGGAAACAC<br>ACCT  | CATTTGGTACAGAGGC<br>ATGG  | 60.1                             | 795                                           | DRR                                               | Ca_09167                            | K                     | GATA        |
| Ca4_P4_45107861  | Ca4                                     | 45107861                      | CATAT/CAT                                                                           | TGTGAGGGTGGGAAAA<br>GAAC  | TGCTTGGCTCACTGTT<br>TCTG  | 59.9                             | 512                                           | DRR                                               | Ca_09170                            | --                    | --          |
| Ca4_P4_45114505  | Ca4                                     | 45114505                      | AT/ATT                                                                              | TGATTAATCTTTTTCGC<br>CCG  | AATGGTGCAAATGAAT<br>GCAA  | 60.0                             | 388                                           | DRR                                               | Ca_09171                            | --                    | MYB_related |
| Ca4_P4_45122277  | Ca4                                     | 45122277                      | TAA/TAAA                                                                            | GCGAGCGTATTGGTAT<br>TGGT  | ATGTGACAAATTGGGG<br>GAAA  | 60.0                             | 551                                           | DRR                                               | Ca_09172                            | T                     | --          |
| Ca4_P4_45122635  | Ca4                                     | 45122635                      | CG/C                                                                                | CCCCCAATTTGTCACA<br>TTCT  | GACCCTCTCTACACCC<br>CCTC  | 59.6                             | 379                                           | DRR                                               | Ca_09172                            | T                     | --          |
| Ca4_P4_45135433  | Ca4                                     | 45135433                      | GACACTAACACT/GACACT                                                                 | CATTCTGCGAGACAG<br>AAAA   | CATGCTGTGACTCGAA<br>AGGA  | 60.0                             | 661                                           | DRR                                               | Ca_09175                            | S                     | --          |
| Ca4_P4_45138231  | Ca4                                     | 45138231                      | CATTATATTATATTATATT/CATTATA<br>TTATATT                                              | ACCACACTCATGCAAC<br>GAAA  | AATAAATCGCAGGGCT<br>TG TG | 60.2                             | 654                                           | DRR                                               | Ca_09177                            | T                     | --          |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_45165137  | Ca4                                     | 45165137                      | A/AC                                                          | TTGTTCTTCTCCCCCT<br>TCT   | TTCAGCCCGCTAGCTA<br>TGAT    | 60.0                             | 669                                           | DRR                                               | Ca_09179                            | P                     | --   |
| Ca4_P4_45199986  | Ca4                                     | 45199986                      | TAAAA/TAAAA                                                   | TATGGGAATGAGGAGG<br>GTGA  | TGGGAGTTAGGAGCCA<br>GAGA    | 60.3                             | 199                                           | DRR                                               | Ca_09182                            | --                    | --   |
| Ca4_P4_45210841  | Ca4                                     | 45210841                      | CAAA/CA                                                       | TGGATCTTTTGTGTC<br>CCCT   | ATGCTAAGCCACCAAC<br>CAAC    | 59.4                             | 680                                           | DRR                                               | Ca_09183                            | O                     | --   |
| Ca4_P4_45211124  | Ca4                                     | 45211124                      | TAAAAAAAA/TAAAAAAAAA                                          | TCCAATCTAAATTATCC<br>CCCA | ATGCTAAGCCACCAAC<br>CAAC    | 58.3                             | 396                                           | DRR                                               | Ca_09183                            | O                     | --   |
| Ca4_P4_45221189  | Ca4                                     | 45221189                      | GTTTT/GTTTT                                                   | GCACTCAAAGAGCACC<br>ATCA  | CTGGCTCCGAAATCTA<br>TTGG    | 60.0                             | 505                                           | DRR                                               | Ca_09184                            | A                     | C2H2 |
| Ca4_P4_45222131  | Ca4                                     | 45222131                      | TA/TAA                                                        | CCACCTTGTTCCCACT<br>CCTA  | TCCAATGAATTTGGAG<br>AGCC    | 60.0                             | 334                                           | DRR                                               | Ca_09184                            | A                     | C2H2 |
| Ca4_P4_45226893  | Ca4                                     | 45226893                      | TTC/TTCGTC                                                    | ATTAGTTCCTGGCCGG<br>TCTC  | GGAGAGAGGACCCACA<br>AACA    | 60.5                             | 868                                           | DRR                                               | Ca_09185                            | S                     | --   |
| Ca4_P4_45245580  | Ca4                                     | 45245580                      | TAAA/TAA                                                      | TGCTTGTGCACAAGT<br>TTCC   | AAAAACGCAGTATCCAT<br>ACAAAA | 59.9                             | 617                                           | DRR                                               | Ca_09188                            | --                    | B3   |
| Ca4_P4_45245680  | Ca4                                     | 45245680                      | TAAAAAAAA/TAAAAA                                              | TGCTTGTGCACAAGT<br>TTCC   | AAAAACGCAGTATCCAT<br>ACAAAA | 59.9                             | 617                                           | DRR                                               | Ca_09188                            | --                    | B3   |
| Ca4_P4_45261134  | Ca4                                     | 45261134                      | ATTTTTTTTT/ATTTTTTTT                                          | TACTCTACCATGCCCA<br>AGGC  | CATAAAGCGGGTGAAG<br>GGTA    | 60.1                             | 479                                           | DRR                                               | Ca_09189                            | O                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_45262079  | Ca4                                     | 45262079                      | ACCCC/ACCC                                                    | TGCATAGGTACAAAA<br>GCCC  | TGAAAAATGGTGACCG<br>TTGA | 58.7                             | 292                                           | DRR                                               | Ca_09189                            | O                     | --  |
| Ca4_P4_45273886  | Ca4                                     | 45273886                      | CATGTGA/CA                                                    | ATGGAAGCATTGTCGG<br>TCTC | TGTGTGGATTGTCGTT<br>CGAG | 60.1                             | 617                                           | DRR                                               | Ca_09191                            | O                     | --  |
| Ca4_P4_45274571  | Ca4                                     | 45274571                      | T/TG                                                          | TCGAACGACAATCCAC<br>ACAT | CGTGGGGGAAATTTT<br>CTTT  | 60.0                             | 518                                           | DRR                                               | Ca_09191                            | O                     | --  |
| Ca4_P4_45274816  | Ca4                                     | 45274816                      | ATTTTTTTT/ATTTTTTTT                                           | TCGAACGACAATCCAC<br>ACAT | TTAACACTTGGAAGGG<br>CGAC | 60.0                             | 811                                           | DRR                                               | Ca_09191                            | O                     | --  |
| Ca4_P4_45274881  | Ca4                                     | 45274881                      | CTTT/CTT                                                      | AAAGAAAAATTTCCCC<br>ACG  | TTAACACTTGGAAGGG<br>CGAC | 60.2                             | 313                                           | DRR                                               | Ca_09191                            | O                     | --  |
| Ca4_P4_45322213  | Ca4                                     | 45322213                      | CTTT/CTTTT                                                    | TGGATACCGCTACTTG<br>GGAG | CACAAGGCAAGGGACA<br>ATTT | 60.1                             | 394                                           | DRR                                               | Ca_09197                            | --                    | --  |
| Ca4_P4_45322675  | Ca4                                     | 45322675                      | ATTTT/ATTTTTT                                                 | AAATTGTCCCTTGCCTT<br>GTG | CCAAGGCAATTCGTT<br>GTTT  | 60.0                             | 595                                           | DRR                                               | Ca_09197                            | --                    | --  |
| Ca4_P4_4533290   | Ca4                                     | 4533290                       | GAAAA/GAAAA                                                   | AAATGCCCGCTATGAG<br>TTTG | GGTGAAAGAGTACGA<br>GGGG  | 60.1                             | 360                                           | DRR                                               | Ca_03805                            | P                     | --  |
| Ca4_P4_45341287  | Ca4                                     | 45341287                      | CATAT/CAT                                                     | TGCTCAAATGGATTGT<br>TGTC | TCCTCCTCTTTGTTGT<br>CCG  | 60.1                             | 798                                           | DRR                                               | Ca_09199                            | F                     | --  |
| Ca4_P4_45341608  | Ca4                                     | 45341608                      | AAGAGAATCGGA/AAGAGAATCGGA<br>GAGAATCGGA                       | GCTGGACAAGTCTGCC<br>AAG  | CTAGTGTGCAGTGGTG<br>CCAT | 59.6                             | 874                                           | DRR                                               | Ca_09198                            | L                     | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_45377587  | Ca4                                     | 45377587                      | ATTTTTTTT/ATTTTTTTT                                           | CTCCATTGGTGGTGTC<br>CTTT  | GTCTGAGCGTTTGCAT<br>GGTA   | 59.8                             | 821                                           | DRR                                               | Ca_09201                            | --                    | --  |
| Ca4_P4_45377807  | Ca4                                     | 45377807                      | AC/A                                                          | TCCCATCATGTTTTGAT<br>AGCC | GTCTGAGCGTTTGCAT<br>GGTA   | 59.8                             | 603                                           | DRR                                               | Ca_09201                            | --                    | --  |
| Ca4_P4_4543916   | Ca4                                     | 4543916                       | TAAAAAAAAA/TAAAAAAAAA                                         | TAGGTCTTCCCTGGG<br>TG TG  | TTAGGCGTGCTTCCTT<br>CACT   | 60.0                             | 384                                           | DRR                                               | Ca_03804                            | --                    | --  |
| Ca4_P4_45513340  | Ca4                                     | 45513340                      | ATTTT/ATTT                                                    | TACCACGTTGAAGTC<br>CTGG   | TGTTTGAGTTGGTGTG<br>GTTC A | 60.9                             | 336                                           | DRR                                               | Ca_09211                            | E                     | --  |
| Ca4_P4_4567851   | Ca4                                     | 4567851                       | AAAAGTT/A                                                     | GTGGGGCATTACGATA<br>CCAC  | GGGGAAGCCATATCAC<br>ATCA   | 60.1                             | 636                                           | DRR                                               | Ca_03802                            | UZ                    | --  |
| Ca4_P4_4568058   | Ca4                                     | 4568058                       | ATTTGATTTT/ATTTGATTTTGTATT<br>T                               | GTGGGGCATTACGATA<br>CCAC  | GGGGAAGCCATATCAC<br>ATCA   | 60.1                             | 636                                           | DRR                                               | Ca_03802                            | UZ                    | --  |
| Ca4_P4_45690560  | Ca4                                     | 45690560                      | TAAAAAAAAAAAAAAAAA/TAAAAAAAAA<br>AAAA                         | CCAATCCCGCAAAATT<br>TCTA  | TAAACCAACCCCAAAAT<br>GAA   | 59.9                             | 701                                           | DRR                                               | Ca_18393                            | --                    | --  |
| Ca4_P4_45858707  | Ca4                                     | 45858707                      | AAATA/AA                                                      | ATGTTGGTCCAAGCAG<br>GAAG  | CGCAGTTTTATGGTGG<br>GTTT   | 60.1                             | 716                                           | DRR                                               | Ca_18375                            | R                     | --  |
| Ca4_P4_4591902   | Ca4                                     | 4591902                       | CA/CACAA                                                      | TCAGACCTGCGTGAT<br>ACTC   | TCTAATTGGCCGACAA<br>ATCC   | 60.0                             | 207                                           | DRR                                               | Ca_03798                            | --                    | --  |
| Ca4_P4_45931997  | Ca4                                     | 45931997                      | CT/CTATAAT                                                    | CCAATAATTAGGGCGG<br>TGTC  | GCTGGTTTGACTCTGG<br>GGTA   | 59.3                             | 574                                           | DRR                                               | Ca_18367                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca4_P4_4593540   | Ca4                                     | 4593540                       | CTAATTAATTAA/CTAATTAA                                         | TTGAGGAATGTAAGGA<br>TGTCCA | TTAATGGCGGCTACGT<br>TTTC | 59.4                             | 928                                           | DRR                                               | Ca_03798                            | --                    | --      |
| Ca4_P4_46057636  | Ca4                                     | 46057636                      | AC/ACGAAGATGATC                                               | CGCATCGGTAAACAAT<br>CTGA   | CGATGCGTAGATCGAC<br>AAAA | 59.7                             | 154                                           | DRR                                               | Ca_18363                            | --                    | --      |
| Ca4_P4_46137643  | Ca4                                     | 46137643                      | AG/AGAAGG                                                     | TTATTCAATGGCTTAG<br>GCGG   | CTCCCGTGCAAAGGAA<br>ATAA | 60.1                             | 665                                           | DRR                                               | Ca_18358                            | --                    | G2-like |
| Ca4_P4_46422010  | Ca4                                     | 46422010                      | ATTTTTTT/ATTTTTTTT                                            | CACTGAAGTCCACGCA<br>CCTA   | TCTTTCTTCCCTCCG<br>ATT   | 59.9                             | 768                                           | DRR                                               | Ca_19272                            | --                    | WOX     |
| Ca4_P4_46732510  | Ca4                                     | 46732510                      | G/GCA                                                         | CGGTATAGCCTGGGAA<br>ATGA   | GATGGAAGGAATGCCA<br>AAGA | 59.9                             | 766                                           | DRR                                               | Ca_19245                            | P                     | --      |
| Ca4_P4_46738774  | Ca4                                     | 46738774                      | GTGTT/GTGTGTT                                                 | CTAGGCTCACCAGCAC<br>CTTC   | GAGCCATTTGAGACGC<br>TTTC | 60.0                             | 318                                           | DRR                                               | Ca_19244                            | --                    | bZIP    |
| Ca4_P4_46767409  | Ca4                                     | 46767409                      | GTT/GT                                                        | GCCAGCTCCTCTTAC<br>AGTG    | ATGCTTTTCAGTGAGG<br>TGGG | 60.0                             | 593                                           | DRR                                               | Ca_19242                            | R                     | bZIP    |
| Ca4_P4_47195956  | Ca4                                     | 47195956                      | TCAATA/T                                                      | GCTTTTGAGTCACGAG<br>GGAG   | TTCAAAGTCATGAACC<br>TCG  | 60.0                             | 387                                           | DRR                                               | Ca_10862                            | --                    | --      |
| Ca4_P4_47211846  | Ca4                                     | 47211846                      | TG/TGG                                                        | TTGAAATGCAACCTTGT<br>CCA   | AAGCCCCTGCTTTGAT<br>TTCT | 60.1                             | 774                                           | DRR                                               | Ca_10861                            | --                    | LBD     |
| Ca4_P4_47233866  | Ca4                                     | 47233866                      | CAAA/CAACAAAA                                                 | ACAGACAAAGCCCAA<br>ATGC    | CATCACGGAATAGGGC<br>AACT | 60.1                             | 331                                           | DRR                                               | Ca_10858                            | --                    | --      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                           |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca4_P4_47247298  | Ca4                                     | 47247298                      | ATTTT/ATTT                                                                | GCGTTGGGAAATACCA<br>AGAA  | GCCAAACAACACAAGC<br>ATGA  | 59.9                             | 663                                           | DRR                                               | Ca_10857                            | --                    | B3          |
| Ca4_P4_47277224  | Ca4                                     | 47277224                      | TGGCTCGGCTCGGCTCGGCTC/TG<br>GCTCGGCTCGGCTC                                | GGACCCATTTGGGACC<br>TTAT  | CTGCCAGTAAGCACC<br>AACT   | 59.9                             | 657                                           | DRR                                               | Ca_10854                            | --                    | G2-like     |
| Ca4_P4_47425741  | Ca4                                     | 47425741                      | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATATAT                     | TGACACACACATGAAA<br>TGCG  | CAGACACAAATTGCTTT<br>CGC  | 60.2                             | 312                                           | DRR                                               | Ca_10845                            | R                     | ERF         |
| Ca4_P4_47597511  | Ca4                                     | 47597511                      | TAA/TAAA                                                                  | GGTACAATTGTTGCAC<br>CACG  | TTTCAATGCGTCAAAG<br>CAG   | 59.9                             | 666                                           | DRR                                               | Ca_10829                            | S                     | --          |
| Ca4_P4_47852567  | Ca4                                     | 47852567                      | TAAAAAAAA/TAAAAAAAA                                                       | AGCAGAGCAAAATTTG<br>GTGG  | TGGTATTGGTCCAACA<br>ACCTG | 60.2                             | 483                                           | DRR                                               | Ca_10809                            | O                     | MYB_related |
| Ca4_P4_47966378  | Ca4                                     | 47966378                      | CTTTTTTTTT/CTTTTTTTTT                                                     | AGCAAATTGGGAACCT<br>TGTG  | CGAGAAACCCATGAGG<br>AAAA  | 60.0                             | 361                                           | DRR                                               | Ca_10792                            | --                    | B3          |
| Ca4_P4_47991117  | Ca4                                     | 47991117                      | GTTTTTT/GTTTTTTTT                                                         | ATTAGCCACGACGATG<br>GTTC  | TGGTGATACATGTAGGC<br>GTGC | 60.0                             | 564                                           | DRR                                               | Ca_10789                            | --                    | B3          |
| Ca4_P4_47991306  | Ca4                                     | 47991306                      | GCA/GTTCACA                                                               | TAATTGCAAGTCATTGC<br>CCA  | CGAGTTGATGTGATTG<br>GTGG  | 60.1                             | 805                                           | DRR                                               | Ca_10789                            | --                    | B3          |
| Ca4_P4_48042400  | Ca4                                     | 48042400                      | AATATATATATATATATATATATAT<br>ATATAT/AATATATATATATATATA<br>TATATATATATATAT | TTTTGGTTCACATTAC<br>CTGAT | GGGCAAAACCCCTCAGA<br>AATA | 59.3                             | 885                                           | DRR                                               | Ca_10784                            | --                    | MYB_related |
| Ca4_P4_48226194  | Ca4                                     | 48226194                      | AGT/AGTGT                                                                 | AAAGAAAAGGGGGTG<br>ATGG   | GGAAGCCATTACCAAC<br>CAAA  | 60.2                             | 251                                           | DRR                                               | Ca_10766                            | --                    | DBB         |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca4_P4_48265483  | Ca4                                     | 48265483                      | ACTAAATTATTTGTTCTAAATTATTT/<br>ACTAAATTATTT                   | TCTTGATTTTACACACC<br>CCAACA | GATGACGGAGCCACAA<br>AGAT  | 59.3                             | 438                                           | DRR                                               | Ca_10761                            | K                     | B3      |
| Ca4_P4_48297107  | Ca4                                     | 48297107                      | AAATTTTAAT/AAATTTTAATTTTAAT                                   | AACAAACACATTTGTG<br>GCGA    | TTCTGACTGTTTAGGC<br>CGCT  | 60.0                             | 678                                           | DRR                                               | Ca_10759                            | --                    | --      |
| Ca4_P4_48303620  | Ca4                                     | 48303620                      | TA/TAA                                                        | AAGTGCAAAAAGTTGA<br>GACGC   | ATTGCATTGTGTGTTTG<br>GGA  | 59.6                             | 631                                           | DRR                                               | Ca_10757                            | B                     | C3H     |
| Ca4_P4_48303926  | Ca4                                     | 48303926                      | AT/ATT                                                        | AAAACCCGTACAACGG<br>ATGA    | CGAAGTTCCAAAACCA<br>CTGC  | 60.2                             | 756                                           | DRR                                               | Ca_10757                            | B                     | C3H     |
| Ca4_P4_48314680  | Ca4                                     | 48314680                      | ATTT/ATTTTT                                                   | GTAATGCGTTTGACCT<br>GCAA    | ATAGGCGCATCTCAAT<br>CACC  | 59.7                             | 649                                           | DRR                                               | Ca_10756                            | --                    | BBR-BPC |
| Ca4_P4_48314877  | Ca4                                     | 48314877                      | TA/T                                                          | TGCGCCTATCTCTCTG<br>TGTG    | TTCGATCCATTTTACCA<br>CCC  | 60.2                             | 365                                           | DRR                                               | Ca_10756                            | --                    | BBR-BPC |
| Ca4_P4_48323095  | Ca4                                     | 48323095                      | AACACACACACA/AACACACACACA<br>CA                               | GCAGCCAAACCAGCTT<br>AGAC    | AATTTGCAAAAATTCGG<br>CTG  | 60.0                             | 515                                           | DRR                                               | Ca_10754                            | Q                     | GeBP    |
| Ca4_P4_48331462  | Ca4                                     | 48331462                      | TTATCTCCCTTAAGATAT/TTAT                                       | CAGCTTGAAGTCCTTG<br>CTCC    | GTGGCCGTTTAATGCA<br>CTTT  | 60.1                             | 834                                           | DRR                                               | Ca_10753                            | J                     | --      |
| Ca4_P4_48332874  | Ca4                                     | 48332874                      | C/CAA                                                         | TTAGCTGTGGAAGGGC<br>ATTT    | AACTGGCAGATTCATC<br>ACACC | 59.7                             | 590                                           | DRR                                               | Ca_10753                            | J                     | --      |
| Ca4_P4_48365846  | Ca4                                     | 48365846                      | GC/G                                                          | GTTGGCCTGTTAGGCA<br>TTGT    | GTGCTTGTTCGGTGG<br>AGAT   | 60.0                             | 274                                           | DRR                                               | Ca_10750                            | A                     | bHLH    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                   |                          |                             |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca4_P4_4839789   | Ca4                                     | 4839789                       | CTTT/CTTTTTTTT                                                    | ACGTAATACTTTGTGG<br>CGGC | TCTCTCCTTTGTGACG<br>GCTT    | 60.0                             | 138                                           | DRR                                                  | Ca_03775                            | --                    | --       |
| Ca4_P4_48459296  | Ca4                                     | 48459296                      | CATAAT/CATAATATAAT                                                | CGAGTGGGTGAGGGA<br>GATTA | GCCCTAAAGCCACCCA<br>CTAT    | 60.1                             | 381                                           | DRR                                                  | Ca_10747                            | --                    | --       |
| Ca4_P4_48459552  | Ca4                                     | 48459552                      | AT/ATT                                                            | TGGTTGGCAGTAAGAT<br>GCAA | CGTTTGTTTGACGAGC<br>ACAA    | 60.3                             | 649                                           | DRR                                                  | Ca_10747                            | --                    | --       |
| Ca4_P4_48500161  | Ca4                                     | 48500161                      | TA/T                                                              | GAAGTACCTGCACGGG<br>TGAT | TTTGGAGGGAAAGGGA<br>AAGT    | 60.0                             | 234                                           | DRR                                                  | Ca_10742                            | V                     | GRAS     |
| Ca4_P4_48673700  | Ca4                                     | 48673700                      | GAAAAAAAA/GAAAAAAAAAAAA                                           | TACCGAACATGCGGTG<br>TAAG | TGACAAAAAGGAGAAG<br>ATAATGC | 59.6                             | 736                                           | DRR                                                  | Ca_23017                            | --                    | --       |
| Ca4_P4_48674038  | Ca4                                     | 48674038                      | ATTTT/ATTTT                                                       | TCCTCTGTGTGTGACA<br>ACCC | TGACCGAATCAAAAAG<br>AAGAAA  | 59.6                             | 694                                           | DRR                                                  | Ca_23017                            | --                    | --       |
| Ca4_P4_48708348  | Ca4                                     | 48708348                      | TAAAAA/TAAAAAA                                                    | GCGCTAGAGGAACTGG<br>ATTG | GGCGATGAATTGGTTT<br>GTTT    | 60.0                             | 944                                           | DRR                                                  | Ca_23020                            | Q                     | Nin-like |
| Ca4_P4_48708876  | Ca4                                     | 48708876                      | TTTTATTT/TTTT                                                     | CGCCACTTGATTTTCAA<br>GCA | GCATCAGCTCTTCCAG<br>CTTC    | 59.9                             | 517                                           | DRR                                                  | Ca_23020                            | Q                     | Nin-like |
| Ca4_P4_48718705  | Ca4                                     | 48718705                      | GATATATATATATATATATATATA<br>TAT/GATATATATATATATATATAT<br>ATATATAT | CGAGAGTGTCCAAAGT<br>GCAA | GCTGGTGGAGAAGGTT<br>TTGA    | 60.0                             | 576                                           | DRR                                                  | Ca_23022                            | --                    | --       |
| Ca4_P4_48834023  | Ca4                                     | 48834023                      | AATA/AATATA                                                       | ACTCTAGACCATCGAC<br>GGCA | GAACACACCAAAAGCT<br>CCGT    | 60.8                             | 398                                           | DRR                                                  | Ca_23026                            | --                    | FAR1     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_4894873   | Ca4                                     | 4894873                       | TAAAAAAAA/TAAAAAAAA                                           | GACTTGGAGCGAAGTG<br>GAAA | GCAATGTTGCGAGAAC<br>AAGA  | 60.4                             | 705                                           | DRR                                               | Ca_03768                            | K                     | --   |
| Ca4_P4_4907090   | Ca4                                     | 4907090                       | CTTT/CTTTT                                                    | ATTGCATCCCAATCCC<br>ATAA | TTAGTCGAGTGTTTGG<br>TGCG  | 60.0                             | 266                                           | DRR                                               | Ca_03767                            | F                     | --   |
| Ca4_P4_4908744   | Ca4                                     | 4908744                       | A/ACCGT                                                       | CACGAACAAAATCAAG<br>CGAA | ATTGCGTGGGAAAAAG<br>TTTG  | 59.8                             | 529                                           | DRR                                               | Ca_03767                            | F                     | --   |
| Ca4_P4_4908883   | Ca4                                     | 4908883                       | T/TA                                                          | CAAACTTTTCCACG<br>CAAT   | TCATCATTGTGCCGTC<br>ATTT  | 60.0                             | 318                                           | DRR                                               | Ca_03767                            | F                     | --   |
| Ca4_P4_49089991  | Ca4                                     | 49089991                      | AGC/AGCGC                                                     | GCTTCCATGCACAGAA<br>GTGA | TGAGAGCACGAAAGGA<br>TG TG | 60.0                             | 190                                           | DRR                                               | Ca_20778                            | R                     | MYB  |
| Ca4_P4_5182858   | Ca4                                     | 5182858                       | TATAATAATAATAATAATAATAT<br>AATAATAATAATAATAA                  | AGGCCAGACCAGACTT<br>TGAA | CAGTGGCTTATGGCCT<br>GACT  | 59.8                             | 606                                           | DRR                                               | Ca_03735                            | E                     | --   |
| Ca4_P4_5469578   | Ca4                                     | 5469578                       | CGTTTAGTTTAGTTTAGTTT/CGTTT<br>AGTTTAGTTTAGTTTAGTTT            | TCCATTGACCAAAGCA<br>TCAA | GCGAATCGAAAACAAG<br>TG GT | 60.0                             | 290                                           | DRR                                               | Ca_03705                            | P                     | --   |
| Ca4_P4_582760    | Ca4                                     | 582760                        | T/TATGGTGCTACTC                                               | CAGGTGACTCATCCCG<br>ATTT | CGCAATTCAGTGAAG<br>CAAA   | 59.9                             | 591                                           | DRR                                               | Ca_07688                            | O                     | FAR1 |
| Ca4_P4_6139965   | Ca4                                     | 6139965                       | GTTTTTTTTTTTT/GTTTTTTTTTT<br>T                                | AATCACATTCCAGTCCT<br>CCG | GGGTTGTGGCTCTCCA<br>TTTA  | 59.9                             | 788                                           | DRR                                               | Ca_03629                            | --                    | --   |
| Ca4_P4_6790926   | Ca4                                     | 6790926                       | AG/AGG                                                        | GAAGCACCCCATGTTC<br>CTAA | AAATGACAAGTTCTACC<br>GCGA | 59.9                             | 956                                           | DRR                                               | Ca_03562                            | QI                    | bHLH |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                     |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca4_P4_7180740   | Ca4                                     | 7180740                       | TT/TTGT                                                             | TGAAGGTGCTCAACAA<br>GGTG    | GGCAATCATCCATGGA<br>ACTC   | 59.9                             | 472                                           | DRR                                               | Ca_03517                            | --                    | GRAS        |
| Ca4_P4_730137    | Ca4                                     | 730137                        | TTATATATATATATATATAT/TTAT<br>ATATATATATATATAT                       | GTCAACCTTGGTGCTT<br>GGTT    | AAGTATTCCGCCTGT<br>CACG    | 60.0                             | 775                                           | DRR                                               | Ca_07702                            | G                     | --          |
| Ca4_P4_7584272   | Ca4                                     | 7584272                       | AATATATATATATATATATATAT<br>AT/AATATATATATATATATATATA<br>TATATATATAT | AAAGTGCACCACACAA<br>GTGC    | TTTGTAACGGTTAAG<br>GGCAA   | 59.8                             | 644                                           | DRR                                               | Ca_03478                            | --                    | --          |
| Ca4_P4_7825515   | Ca4                                     | 7825515                       | TAAAAAAAAA/TAAAAAAAAA                                               | TGCACAAAAATAAAAC<br>ATTTCAA | AAAGGATGGAAGCCCA<br>TTTT   | 58.7                             | 959                                           | DRR                                               | Ca_03457                            | G                     | NAC         |
| Ca4_P4_8167017   | Ca4                                     | 8167017                       | CAAAA/CAAA                                                          | GGGTGGGTTTAGAGGA<br>CCAT    | TTTCTTGAATGGGCAAA<br>ACC   | 60.1                             | 259                                           | DRR                                               | Ca_08305                            | V                     | GRAS        |
| Ca4_P4_8167238   | Ca4                                     | 8167238                       | ATCTT/ATCTTCTT                                                      | GGGTGGGTTTAGAGGA<br>CCAT    | TGAAGCTTTTGTCTACA<br>AGGAA | 60.1                             | 737                                           | DRR                                               | Ca_08305                            | V                     | GRAS        |
| Ca4_P4_8167347   | Ca4                                     | 8167347                       | ATATTATTTTA/ATATTATTTTATT<br>ATTTTAA                                | GGGTGGGTTTAGAGGA<br>CCAT    | TGAAGCTTTTGTCTACA<br>AGGAA | 60.1                             | 737                                           | DRR                                               | Ca_08305                            | V                     | GRAS        |
| Ca4_P4_8184653   | Ca4                                     | 8184653                       | CTTTTTTT/CTTTTTTT                                                   | GCTGTCTTTTCGTCC<br>TGCT     | GTATTGGCCAACCAGA<br>CCAC   | 59.6                             | 856                                           | DRR                                               | Ca_08308                            | T                     | --          |
| Ca4_P4_8193266   | Ca4                                     | 8193266                       | TAAAAAAAAA/TAAAAAAAAA                                               | GCATCTCTCCAAGATG<br>TCTGC   | TGGGAATTGGGAGCTA<br>TCAG   | 60.0                             | 620                                           | DRR                                               | Ca_08309                            | R                     | --          |
| Ca4_P4_8203373   | Ca4                                     | 8203373                       | ATTTCTTTCTTTCTTCT/ATTTCTTT<br>CTTTCT                                | CGTGAAGGATAGAAA<br>TCGG     | GCAGCTTCTGAATGGA<br>AACC   | 59.5                             | 536                                           | DRR                                               | Ca_08310                            | T                     | MYB_related |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_8221604   | Ca4                                     | 8221604                       | TAAAAAA/TATTAAAAAAA                                           | AACACAAGGAGGGAAA<br>CACG | CAAGAACTGCCAATG<br>CAAA   | 60.0                             | 644                                           | DRR                                               | Ca_08311                            | T                     | bHLH |
| Ca4_P4_8222289   | Ca4                                     | 8222289                       | TAAAAAAAA/TAAAAAAAAA                                          | TTTGCATTGGCAGTTT<br>CTTG | CCGCAACAACAAAGAC<br>AGAA  | 59.8                             | 609                                           | DRR                                               | Ca_08312                            | --                    | --   |
| Ca4_P4_8244322   | Ca4                                     | 8244322                       | TT/TTCT                                                       | GCATTCTGGTCGGTT<br>TGTT  | ACACCACACAAAGCA<br>GTGA   | 60.0                             | 164                                           | DRR                                               | Ca_08315                            | S                     | --   |
| Ca4_P4_8245965   | Ca4                                     | 8245965                       | GATATATATATAT/GATATATAT<br>ATATATATATATAT                     | TCAAATTTTCTTATGCG<br>GGC | TGAGGAAACACCACCA<br>CGTA  | 60.0                             | 790                                           | DRR                                               | Ca_08314                            | KB                    | --   |
| Ca4_P4_8289104   | Ca4                                     | 8289104                       | CAA/CA                                                        | GCGGGGTTCAAATCCT<br>AAAT | ATAGACGCCCCAAGT<br>ATCC   | 60.2                             | 355                                           | DRR                                               | Ca_08316                            | --                    | NAC  |
| Ca4_P4_8292742   | Ca4                                     | 8292742                       | GATA/GATATATA                                                 | AGAGAAAGGACGAGC<br>ATCA  | AGGCATTTTCGTGACG<br>AGTT  | 60.0                             | 649                                           | DRR                                               | Ca_08317                            | --                    | --   |
| Ca4_P4_8301399   | Ca4                                     | 8301399                       | GCAACCTAATGTTCAACCTAA/GCAA<br>CCTAA                           | CACAATGATGTTTGGT<br>TCGG | AGGGGTGTTTACGCAT<br>TGAG  | 59.8                             | 483                                           | DRR                                               | Ca_08318                            | S                     | --   |
| Ca4_P4_8301438   | Ca4                                     | 8301438                       | AG/A                                                          | CACAATGATGTTTGGT<br>TCGG | AGGGGTGTTTACGCAT<br>TGAG  | 59.8                             | 483                                           | DRR                                               | Ca_08318                            | S                     | --   |
| Ca4_P4_8335376   | Ca4                                     | 8335376                       | ATTTT/ATTT                                                    | CGACAAAAGTGAGGG<br>GAAA  | GCAATGCGTTGTCTGT<br>GTCT  | 60.1                             | 192                                           | DRR                                               | Ca_08321                            | --                    | --   |
| Ca4_P4_8344606   | Ca4                                     | 8344606                       | TAAAAAA/TAAAAA                                                | GAGCAGAACGAGTGAA<br>AGGG | CTCCTTCGCATTTCTGTC<br>TTC | 60.0                             | 545                                           | DRR                                               | Ca_08322                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_8345457   | Ca4                                     | 8345457                       | T/TA                                                          | TCTTTGCTTTCAACGCT<br>GTTT | AGGAGGTGCATCGAGG<br>TATG  | 60.0                             | 915                                           | DRR                                               | Ca_08322                            | --                    | --   |
| Ca4_P4_8351185   | Ca4                                     | 8351185                       | TAAAAAAAA/TAAAAAAA                                            | ATTTTCGGTTTCCCTTC<br>CAC  | CGATTTCCCTTGGTCC<br>AAAT  | 60.2                             | 960                                           | DRR                                               | Ca_08323                            | --                    | --   |
| Ca4_P4_8354913   | Ca4                                     | 8354913                       | ATTTTTTTTT/ATTTTTTTT                                          | TTGATTTGGGGGCTTT<br>GATA  | GGAGCAGTTGTCCCAT<br>TTGT  | 60.3                             | 765                                           | DRR                                               | Ca_08324                            | T                     | bZIP |
| Ca4_P4_8355635   | Ca4                                     | 8355635                       | T/TC                                                          | GGACAAC TGCTCCCTC<br>TTGA | TTGGGAATCGGTGAAA<br>ACTT  | 60.4                             | 857                                           | DRR                                               | Ca_08324                            | T                     | bZIP |
| Ca4_P4_8377254   | Ca4                                     | 8377254                       | ATTTTTTTTTT/ATTTTTTTTTTTT                                     | CCACATATATCTGCC<br>CACC   | TGACTGTGTGCACTGA<br>AACAA | 60.0                             | 563                                           | DRR                                               | Ca_08327                            | KL                    | --   |
| Ca4_P4_8377484   | Ca4                                     | 8377484                       | ATTTTTTTTTT/ATTTTTTTT                                         | TTCGTCCATTGAATCC<br>TGA   | GGGTGAGACTGAAGCT<br>GGTC  | 59.0                             | 720                                           | DRR                                               | Ca_08327                            | KL                    | --   |
| Ca4_P4_8377585   | Ca4                                     | 8377585                       | ATTT/ATT                                                      | TTCGTCCATTGAATCC<br>TGA   | CCTGCAAGCACTTACG<br>ACAA  | 59.0                             | 891                                           | DRR                                               | Ca_08327                            | KL                    | --   |
| Ca4_P4_8396244   | Ca4                                     | 8396244                       | CAAA/CA                                                       | TTTACAACACATTGCG<br>CACC  | CGTTTATTGACGGAAG<br>GCAT  | 60.6                             | 681                                           | DRR                                               | Ca_08328                            | R                     | AP2  |
| Ca4_P4_8417735   | Ca4                                     | 8417735                       | ATTTTT/ATTTT                                                  | CACAGGGGAATAAGGT<br>TGGA  | ACAAGAGGCGGAGACA<br>GGTA  | 59.8                             | 862                                           | DRR                                               | Ca_08331                            | --                    | ERF  |
| Ca4_P4_8430074   | Ca4                                     | 8430074                       | AAT/AATAT                                                     | TTTTGGCATGAAAAAG<br>GGAC  | GAAATTTACCGCTTGA<br>CCGA  | 59.9                             | 772                                           | DRR                                               | Ca_08334                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca4_P4_8449229   | Ca4                                     | 8449229                       | ATTTTTTTTT/ATTTTTTTT                                          | TGGAGTTTTAGCCACT<br>TCCA | TCTCGCCAAATATCTAC<br>AATCG | 58.4                             | 337                                           | DRR                                               | Ca_08335                            | R                     | --      |
| Ca4_P4_8449477   | Ca4                                     | 8449477                       | TG/T                                                          | TGGAGTTTTAGCCACT<br>TCCA | TCTCGCCAAATATCTAC<br>AATCG | 58.4                             | 337                                           | DRR                                               | Ca_08336                            | --                    | --      |
| Ca4_P4_8454111   | Ca4                                     | 8454111                       | T/TTTTC                                                       | TTCTTTGGGTCTCCCA<br>ACAC | TTATGAGCTTTGGATTG<br>GGC   | 59.9                             | 631                                           | DRR                                               | Ca_08337                            | R                     | MYB     |
| Ca4_P4_8483192   | Ca4                                     | 8483192                       | A/ACT                                                         | ATTTGAGGAAAAGGG<br>AGGA  | GACCCTATCAGAGTGG<br>CAGC   | 60.0                             | 886                                           | DRR                                               | Ca_08340                            | R                     | --      |
| Ca4_P4_8499889   | Ca4                                     | 8499889                       | AG/A                                                          | TTCCCAAATTCCTGCA<br>TCT  | AGCCATACITTCATGG<br>TGCC   | 59.5                             | 958                                           | DRR                                               | Ca_08342                            | C                     | --      |
| Ca4_P4_8514977   | Ca4                                     | 8514977                       | G/GT                                                          | CACACCCCTAGCTTTG<br>CTTC | CACGAACGCCTGTGAA<br>CTTA   | 59.9                             | 547                                           | DRR                                               | Ca_08343                            | YU                    | --      |
| Ca4_P4_8515876   | Ca4                                     | 8515876                       | AATG/A                                                        | GAAATGTTGGTGAGGG<br>ATGG | AACATTTTGTAGTCCCA<br>CGC   | 60.2                             | 550                                           | DRR                                               | Ca_08344                            | --                    | --      |
| Ca4_P4_8616583   | Ca4                                     | 8616583                       | GATGT/GATGTATGT                                               | GCGAGAATACAATTC<br>CAGCA | ACTCGATCGTGAAGC<br>AAGT    | 60.2                             | 324                                           | DRR                                               | Ca_08355                            | O                     | --      |
| Ca4_P4_8639881   | Ca4                                     | 8639881                       | TA/TACAA                                                      | ACTCCCTCAATGGCAA<br>CATC | ACACCACGAACGCAAC<br>AATA   | 59.9                             | 652                                           | DRR                                               | Ca_08357                            | --                    | --      |
| Ca4_P4_8650272   | Ca4                                     | 8650272                       | T/TTTGGATTACACAATAGAG                                         | TTCCCTTTGAGTGGGA<br>TTTG | TCTTCCGTTTAGCTTA<br>TATCCA | 59.9                             | 597                                           | DRR                                               | Ca_08358                            | --                    | G2-like |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_8701352   | Ca4                                     | 8701352                       | ATTTTTTT/ATTTTT                                               | TTACGACTTTGAATGC<br>CACG | TGTTTCGCAATTTAGG<br>GGAG   | 59.7                             | 503                                           | DRR                                               | Ca_08365                            | G                     | --   |
| Ca4_P4_8716168   | Ca4                                     | 8716168                       | AATTA/AA                                                      | GGTGCCATTAAAGAGC<br>TTGC | CAACTAAATCACGTAG<br>GTCCCA | 59.9                             | 566                                           | DRR                                               | Ca_08368                            | Q                     | --   |
| Ca4_P4_8734624   | Ca4                                     | 8734624                       | TAAAAAAAA/TAAAAAAAAA                                          | CCGGTCAATCTATTGC<br>GACT | TGGGTCATGTGGAAGG<br>AAGT   | 60.1                             | 537                                           | DRR                                               | Ca_08370                            | R                     | WOX  |
| Ca4_P4_8756554   | Ca4                                     | 8756554                       | TT/TTGT                                                       | GCTAACCTTTCCAATT<br>CCC  | TGAATTGGCCAAAACT<br>CAA    | 59.8                             | 458                                           | DRR                                               | Ca_08371                            | --                    | NAC  |
| Ca4_P4_8757082   | Ca4                                     | 8757082                       | GATGGATATGGATA/GATGGATA                                       | TGAGTTTTTGGCCAATT<br>CAA | GCAGGTGCAGAAAGAT<br>TACCA  | 59.1                             | 605                                           | DRR                                               | Ca_08371                            | --                    | NAC  |
| Ca4_P4_8774335   | Ca4                                     | 8774335                       | CT/C                                                          | GACGATTGCGAATTTG<br>AGGT | TGATTTATGTTTGTGGC<br>GGA   | 60.1                             | 295                                           | DRR                                               | Ca_08373                            | C                     | --   |
| Ca4_P4_8775167   | Ca4                                     | 8775167                       | ATT/ATTT                                                      | TGTTCCCTGCAATTCA<br>CATC | ACGGGTCTCGATCAAT<br>GTGT   | 59.5                             | 360                                           | DRR                                               | Ca_08373                            | C                     | --   |
| Ca4_P4_8802549   | Ca4                                     | 8802549                       | TA/T                                                          | TCACAAAGCGCCATTA<br>AACA | TGTACGCAGTGTGCTT<br>GTCA   | 60.3                             | 370                                           | DRR                                               | Ca_08378                            | AR                    | MYB  |
| Ca4_P4_8850307   | Ca4                                     | 8850307                       | GAAAAA/GAAAAA                                                 | CTCCGATTGTTGAGGT<br>GGTT | AAATTAGCTTTGGCTG<br>GGGT   | 60.0                             | 548                                           | DRR                                               | Ca_08382                            | --                    | MIKC |
| Ca4_P4_8891981   | Ca4                                     | 8891981                       | CAAA/CAA                                                      | ATACACCACAACGCGT<br>CAAA | AAGCATGGTATTCGGG<br>AGTG   | 60.0                             | 204                                           | DRR                                               | Ca_08386                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                              |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca4_P4_8993223   | Ca4                                     | 8993223                       | CATAAATAAATAAATAAATAAATAA<br>TAAA/CATAAATAAATAAATAAATAA<br>TAAA                              | TCACAAATCACATTAC<br>CCC     | GGCGGTTTGACAGTAG<br>GAAA  | 59.2                             | 314                                           | DRR                                               | Ca_08394                            | GMW                   | --       |
| Ca4_P4_9017988   | Ca4                                     | 9017988                       | TTATATATATATATATA/TTATATATA<br>TATATA                                                        | GCGTGGCATCAATATT<br>CCTT    | ATAGATTGATCGGGAC<br>GGTG  | 59.9                             | 633                                           | DRR                                               | Ca_08396                            | AD                    | --       |
| Ca4_P4_9049540   | Ca4                                     | 9049540                       | TA/TACA                                                                                      | AAGAATTGTCAACCA<br>GTTCTACC | AACATGGCGTTTTGGT<br>TGAT  | 57.8                             | 667                                           | DRR                                               | Ca_08398                            | Q                     | B3       |
| Ca4_P4_9197695   | Ca4                                     | 9197695                       | AAAC/AAACAAC                                                                                 | TGCACCAATCGAACTA<br>ATCG    | TTTCTCGTCTTGGTGC<br>AGTG  | 59.7                             | 369                                           | DRR                                               | Ca_08410                            | I                     | --       |
| Ca4_P4_9321669   | Ca4                                     | 9321669                       | GTATTATTAT/GTATTAT                                                                           | GTTGTGTCCGTGTCAG<br>ATGC    | GTCCTTGACATTGGTG<br>GGAG  | 60.2                             | 439                                           | DRR                                               | Ca_08420                            | A                     | bZIP     |
| Ca4_P4_9463038   | Ca4                                     | 9463038                       | ATTAATTTT/ATT                                                                                | CAAGAGGAAACATGGA<br>GGGA    | CCAAAAAGCAACTTTCA<br>AGCC | 60.0                             | 632                                           | DRR                                               | Ca_08435                            | R                     | C2H2     |
| Ca4_P4_9704009   | Ca4                                     | 9704009                       | AAGTTAGGAGTTAGGAGTTAGGAG<br>TTAGGAGTTAGG/AAGTTAGGAGTT<br>AGGAGTTAGGAGTTAGGAGTTAGG<br>AGTTAGG | TTCCAAAAGCAAACAC<br>ACCA    | CTCTTTCTTGACCTGCC<br>CTG  | 60.1                             | 745                                           | DRR                                               | Ca_08447                            | Q                     | Nin-like |
| Ca4_P4_9727283   | Ca4                                     | 9727283                       | AT/A                                                                                         | TGTCTGCGGTCACAAA<br>ACTC    | TGGTGTCCATTTTGCA<br>CAT   | 59.9                             | 504                                           | DRR                                               | Ca_08452                            | E                     | --       |
| Ca4_P4_9827543   | Ca4                                     | 9827543                       | GAAAAAAAAA/GAAAAAAAAA                                                                        | CGGTCACCGGTACCA<br>CTTT     | CAATCTGCCATGTCAAT<br>GAA  | 60.9                             | 332                                           | DRR                                               | Ca_08460                            | --                    | --       |
| Ca5_P4_10511669  | Ca5                                     | 10511669                      | TC/T                                                                                         | CACTACTTGGTTGGGG<br>CCTA    | TTGTTGGGATCCGACT<br>TTGT  | 60.0                             | 364                                           | DRR                                               | Ca_21230                            | --                    | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca5_P4_10668285  | Ca5                                     | 10668285                      | TAAAAAAAAA/TAAAAAAAAA                                         | GGGCGATTATATACCA<br>GCGA  | TGGCAACTATTTTGAG<br>CTTTTTC | 59.9                             | 564                                           | DRR                                               | Ca_21221                            | --                    | --   |
| Ca5_P4_11983861  | Ca5                                     | 11983861                      | GTCT/GATCTTCGATCCTTCT                                         | CTGCTGTCAACTCCAC<br>TCCA  | TCAAAATCCCCCAATAA<br>CCA    | 60.0                             | 713                                           | DRR                                               | Ca_17106                            | --                    | --   |
| Ca5_P4_12659145  | Ca5                                     | 12659145                      | TTAGTCGTAGTCGTAGTCGT/TTAG<br>TCGTAGTCGTAGTCGTAGTCGT           | GTGACTGGGGACTGGT<br>GACT  | GACGGACGGTGTAGCA<br>AAAT    | 60.0                             | 451                                           | DRR                                               | Ca_17066                            | --                    | FAR1 |
| Ca5_P4_1269046   | Ca5                                     | 1269046                       | AAATT/A                                                       | TCCGGTACACAACTTTT<br>CCC  | ACCCATCATTCCAACC<br>AAC     | 59.8                             | 376                                           | DRR                                               | Ca_26280                            | E                     | --   |
| Ca5_P4_14059187  | Ca5                                     | 14059187                      | CTTGTTAGTTG/CTTGTTAGTTGTTA<br>GTTG                            | CGGTCTCAACCTCTCC<br>CATA  | TTTCCCAATCGATTTCG<br>TTC    | 60.1                             | 706                                           | DRR                                               | Ca_20824                            | R                     | --   |
| Ca5_P4_143697    | Ca5                                     | 143697                        | A/AT                                                          | AGCAAGAGGAGCAAAA<br>CTGG  | CCACCGCAGACTTAAA<br>CCAT    | 59.6                             | 706                                           | DRR                                               | Ca_18170                            | --                    | --   |
| Ca5_P4_16765808  | Ca5                                     | 16765808                      | TAGA/TA                                                       | CGATCGTGCTACGTCT<br>TCAA  | TGGTGGGAATGTTGTG<br>ATTG    | 60.0                             | 677                                           | DRR                                               | Ca_17941                            | R                     | HSF  |
| Ca5_P4_168246    | Ca5                                     | 168246                        | GATTTATTTATTTATTTATTT/GATTT<br>ATTTATTTATTTATTTATTT           | TCAGATACACGCATCC<br>CTTT  | CGAGACCATTGAGTCC<br>AAAAA   | 58.2                             | 467                                           | DRR                                               | Ca_18171                            | --                    | NAC  |
| Ca5_P4_172991    | Ca5                                     | 172991                        | TAAAAAAAAA/TAAAAAAAAA                                         | GCGAATGACAAGCAAA<br>AAGA  | ACCGTGAGATGCCACA<br>TTTT    | 59.0                             | 907                                           | DRR                                               | Ca_18172                            | J                     | --   |
| Ca5_P4_173324    | Ca5                                     | 173324                        | ATTTTTTTTTTT/ATTTTTTTTTTT                                     | TGTTTATCCACAAGCTT<br>TCCG | ACCGTGAGATGCCACA<br>TTTT    | 60.1                             | 270                                           | DRR                                               | Ca_18172                            | J                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                   |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca5_P4_198698    | Ca5                                     | 198698                        | AA/AAGA                                                           | CCGGAGCACGTAAAGC<br>TTAG  | GTGGCATCCACAATGA<br>CAAA | 60.0                             | 488                                           | DRR                                               | Ca_18174                            | L                     | --       |
| Ca5_P4_20542450  | Ca5                                     | 20542450                      | AT/ATT                                                            | ATGCATTACCTGTGG<br>CATA   | ACTCCTTCCTTTCGTCC<br>CAT | 60.0                             | 331                                           | DRR                                               | Ca_18213                            | --                    | HB-other |
| Ca5_P4_20781552  | Ca5                                     | 20781552                      | GATATATATATATATATATATATA<br>TAT/GATATATATATATATATATAT<br>ATATATAT | GCTGAGGTGGGAAACA<br>TTTG  | CCAAATCAGAACCAAA<br>GGCA | 60.5                             | 598                                           | DRR                                               | Ca_18223                            | --                    | ARF      |
| Ca5_P4_209072    | Ca5                                     | 209072                        | GTTTTT/GTTTTTTT                                                   | TGGCATCACCATCACT<br>TGTT  | ACGTTTATGGGATGCT<br>TCAA | 60.0                             | 607                                           | DRR                                               | Ca_18176                            | --                    | C2H2     |
| Ca5_P4_209466    | Ca5                                     | 209466                        | AAAAAAGCTTAAAACTTAAAA/AAAA<br>AACTTAAAAACTTAAAAACTTAAAA           | AATTGAAGCATCCCAT<br>AAACG | TTAGACCATCCACAACA<br>CGG | 59.0                             | 698                                           | DRR                                               | Ca_18176                            | --                    | C2H2     |
| Ca5_P4_209690    | Ca5                                     | 209690                        | ATTTTTTT/ATTTTTTTT                                                | AAAACATTCAACCAACC<br>ACCA | TTAGACCATCCACAACA<br>CGG | 60.1                             | 320                                           | DRR                                               | Ca_18176                            | --                    | C2H2     |
| Ca5_P4_209767    | Ca5                                     | 209767                        | GAAAAAAAA/GAAAAAAAAAA                                             | AAAACATTCAACCAACC<br>ACCA | TTAGACCATCCACAACA<br>CGG | 60.1                             | 320                                           | DRR                                               | Ca_18176                            | --                    | C2H2     |
| Ca5_P4_209793    | Ca5                                     | 209793                        | AAATTAAT/AAATTAATTAAT                                             | AAAACATTCAACCAACC<br>ACCA | TTAGACCATCCACAACA<br>CGG | 60.1                             | 320                                           | DRR                                               | Ca_18176                            | --                    | C2H2     |
| Ca5_P4_210200    | Ca5                                     | 210200                        | ATTTTTTTTT/ATTTTTTTTTT                                            | TTAAACACCCGTGTTG<br>TGGA  | AAATGGCTTAGGGAGG<br>GAGA | 59.9                             | 607                                           | DRR                                               | Ca_18176                            | --                    | C2H2     |
| Ca5_P4_210510    | Ca5                                     | 210510                        | ATT/ATTT                                                          | TCTCCCTCCCTAAGCC<br>ATTT  | GAATTATCCGCTGCTT<br>GCAT | 60.0                             | 201                                           | DRR                                               | Ca_18176                            | --                    | C2H2     |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca5_P4_210754    | Ca5                                     | 210754                        | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA<br>A                            | TCTCCCTCCCTAAGCC<br>ATT  | TGGCTCAGAGCTGATT<br>CTGAT | 60.0                             | 746                                           | DRR                                               | Ca_18176                            | --                    | C2H2  |
| Ca5_P4_21281623  | Ca5                                     | 21281623                      | TC/T                                                          | CAGGCTGATGAAGATG<br>ACGA | TCATTGATCCCCCGTA<br>ATGT  | 59.9                             | 613                                           | DRR                                               | Ca_18240                            | --                    | --    |
| Ca5_P4_21853723  | Ca5                                     | 21853723                      | TAA/TAAAAAATCAA                                               | AGCCCTATGTCACGAC<br>CAAC | TTTTTGCATGACGACTC<br>CAG  | 60.0                             | 834                                           | DRR                                               | Ca_24465                            | --                    | --    |
| Ca5_P4_22069880  | Ca5                                     | 22069880                      | GATATA/GATA                                                   | TTCGTATGCGTGCCAA<br>TATC | GCATGTTCTTTCGTTT<br>GTCA  | 59.5                             | 129                                           | DRR                                               | Ca_21161                            | --                    | --    |
| Ca5_P4_225405    | Ca5                                     | 225405                        | TTCTCTC/TTCTCTC                                               | CGGATATGCCATCACA<br>GTTG | GGCCCCATTGATGGTT<br>ACTA  | 59.9                             | 834                                           | DRR                                               | Ca_18177                            | --                    | ZF-HD |
| Ca5_P4_225505    | Ca5                                     | 225505                        | ATTTTTTTTT/ATTTTTTTTT                                         | CGGATATGCCATCACA<br>GTTG | GGCCCCATTGATGGTT<br>ACTA  | 59.9                             | 834                                           | DRR                                               | Ca_18177                            | --                    | ZF-HD |
| Ca5_P4_22695785  | Ca5                                     | 22695785                      | C/CGGAGAGGAGGG                                                | CTAACCAGAAAAGGCA<br>GCAG | ACAATATTCCCCGGGC<br>TAAC  | 60.0                             | 358                                           | DRR                                               | Ca_20069                            | C                     | --    |
| Ca5_P4_22919631  | Ca5                                     | 22919631                      | AG/A                                                          | GATTTGGTGGAATCTC<br>CGAA | GCCACCGACTACTTCT<br>CCCT  | 59.9                             | 336                                           | DRR                                               | Ca_21962                            | --                    | --    |
| Ca5_P4_22919722  | Ca5                                     | 22919722                      | GTT/GT                                                        | GATTTGGTGGAATCTC<br>CGAA | GCCACCGACTACTTCT<br>CCCT  | 59.9                             | 336                                           | DRR                                               | Ca_21962                            | --                    | --    |
| Ca5_P4_230199    | Ca5                                     | 230199                        | ATTTTT/ATTTT                                                  | CAGTTTGGATCTGATG<br>GGTT | CAATTGTGGAATGCAA<br>CCAG  | 59.8                             | 576                                           | DRR                                               | Ca_18178                            | S                     | --    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca5_P4_23945434  | Ca5                                     | 23945434                      | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATAT       | AAAACAGCTTGTAAATC<br>CGTGA | TTTTTCGTCAATTAAC<br>TTTCCA   | 58.8                             | 790                                           | DRR                                               | Ca_17664                            | O                     | bHLH |
| Ca5_P4_24267648  | Ca5                                     | 24267648                      | AGGGGGG/AGGGGGGG                                              | GCAAGATGATCCCGAC<br>TCTC   | GACTGGACGTAACCCA<br>CGTT     | 59.8                             | 528                                           | DRR                                               | Ca_15569                            | --                    | --   |
| Ca5_P4_25186556  | Ca5                                     | 25186556                      | GAAAAAAAA/GAAAAAAAAA                                          | TCAGAGGTACATTCGC<br>CAGA   | GTCAATTTGATAGGCC<br>CCCT     | 59.4                             | 686                                           | DRR                                               | Ca_15627                            | L                     | --   |
| Ca5_P4_25186591  | Ca5                                     | 25186591                      | CAAAAAAAAA/CAAAAAAAAAA                                        | TCAGAGGTACATTCGC<br>CAGA   | GTCAATTTGATAGGCC<br>CCCT     | 59.4                             | 686                                           | DRR                                               | Ca_15627                            | L                     | --   |
| Ca5_P4_25803856  | Ca5                                     | 25803856                      | TAAAAAAAAAAAAA/TAAAAAAAAA                                     | ATCCGATAAATCGCATT<br>GTG   | CCCACAAGGTCCGAGA<br>ATTA     | 58.5                             | 203                                           | DRR                                               | Ca_09020                            | --                    | --   |
| Ca5_P4_25896623  | Ca5                                     | 25896623                      | AT/ATAAAGT                                                    | TCCACGTTAGGGGGTT<br>ACCT   | TCAGACCGATCTTGA<br>TGAC      | 60.6                             | 839                                           | DRR                                               | Ca_09015                            | S                     | --   |
| Ca5_P4_260923    | Ca5                                     | 260923                        | CATAT/CATATAT                                                 | CTTCGGCCTAAAGATT<br>TTGC   | ATTGCGGTTGTTCGGT<br>TATC     | 59.0                             | 358                                           | DRR                                               | Ca_18180                            | A                     | --   |
| Ca5_P4_261320    | Ca5                                     | 261320                        | TCAC/TC                                                       | GATAACCGAACAACCG<br>CAAT   | CGGAGCTTCGGTAGGA<br>CATA     | 59.8                             | 754                                           | DRR                                               | Ca_18179                            | R                     | --   |
| Ca5_P4_26559939  | Ca5                                     | 26559939                      | AATATATATATATAT/AATATATAT<br>ATATATATAT                       | TTTTTGGGTTGAGGAC<br>AAGG   | GCACTATCCTATCAAA<br>GGTCTCTC | 59.9                             | 145                                           | DRR                                               | Ca_08966                            | --                    | bHLH |
| Ca5_P4_26571749  | Ca5                                     | 26571749                      | TTTCATGACTTCAT/TTTCAT                                         | TCCTAAACGTCGAAA<br>CCAAA   | TCACAATCTTAAATGC<br>GAAAAA   | 59.6                             | 371                                           | DRR                                               | Ca_08965                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                              |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca5_P4_26873199  | Ca5                                     | 26873199                      | AATATATATATATATATAT/AAAT<br>ATATATATATATATATAT                | TCAAAATTTTCGATCAA<br>AAGCC   | TTGCGTAACATTACAC<br>AAAAA | 60.2                             | 852                                           | DRR                                               | Ca_08941                            | K                     | M-type   |
| Ca5_P4_26994998  | Ca5                                     | 26994998                      | TC/TCC                                                        | GGAGCGGGAATATGAC<br>TGAA     | GGGAGAGGTTGGGAG<br>CTTAC  | 60.0                             | 492                                           | DRR                                               | Ca_08931                            | R                     | MYB      |
| Ca5_P4_26995171  | Ca5                                     | 26995171                      | TAG/TAGCACAAGCACTAAG                                          | GGAGCGGGAATATGAC<br>TGAA     | GCGGCAGAAGAACCTA<br>TTTG  | 60.0                             | 576                                           | DRR                                               | Ca_08931                            | R                     | MYB      |
| Ca5_P4_26996169  | Ca5                                     | 26996169                      | TG/TGATCG                                                     | ATGTTGGGAAGCTTGCA<br>CTCC    | AACTATGTCCTGTGGA<br>CCGC  | 60.0                             | 458                                           | DRR                                               | Ca_08931                            | R                     | MYB      |
| Ca5_P4_27950124  | Ca5                                     | 27950124                      | TATCCAAAAT/TATCCAAAATTATTT<br>GATCCAAAAT                      | TTGCAACAAAGCGCTG<br>TAAC     | CTTGCCAATTCCAGTC<br>CAT   | 60.1                             | 640                                           | DRR                                               | Ca_13422                            | --                    | Trihelix |
| Ca5_P4_28012407  | Ca5                                     | 28012407                      | AATATATATATATAT/AAATATAT<br>ATATAT                            | TTGAAGGAAGATGAAT<br>CGTTGA   | ATGCGGATACTCTCTG<br>CCAC  | 59.7                             | 622                                           | DRR                                               | Ca_13417                            | S                     | --       |
| Ca5_P4_280542    | Ca5                                     | 280542                        | AATTATTATTATT/AATTATTATTATT<br>ATT                            | CAAACAAGCTTTTTCAC<br>TTTCTCA | AGGACCTCCCTTTTCT<br>CCA   | 60.0                             | 636                                           | DRR                                               | Ca_18183                            | --                    | ARF      |
| Ca5_P4_28150139  | Ca5                                     | 28150139                      | TGG/TGGACAGG                                                  | ATTGTGCAATGAATGT<br>CCGA     | CACTTGTGCGCTACAC<br>CACT  | 59.9                             | 199                                           | DRR                                               | Ca_13406                            | --                    | --       |
| Ca5_P4_28241837  | Ca5                                     | 28241837                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATATAT                 | TCGACCATAAACTATG<br>CAGACA   | TTCGTTCAAAGAACC<br>CA     | 59.7                             | 781                                           | DRR                                               | Ca_13400                            | --                    | ARF      |
| Ca5_P4_28281944  | Ca5                                     | 28281944                      | CTATATATATATATATATAT/CTAT<br>ATATATATATATATAT                 | GCAGAACAAAGACGTCA<br>GTATCG  | AAATGTTTCATCCGCCTT<br>CTG | 59.9                             | 702                                           | DRR                                               | Ca_13397                            | D                     | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                                 |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca5_P4_288048    | Ca5                                     | 288048                        | CTT/CTTTT                                                                       | GGACCAGCAAGAAGCA<br>ACTC | TGTGAGAAATGGAAT<br>TGGA   | 60.0                             | 933                                           | DRR                                               | Ca_18185                            | R                     | B3   |
| Ca5_P4_288684    | Ca5                                     | 288684                        | ATACTTACTT/ATACTT                                                               | CTTGGACTCCAGTGCC<br>TCAT | GTGCATTTTGCAGGCA<br>ATTA  | 60.3                             | 474                                           | DRR                                               | Ca_18185                            | R                     | B3   |
| Ca5_P4_291688    | Ca5                                     | 291688                        | ATTTTTT/ATTTTTTTT                                                               | AAAGAGCCAAAGAAGC<br>ACCA | AGCAAATGCGACTGTG<br>ATTG  | 60.0                             | 722                                           | DRR                                               | Ca_18186                            | --                    | --   |
| Ca5_P4_291943    | Ca5                                     | 291943                        | GCGCAACCGCAA/GCGCAACCGCA<br>ACCGCAA                                             | TTCGTGGCTTAATCCC<br>ACTC | GTCTGGTGCTCTTCCC<br>AATC  | 60.1                             | 517                                           | DRR                                               | Ca_18186                            | --                    | --   |
| Ca5_P4_292149    | Ca5                                     | 292149                        | A/AC                                                                            | AAAGTGCCGAAGTTTG<br>CAGT | TGCTTCCCTTCAACAG<br>TCA   | 59.9                             | 485                                           | DRR                                               | Ca_18186                            | --                    | --   |
| Ca5_P4_29735774  | Ca5                                     | 29735774                      | CATATATATATATATATATATATA<br>TATATATATA/CATATATATATATATA<br>TATATATATATATATATATA | GTTAATACCGCGGGGA<br>AAAT | CTCTCCAACCTCAATGCA<br>CCA | 60.0                             | 705                                           | DRR                                               | Ca_16655                            | R                     | --   |
| Ca5_P4_29938246  | Ca5                                     | 29938246                      | ATT/ATTT                                                                        | GCAAAAACAGCGACAC<br>TGAA | TTGTGTGGGAAAGGTG<br>ACAA  | 60.0                             | 764                                           | DRR                                               | Ca_16674                            | --                    | --   |
| Ca5_P4_29938358  | Ca5                                     | 29938358                      | ATT/AT                                                                          | AGCTTTGAATGGCAAT<br>GGAC | TTGTGTGGGAAAGGTG<br>ACAA  | 60.1                             | 380                                           | DRR                                               | Ca_16674                            | --                    | --   |
| Ca5_P4_31133950  | Ca5                                     | 31133950                      | A/AC                                                                            | GAGGAGATTGGGGAG<br>CAACT | CTCATTGGCCATGAAA<br>GGAT  | 60.6                             | 539                                           | DRR                                               | Ca_04815                            | --                    | --   |
| Ca5_P4_31147221  | Ca5                                     | 31147221                      | CG/CGG                                                                          | CTTGTCAGCAACCAA<br>CGTA  | ACCCTGGATATTAGGG<br>TGGC  | 59.8                             | 378                                           | DRR                                               | Ca_04818                            | --                    | GRAS |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                           |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca5_P4_31161168  | Ca5                                     | 31161168                      | TTATATATATATATATATATATATATATATATAT/TTATATATATATATATATATATATATATATATATATAT | TTCTTTGAAAGCATGG<br>ACCC  | TCTCGGAATCTTTCC<br>AAAC    | 60.1                             | 469                                           | DRR                                               | Ca_04820                            | S                     | CPP         |
| Ca5_P4_31183021  | Ca5                                     | 31183021                      | ATTT/ATTTTTT                                                              | CCAAACACTCAAACCG<br>ACTC  | AAAGACCAAATTGGAC<br>ACTTCA | 58.2                             | 817                                           | DRR                                               | Ca_04823                            | --                    | WOX         |
| Ca5_P4_31512273  | Ca5                                     | 31512273                      | AT/ATATATCT                                                               | GCCATGATCAATGCAA<br>GAGA  | TTTCCAACCCACAAAAT<br>CAA   | 59.8                             | 450                                           | DRR                                               | Ca_04853                            | Q                     | --          |
| Ca5_P4_31691419  | Ca5                                     | 31691419                      | TACATACAC/TAC                                                             | CCGTTCAACCTCTGCA<br>TCTT  | TCTGTCATCCAATCTCA<br>ACTCG | 60.3                             | 216                                           | DRR                                               | Ca_04871                            | OJ                    | bZIP        |
| Ca5_P4_31813449  | Ca5                                     | 31813449                      | TTAT/TT                                                                   | TTTTCAACCTTTTCGTT<br>CCAA | GGTCAGCGTTATATCC<br>CACAA  | 59.6                             | 696                                           | DRR                                               | Ca_04886                            | Z                     | --          |
| Ca5_P4_32005288  | Ca5                                     | 32005288                      | CAATAACAAATAACAAA/CAATAACA<br>AATAACAAATAACAAA                            | AAACCCGATAAAAAGC<br>GTGA  | ACAGAAAAAGCGGATA<br>GGCA   | 59.6                             | 526                                           | DRR                                               | Ca_04904                            | Z                     | MYB_related |
| Ca5_P4_32233     | Ca5                                     | 32233                         | ATTTTTTTTTT/ATTTTTTTTTT                                                   | TTTTGGTTTGGGATGG<br>TTGT  | GGAGATCACTCGGGTT<br>GTGT   | 60.1                             | 585                                           | DRR                                               | Ca_18158                            | --                    | --          |
| Ca5_P4_32388967  | Ca5                                     | 32388967                      | CTATTATTTTATTATTTTATTA/CTAT<br>TATTTATTATTTTATTATTTTATTA                  | AATTGCGATAAGCAATT<br>GGG  | TAGGATTACACGGGCG<br>AGAC   | 59.9                             | 821                                           | DRR                                               | Ca_04938                            | --                    | bZIP        |
| Ca5_P4_33146690  | Ca5                                     | 33146690                      | TAAAAAAAAA/TAAAAAAAAA                                                     | TACCCGAACAACTTTG<br>ACCC  | TGCTTTCGTGATTCCAA<br>CAA   | 59.8                             | 731                                           | DRR                                               | Ca_05009                            | D                     | YABBY       |
| Ca5_P4_3337230   | Ca5                                     | 3337230                       | CATATATATATAT/CATATATATATAT<br>ATAT                                       | TCATCCCGAATCAGTT<br>CACA  | GGCATGATGCAAGGGA<br>TAGT   | 60.0                             | 291                                           | DRR                                               | Ca_18697                            | --                    | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                           |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca5_P4_33444959  | Ca5                                     | 33444959                      | GATATA/GATATATA                                               | TTATGGAGGCCACATT<br>CACA  | GAAATTAAGGCCTCTT<br>GATCTTTTT | 59.9                             | 961                                           | DRR                                               | Ca_01912                            | O                     | MYB_related |
| Ca5_P4_33456475  | Ca5                                     | 33456475                      | TTATGTTAAATATGTTAA/TTATGTTA<br>AATATGTTAAATATGTTAA            | GATGAAGTGCTGATCA<br>GAGGC | ACCAGGAAACATTGCC<br>AGAC      | 60.0                             | 789                                           | DRR                                               | Ca_01911                            | O                     | MYB_related |
| Ca5_P4_33457459  | Ca5                                     | 33457459                      | ATT/ATTT                                                      | TCTTCAAATTAATTC<br>CACCCA | GTTGAAATTTGGGTG<br>TCGG       | 59.7                             | 750                                           | DRR                                               | Ca_01911                            | O                     | MYB_related |
| Ca5_P4_33457924  | Ca5                                     | 33457924                      | ATTTTTTT/ATTTTTTTT                                            | CCGACACCCAAATTT<br>CAAC   | GCCCTCAGATGAGAGT<br>CAGG      | 60.2                             | 680                                           | DRR                                               | Ca_01911                            | O                     | MYB_related |
| Ca5_P4_33525483  | Ca5                                     | 33525483                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATAT               | CAACATGCATCAGGCG<br>TATC  | TTGGATTGGACGTTGT<br>TGTT      | 60.1                             | 433                                           | DRR                                               | Ca_01906                            | --                    | --          |
| Ca5_P4_33600042  | Ca5                                     | 33600042                      | CT/C                                                          | TAACCATTCACAGCC<br>ACAA   | CTTAGAGGTCGCTTCA<br>ACGG      | 60.0                             | 680                                           | DRR                                               | Ca_01896                            | --                    | --          |
| Ca5_P4_33600975  | Ca5                                     | 33600975                      | C/CAACCTA                                                     | CGTTGAGGACTTACCC<br>GAAA  | CCGTTGGTGTTAAAGG<br>GAGA      | 60.1                             | 351                                           | DRR                                               | Ca_01896                            | --                    | --          |
| Ca5_P4_336785    | Ca5                                     | 336785                        | CAAAAAAAAA/CAAAAAAAAA                                         | GCCTACGTCAGACCGA<br>TGTT  | TCCTGGCAGAAATTTG<br>GTTC      | 60.1                             | 458                                           | DRR                                               | Ca_18190                            | H                     | --          |
| Ca5_P4_337016    | Ca5                                     | 337016                        | ATTT/ATTTT                                                    | CCAAACTGGGGAGAA<br>ACAA   | TGATATTGGAGGGGGC<br>ATAA      | 59.9                             | 306                                           | DRR                                               | Ca_18190                            | H                     | --          |
| Ca5_P4_3406072   | Ca5                                     | 3406072                       | TAAAA/TAAAA                                                   | TTCACCCATTGTATGCT<br>TTGA | GCGGTGTTGAAAAGGA<br>AAAG      | 59.0                             | 832                                           | DRR                                               | Ca_18699                            | K                     | MYB         |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                 |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_34191964  | Ca5                                     | 34191964                      | AAATAATAATAATAATAATAATA<br>AT/AAATAATAATAATAATAATAA<br>TAATAAT  | AGGCAAAATGTTTTCA<br>CGG    | TTTGTTTTGGCACATGC<br>ACT   | 60.0                             | 561                                           | DRR                                               | Ca_01828                            | --                    | --  |
| Ca5_P4_34332054  | Ca5                                     | 34332054                      | AATATATATATATATATATAT/AAT<br>ATATATATATATATATATATATATA<br>TAT   | AAATTGCAAAGACCAAT<br>GAACA | CAACAAAAGTGGCACA<br>ATCC   | 59.5                             | 659                                           | DRR                                               | Ca_01814                            | --                    | --  |
| Ca5_P4_34771204  | Ca5                                     | 34771204                      | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATA<br>TATAT | TCTCATGTTTCCCAACC<br>ACA   | CTGGACCACATTCTGG<br>CTCT   | 59.9                             | 487                                           | DRR                                               | Ca_01764                            | --                    | ERF |
| Ca5_P4_34854970  | Ca5                                     | 34854970                      | AAATAATAATAATAATA/AAATAA<br>TAATAATAATAATAATA                   | TCCCACCGTGATCGTT<br>TTAT   | CAAGGAACTTGGACCG<br>TCAT   | 60.2                             | 732                                           | DRR                                               | Ca_01754                            | --                    | ARF |
| Ca5_P4_35176516  | Ca5                                     | 35176516                      | GATATATATATATATAT/GATATAT<br>ATATATATATATAT                     | TTTGATAACAAGCCA<br>GCAC    | AGGCTGTCCCCATCAT<br>TGTA   | 59.9                             | 490                                           | DRR                                               | Ca_01718                            | R                     | --  |
| Ca5_P4_35689449  | Ca5                                     | 35689449                      | TC/T                                                            | CGTTGCAACAGAAGCA<br>GAAG   | GATCCAAAGCCCTCAA<br>TGAA   | 59.8                             | 566                                           | DRR                                               | Ca_01660                            | M                     | --  |
| Ca5_P4_360986    | Ca5                                     | 360986                        | ATTTTTTTTT/ATTTTTTTTT                                           | TGTGAGTTTAAGGGAG<br>GGGA   | GCATCCAGGATCAGAG<br>GTGT   | 59.5                             | 390                                           | DRR                                               | Ca_18192                            | P                     | --  |
| Ca5_P4_36176137  | Ca5                                     | 36176137                      | AATATATATATAT/AATATATATAT<br>AT                                 | TCATTGACATTTTGTCC<br>CCA   | TTGATTGGAAGGTTT<br>GTCA    | 59.8                             | 617                                           | DRR                                               | Ca_01608                            | --                    | --  |
| Ca5_P4_36212540  | Ca5                                     | 36212540                      | GTT/GTTAGATT                                                    | TTTCATTGTTCCGTCA<br>CCA    | TTGAGTCAATGCAAGA<br>GTCCCT | 59.9                             | 874                                           | DRR                                               | Ca_01603                            | I                     | B3  |
| Ca5_P4_36308359  | Ca5                                     | 36308359                      | TTTATT/TTTATTGGTATTATTATT<br>T                                  | GTTTGTGGCGGATTT<br>GTTT    | CCGATACAACGGAATT<br>GTCC   | 59.8                             | 423                                           | DRR                                               | Ca_01593                            | Z                     | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                             |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca5_P4_36410469  | Ca5                                     | 36410469                      | AG/A                                                          | TGGAAACGAGTCCAAC<br>AACA    | ACCTCCCTGTTTGTCAA<br>TCG      | 60.1                             | 452                                           | DRR                                               | Ca_01583                            | E                     | --          |
| Ca5_P4_36432725  | Ca5                                     | 36432725                      | AG/A                                                          | TCTCCAAAACACCGAG<br>ACAA    | TGGATCAACATTTCCCA<br>ATTC     | 59.3                             | 679                                           | DRR                                               | Ca_01577                            | --                    | --          |
| Ca5_P4_37107723  | Ca5                                     | 37107723                      | TAAAAAAAAA/TAAAAAAAAA                                         | TTACCCGCTGAAAACC<br>TTTG    | GAGCAGAGGCGGATGT<br>TTTA      | 60.1                             | 445                                           | DRR                                               | Ca_01506                            | D                     | LBD         |
| Ca5_P4_37460031  | Ca5                                     | 37460031                      | CATATATATATATATAT/CATATAT<br>ATATATATAT                       | GGACAGCCCTGGTAAT<br>CAAA    | CCTGCAAAACCACATTTT<br>CCT     | 59.9                             | 958                                           | DRR                                               | Ca_01474                            | U                     | --          |
| Ca5_P4_37799581  | Ca5                                     | 37799581                      | CTTTTT/CTTTTTT                                                | GCACCGTGATTTTGAT<br>GATG    | ATCAAGTCAGTGTGTC<br>ATCG      | 59.9                             | 594                                           | DRR                                               | Ca_01443                            | --                    | --          |
| Ca5_P4_37981188  | Ca5                                     | 37981188                      | TAAAA/TAAAAA                                                  | AAGGAAACACGCATCC<br>AAAC    | TGCGCAAAATCGTAGA<br>CAAG      | 60.0                             | 311                                           | DRR                                               | Ca_01422                            | B                     | MYB_related |
| Ca5_P4_37981277  | Ca5                                     | 37981277                      | ATT/AT                                                        | AAGGAAACACGCATCC<br>AAAC    | TGCGCAAAATCGTAGA<br>CAAG      | 60.0                             | 311                                           | DRR                                               | Ca_01422                            | B                     | MYB_related |
| Ca5_P4_38028193  | Ca5                                     | 38028193                      | AT/A                                                          | TGGCAAGAATACCTTG<br>TAAGCA  | TCAAATTCGTAAC TCA<br>ATCTTCAA | 59.8                             | 595                                           | DRR                                               | Ca_01418                            | R                     | DBB         |
| Ca5_P4_38028753  | Ca5                                     | 38028753                      | A/AC                                                          | TGGACCACGTGTACTA<br>TTTAACC | CCAAGTGTATTGGAG<br>GGAGA      | 58.0                             | 524                                           | DRR                                               | Ca_01418                            | R                     | DBB         |
| Ca5_P4_38028815  | Ca5                                     | 38028815                      | TAAAAAAAA/TAAAAA                                              | TCAATCACCTTAGAATC<br>TCACCC | TCCAAGTGTATTGGA<br>GGGAG      | 59.5                             | 287                                           | DRR                                               | Ca_01418                            | R                     | DBB         |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca5_P4_38030046  | Ca5                                     | 38030046                      | AAT/AATAT                                                     | TCAAAAACGGACATGA<br>GCA  | TTTATGGACAGCTCCC<br>GAAC   | 60.2                             | 614                                           | DRR                                               | Ca_01418                            | R                     | DBB         |
| Ca5_P4_38059062  | Ca5                                     | 38059062                      | ATTTTTTTTT/ATTTTTTT                                           | CGGCCTAAATAGTACC<br>GCA  | TTTGTGGCACCACACA<br>AGAT   | 60.1                             | 728                                           | DRR                                               | Ca_01417                            | R                     | --          |
| Ca5_P4_38061782  | Ca5                                     | 38061782                      | ATTTT/ATT                                                     | CCCTCCGTGTTTATTTA<br>CCG | CACTCTAGCTTTGGGC<br>TTGG   | 59.3                             | 687                                           | DRR                                               | Ca_01416                            | --                    | --          |
| Ca5_P4_38067755  | Ca5                                     | 38067755                      | AGACAG/A                                                      | AGCAATGTGCACAATC<br>CAAA | GCGACAGATTCAACTC<br>ACAGA  | 60.1                             | 106                                           | DRR                                               | Ca_01413                            | --                    | --          |
| Ca5_P4_38068074  | Ca5                                     | 38068074                      | ATTTTTTTTT/ATTTTTTT                                           | GCAATGTGCACAATCC<br>AAAC | CCCTTACCTGCTAAGC<br>GAAA   | 60.0                             | 580                                           | DRR                                               | Ca_01413                            | --                    | --          |
| Ca5_P4_38068190  | Ca5                                     | 38068190                      | GAAAAGAAAAGA/GAAAAGAAAA<br>GAAAAGA                            | GCAATGTGCACAATCC<br>AAAC | CCCTTACCTGCTAAGC<br>GAAA   | 60.0                             | 580                                           | DRR                                               | Ca_01413                            | --                    | --          |
| Ca5_P4_38076271  | Ca5                                     | 38076271                      | T/TTAACAAATG                                                  | CCGAATTTGTTTGCTA<br>CCGT | TTTTGACACATCTATCC<br>AATCG | 60.0                             | 388                                           | DRR                                               | Ca_01412                            | O                     | MYB_related |
| Ca5_P4_38087876  | Ca5                                     | 38087876                      | ACCTCAAC/ACCTCAACAGTCCTCA<br>AC                               | CCTTGTTTTCGTGAAT<br>GCCT | GCATTTTGAATGCCTC<br>CACT   | 60.1                             | 567                                           | DRR                                               | Ca_01409                            | --                    | --          |
| Ca5_P4_38104582  | Ca5                                     | 38104582                      | TAAAAAAA/TAAAAAAA                                             | TACTGGTGGATTGATC<br>CGGT | TGGGCATCCCAGTGT<br>TAAT    | 60.2                             | 641                                           | DRR                                               | Ca_01408                            | P                     | --          |
| Ca5_P4_38110814  | Ca5                                     | 38110814                      | AATATAT/AATATATAT                                             | ACCAATCCAGCAGAC<br>AATC  | CAATCTGTTTTCGTGGT<br>CTTTG | 59.9                             | 243                                           | DRR                                               | Ca_01407                            | S                     | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                 | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca5_P4_38128399  | Ca5                                     | 38128399                      | GCAACACAACCA/GCA                                                                              | GGAAGTTGGCATTCA<br>CTGT  | GCTGGTCTTTTCCCTT<br>GTG  | 60.0                             | 693                                           | DRR                                               | Ca_01405                            | A                     | --     |
| Ca5_P4_38142286  | Ca5                                     | 38142286                      | GACACA/GACA                                                                                   | TTGTTCCCTTTTGGAT<br>GAGG | ACTTTGCTGGCAATGT<br>GTGT | 59.9                             | 526                                           | DRR                                               | Ca_01403                            | R                     | NAC    |
| Ca5_P4_38142542  | Ca5                                     | 38142542                      | ATTTTT/ATTTTTTTTT                                                                             | TGCAACATGAAGGTCA<br>CACA | ATCGATCGTCAGCTGA<br>TTCC | 59.7                             | 466                                           | DRR                                               | Ca_01403                            | R                     | NAC    |
| Ca5_P4_38149695  | Ca5                                     | 38149695                      | TGATGTAGATGTAGA/TGATGTAGA<br>TGATAGGTAGA                                                      | ATGGCCAGTCATGTCA<br>CAAA | TGGAGGAAGAACCGAA<br>AATG | 60.0                             | 330                                           | DRR                                               | Ca_01402                            | --                    | bHLH   |
| Ca5_P4_38364224  | Ca5                                     | 38364224                      | CTATATATATATATATATATATATA<br>ATA/CTATATATATATATATATATATA<br>TATA                              | TCGCAATTTGGAAGA<br>GTTTT | ACGTCGGTGGACTCAA<br>ATTC | 58.9                             | 333                                           | DRR                                               | Ca_01388                            | --                    | --     |
| Ca5_P4_38382482  | Ca5                                     | 38382482                      | TATAATAATAATAATAATAATAATA<br>TAATAATAATAAT/TATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAAT | GGTGGAGACGTGGAA<br>CAACT | CCGACGGAAATGTACC<br>AATC | 60.0                             | 806                                           | DRR                                               | Ca_01386                            | --                    | LFY    |
| Ca5_P4_38726886  | Ca5                                     | 38726886                      | AATCAATCTTCCATCA/AATCAATCT<br>TCCATCATCAATCTTCCATCA                                           | CGAGTTTGTGGGGA<br>GATTA  | TGGAGGAGGCAAAATC<br>TGTC | 59.9                             | 465                                           | DRR                                               | Ca_07423                            | O                     | --     |
| Ca5_P4_39793489  | Ca5                                     | 39793489                      | CAAAAAAAAA/CAAAAAAAAA                                                                         | AGGGCACTTTGTCTCC<br>TCAA | ACCAAATCGATGGAAT<br>GACC | 59.8                             | 529                                           | DRR                                               | Ca_07506                            | S                     | bZIP   |
| Ca5_P4_39872057  | Ca5                                     | 39872057                      | GATATATATATATATATATATATA<br>TAT/GATATATATATATATATATATA<br>TATATA                              | AGGAAAACATTGGTG<br>GACA  | ATCAAACAACCGAAAGT<br>GCC | 60.2                             | 656                                           | DRR                                               | Ca_07512                            | F                     | --     |
| Ca5_P4_40858234  | Ca5                                     | 40858234                      | GATATATATATATATATATATATA<br>TATATATATATA/GATATATATATATA<br>TATATATATATATATATATA               | AGGCATGGTGTGGAG<br>TCAT  | TCCGACAAGGAGAATA<br>ACCG | 60.4                             | 650                                           | DRR                                               | Ca_07607                            | K                     | M-type |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                                                                 |                              |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca5_P4_41377707  | Ca5                                     | 41377707                      | TG/TGGTTAGGG                                                                                    | AAGAAACGGGTATGTG<br>GCTG     | TTGCAATCGCACTCCA<br>ATAG     | 60.0                             | 575                                           | DRR                                               | Ca_19238                            | --                    | --      |
| Ca5_P4_42076019  | Ca5                                     | 42076019                      | GTTTTTTTTTTT/GTTTTTTTTTTT                                                                       | TGAGAATCCAATTCG<br>GGAC      | TTGTTACGATTCTCGCA<br>GGT     | 59.9                             | 197                                           | DRR                                               | Ca_11404                            | R                     | G2-like |
| Ca5_P4_42657457  | Ca5                                     | 42657457                      | AT/ATT                                                                                          | TGTCAAATTGGCCTGC<br>ATTA     | GTGCAACAGCTGCAAT<br>AGGA     | 60.1                             | 222                                           | DRR                                               | Ca_11347                            | B                     | C3H     |
| Ca5_P4_42948243  | Ca5                                     | 42948243                      | TTA/TTATA                                                                                       | GGGAAGGAGTTTACG<br>GAGG      | GAACGACAAGTCAACA<br>AAGTCC   | 59.9                             | 679                                           | DRR                                               | Ca_11314                            | O                     | --      |
| Ca5_P4_43007181  | Ca5                                     | 43007181                      | AATATATATATATATATATATATAT<br>ATATA/AATATATATATATATATATAT<br>ATATATA                             | ACCGATGGAATGCAAC<br>ACTT     | CCCGAAATTAAGTTAAG<br>GGACC   | 60.4                             | 657                                           | DRR                                               | Ca_11308                            | --                    | bHLH    |
| Ca5_P4_43179356  | Ca5                                     | 43179356                      | AAACAATAACAA/AAACAA                                                                             | GGAAACATGGTCAGCT<br>GCTT     | GCATTTTCTTCACTAGG<br>CCC     | 60.3                             | 757                                           | DRR                                               | Ca_12741                            | --                    | --      |
| Ca5_P4_43298677  | Ca5                                     | 43298677                      | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATATAT<br>ATATA                               | TCAAATTTGCAAAGACA<br>GATTTTC | TTTTGGTGTCACCTTAAG<br>AGTGGA | 59.7                             | 893                                           | DRR                                               | Ca_12727                            | --                    | --      |
| Ca5_P4_43299130  | Ca5                                     | 43299130                      | TC/T                                                                                            | TTGGTTTACGAATTTTA<br>TGGTGAA | CTGCATAGGCAGGGTG<br>GTAG     | 59.7                             | 385                                           | DRR                                               | Ca_12727                            | --                    | --      |
| Ca5_P4_43366856  | Ca5                                     | 43366856                      | CAAC/CAACATAAATGATAAC                                                                           | TGTAGATTGGGTGTGG<br>CAGA     | ATTGGGTGCTCAAGGA<br>CAAG     | 60.1                             | 970                                           | DRR                                               | Ca_12719                            | --                    | SAP     |
| Ca5_P4_43861667  | Ca5                                     | 43861667                      | CAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATA/CAATAATA<br>ATAATAATAATAATAATAATAATAAT<br>AATAATA | TCTTCCCATGTGCCCT<br>TTAG     | AAGAGGCAAGTTTGAA<br>CTCGTAA  | 60.1                             | 467                                           | DRR                                               | Ca_12668                            | I                     | G2-like |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                                 |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca5_P4_44522099  | Ca5                                     | 44522099                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>TTATTATTATTATTATTATTATT                 | TAGCCGCTACCAATTA<br>TCGC   | CTTTTAATGGCAAATGG<br>CGT     | 60.2                             | 663                                           | DRR                                               | Ca_03897                            | R                     | --       |
| Ca5_P4_45182561  | Ca5                                     | 45182561                      | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATAT<br>TATAT                                | TAGATATCCGAATCGG<br>CCTG   | TGACTTGATTCGGGTG<br>ATGA     | 60.0                             | 272                                           | DRR                                               | Ca_03960                            | --                    | Trihelix |
| Ca5_P4_45327318  | Ca5                                     | 45327318                      | CGGTGATGGTGATGGTGATGGTGA<br>TGGTGATGGTGATG/CGGTGATGGT<br>GATGGTGATGGTGATGGTGATGGT<br>GATGGTGATG | AGGAATGTAGTTTGGC<br>GTGG   | TCCATAGATAAAACAAA<br>GGGGAAA | 60.0                             | 770                                           | DRR                                               | Ca_03975                            | QR                    | B3       |
| Ca5_P4_45523588  | Ca5                                     | 45523588                      | TAAAAATTAAAAATTAAAAATTAA<br>AAAA/TAAAAATTAAAAATTAAAAA                                           | TCCACATGTTTTCCGAT<br>AGTTG | TCGGTACAAAAGGTGT<br>TTTCG    | 59.9                             | 585                                           | DRR                                               | Ca_04000                            | YU                    | --       |
| Ca5_P4_457302    | Ca5                                     | 457302                        | CGT/CAAAGACCGTTGTGT                                                                             | CACAAGAAAGGGAATG<br>ACACTG | ACCACACAACCTTTGGG<br>CTTC    | 59.6                             | 643                                           | DRR                                               | Ca_18199                            | --                    | --       |
| Ca5_P4_45746975  | Ca5                                     | 45746975                      | ATT/ATTACACTCTTT                                                                                | GGAGTTGCAAAAGAGC<br>ATGA   | TGGTTAACTGGAGA<br>GGGG       | 59.0                             | 136                                           | DRR                                               | Ca_04024                            | G                     | --       |
| Ca5_P4_46305506  | Ca5                                     | 46305506                      | GATATATATATATATATATATATAT<br>TATATATATAT/GATATATATATAT<br>ATATATATATATATATATATATATAT<br>TAT     | TGCCCTCAATCTGAAA<br>ACAA   | GAACAAGAGCGGTCTC<br>ACAA     | 59.2                             | 876                                           | DRR                                               | Ca_04084                            | --                    | --       |
| Ca5_P4_46946905  | Ca5                                     | 46946905                      | AATATATATATATATATAT/AATATAT<br>ATATATATATATATAT                                                 | CATCCGTGGTCCTTTG<br>ACTT   | TGGTCATTGCATTTTCC<br>TCA     | 60.0                             | 482                                           | DRR                                               | Ca_04149                            | K                     | ERF      |
| Ca5_P4_47632016  | Ca5                                     | 47632016                      | CAGTGT/C                                                                                        | GGAGGTCGCTTGCTAA<br>GTTG   | AATGGCCCAACTCCTA<br>TTCC     | 60.0                             | 695                                           | DRR                                               | Ca_04223                            | S                     | --       |
| Ca5_P4_47692025  | Ca5                                     | 47692025                      | ATTTTTTTTT/ATTTTTTTT                                                                            | CACCAAAAGCAGGGTC<br>TCTC   | GCCTTAAAGCTTTGGG<br>TGAA     | 59.8                             | 346                                           | DRR                                               | Ca_04228                            | --                    | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca5_P4_479066    | Ca5                                     | 479066                        | TAAAAAAAAA/TAAAAAAAAA                                                         | CCTGTTCTGTAGTGGG<br>AGCC   | TCCATGTTACTTCTCCG<br>CCT | 59.7                             | 508                                           | DRR                                               | Ca_18200                            | U                     | --   |
| Ca5_P4_479350    | Ca5                                     | 479350                        | CATATATATATATATA/CATATATATA<br>TATATATA                                       | TTGTCACACAATAAGG<br>CGGA   | TCATCACGATCTGAATC<br>CCA | 60.1                             | 674                                           | DRR                                               | Ca_18200                            | U                     | --   |
| Ca5_P4_480514    | Ca5                                     | 480514                        | AATAATAATAAT/AATAATAATAATTA<br>TAATAATAAT                                     | AAGAACTTGAACAAT<br>GAGGTGG | GATCAGGATGAACGG<br>AAGA  | 59.6                             | 610                                           | DRR                                               | Ca_18201                            | --                    | --   |
| Ca5_P4_482095    | Ca5                                     | 482095                        | GC/G                                                                          | TTGCATCTGTCAGCGA<br>ACTC   | TTTTTCGGGGTCAAA<br>TGTA  | 60.1                             | 800                                           | DRR                                               | Ca_18201                            | --                    | --   |
| Ca5_P4_5292404   | Ca5                                     | 5292404                       | GA/G                                                                          | GGGAGGATTGTAACAG<br>CGAA   | GCTGCAAGAATCAACG<br>TCAA | 60.1                             | 177                                           | DRR                                               | Ca_22623                            | --                    | --   |
| Ca5_P4_667833    | Ca5                                     | 667833                        | GC/G                                                                          | TGAGCCACTGTTTGGA<br>ACAC   | TGTTGCTCCTCACGAA<br>TCTG | 59.7                             | 473                                           | DRR                                               | Ca_23223                            | --                    | --   |
| Ca5_P4_668104    | Ca5                                     | 668104                        | ATT/AT                                                                        | CAGATTCGTGAGGAGC<br>AACA   | TGAATCCCCTCTGATC<br>CTTG | 60.0                             | 331                                           | DRR                                               | Ca_23223                            | --                    | --   |
| Ca5_P4_71060     | Ca5                                     | 71060                         | GC/GCCTCTGTTATGAAAC                                                           | GGTGGGGATGGATGTA<br>GATG   | TGAACAAACATTGGG<br>CAAA  | 60.0                             | 627                                           | DRR                                               | Ca_18161                            | R                     | FAR1 |
| Ca5_P4_7639595   | Ca5                                     | 7639595                       | AAGAGAGAGAGAGAGAGAGAGA<br>GAGAGAGAGA/AAGAGAGAGAGAG<br>AGAGAGAGAGAGAGAGAGAGAGA | AACCAAGCCAACCTCA<br>ACAG   | CCCTTTCATGCCAACAA<br>AAT | 60.1                             | 392                                           | DRR                                               | Ca_18738                            | --                    | B3   |
| Ca5_P4_7726586   | Ca5                                     | 7726586                       | GTT/GTTT                                                                      | CTGGAAATCCTCCTC<br>CTCC    | TTGTCTCAACAATCTCC<br>CCC | 60.0                             | 339                                           | DRR                                               | Ca_18731                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                      | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                    |                               |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca5_P4_7920333   | Ca5                                     | 7920333                       | AATATA/AATATATA                                                                    | ATGCTTAGCGGAGTGG<br>AAAA      | GATATTGTTGGCGTT<br>GGAG    | 59.8                             | 193                                           | DRR                                               | Ca_18721                            | T                     | M-type   |
| Ca5_P4_8824148   | Ca5                                     | 8824148                       | A/ATGT                                                                             | GGAGCTGAGGTTGAG<br>GTTGA      | CAATATCGGCAAATTGA<br>AGTGA | 60.4                             | 476                                           | DRR                                               | Ca_20336                            | A                     | --       |
| Ca5_P4_9360000   | Ca5                                     | 9360000                       | TAAAAA/TAAAAA                                                                      | GGCTGATGTTATTGCC<br>TGGA      | TCGTCATCACTTGTGG<br>TGGT   | 61.0                             | 791                                           | DRR                                               | Ca_19977                            | T                     | --       |
| Ca5_P4_9787406   | Ca5                                     | 9787406                       | CT/CTTTATCTGT                                                                      | CACGTCGAAAAGTCAC<br>ATCG      | TGCATTACCTCCCCTC<br>AAG    | 60.3                             | 728                                           | DRR                                               | Ca_20498                            | S                     | --       |
| Ca5_P4_9820324   | Ca5                                     | 9820324                       | CTTTT/CTT                                                                          | CAGAACTCAACTTGCA<br>CCGA      | TTGGCACCGAGAAGTT<br>CTTT   | 60.0                             | 701                                           | DRR                                               | Ca_20501                            | O                     | --       |
| Ca6_P4_10090816  | Ca6                                     | 10090816                      | ATTATTTATTTATTTATTTATTT<br>ATTTATTTATTTATT/ATTATTTATTT<br>ATTTATTTATTTATTTATTTATTT | CCCGCAAAATTAAGTG<br>GGTA      | CCCATACCCGTTATCC<br>ACAC   | 59.8                             | 560                                           | DRR                                               | Ca_08583                            | Z                     | Trihelix |
| Ca6_P4_10120649  | Ca6                                     | 10120649                      | TAAAAAAAAA/TAAAAAAAAA                                                              | TGTTATTTGAACGCAAA<br>TGG      | AATCAGAAGGAGGGAC<br>CAAAA  | 57.2                             | 786                                           | DRR                                               | Ca_08580                            | J                     | --       |
| Ca6_P4_10566584  | Ca6                                     | 10566584                      | C/CTT                                                                              | TTTTGTCAATTTGGTATT<br>CATTTCA | GGCTTGCAACCCAATT<br>ATTTT  | 58.5                             | 600                                           | DRR                                               | Ca_08541                            | --                    | --       |
| Ca6_P4_10606087  | Ca6                                     | 10606087                      | TTCT/TTCTCT                                                                        | GAAGGTTTACGTTTTG<br>CCCA      | GGCTACCAAGAATTG<br>GACG    | 60.0                             | 533                                           | DRR                                               | Ca_08537                            | H                     | --       |
| Ca6_P4_10611238  | Ca6                                     | 10611238                      | AG/A                                                                               | TCTGACATGACAAAT<br>GGTGG      | TCGGAATTGGTCCGAA<br>ATTA   | 59.4                             | 409                                           | DRR                                               | Ca_08536                            | K                     | HSF      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                              | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                                                            |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca6_P4_10611559  | Ca6                                     | 10611559                      | AG/AGTTTACACTCCGATG                                                                                        | ATATTTTCTCCAAGG<br>CGG    | TTGTTTGTTCAAGG<br>AAGG     | 60.3                             | 711                                           | DRR                                               | Ca_08536                            | K                     | HSF  |
| Ca6_P4_10649780  | Ca6                                     | 10649780                      | TAA/TAA                                                                                                    | GACGGTTATGGAGCCT<br>TCAA  | TTGCATATCTTGTGCCT<br>CCC   | 60.1                             | 363                                           | DRR                                               | Ca_08532                            | --                    | HSF  |
| Ca6_P4_10649918  | Ca6                                     | 10649918                      | GTTTGTTTTGTTTTGTTTT/GTTTGT<br>TTTGTTTTGTTTTGTTTT                                                           | GACGGTTATGGAGCCT<br>TCAA  | TTGCATATCTTGTGCCT<br>CCC   | 60.1                             | 363                                           | DRR                                               | Ca_08531                            | I                     | --   |
| Ca6_P4_10695609  | Ca6                                     | 10695609                      | TAAAAAAAAAAAA/TAAAAAAAAA                                                                                   | CTCCGTAATGAAACCC<br>GAGA  | AGGAAGGGGAACGACC<br>TAGA   | 60.1                             | 744                                           | DRR                                               | Ca_08528                            | --                    | bHLH |
| Ca6_P4_10708022  | Ca6                                     | 10708022                      | GCT/GCTGAATCT                                                                                              | CCAAGGGTTGGCTAGA<br>ACTG  | TGGAAAATATGTGTGG<br>GATCAG | 59.7                             | 689                                           | DRR                                               | Ca_08527                            | GC                    | HSF  |
| Ca6_P4_10708200  | Ca6                                     | 10708200                      | TATTAATTA/TATTA                                                                                            | GTGGGTACAGAAACAT<br>GGCA  | TGGAAAATATGTGTGG<br>GATCAG | 59.4                             | 539                                           | DRR                                               | Ca_08527                            | GC                    | HSF  |
| Ca6_P4_10708661  | Ca6                                     | 10708661                      | TAAAAAA/TAAAAA                                                                                             | TGAAATTCAACTGATCC<br>CACA | TCCTTTGGTGGTGT<br>CCTC     | 59.0                             | 811                                           | DRR                                               | Ca_08527                            | GC                    | HSF  |
| Ca6_P4_1094043   | Ca6                                     | 1094043                       | ATTTT/ATTTT                                                                                                | TGTCATGGCAACATTC<br>ACAA  | TCCTGCCACCATCTTTA<br>ACC   | 59.5                             | 572                                           | DRR                                               | Ca_13316                            | --                    | --   |
| Ca6_P4_10953097  | Ca6                                     | 10953097                      | CTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>/CTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTA | TTGGCTTCTCGTTGGA<br>TTTT  | AGTTTCGGGGTTCCTT<br>CTTT   | 59.7                             | 298                                           | DRR                                               | Ca_20466                            | QR                    | B3   |
| Ca6_P4_11513553  | Ca6                                     | 11513553                      | ATGTGTGTGTGT/ATGTGTGTGT                                                                                    | ATGCCACCCATAATT<br>TCA    | CTTGCCAATTCCAGTC<br>CAT    | 60.0                             | 404                                           | DRR                                               | Ca_23432                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca6_P4_11632067  | Ca6                                     | 11632067                      | GGTGTG/GGTG                                                   | CCAAAGTTAGCCCTTC<br>CTCC   | AGCACTGACCTTTTGA<br>GCGT | 60.1                             | 445                                           | DRR                                               | Ca_25057                            | S                     | --          |
| Ca6_P4_11649630  | Ca6                                     | 11649630                      | GACTA/GACTAACTA                                               | TTGCTTGTGCAAAAGA<br>ATGC   | TACTATGCGTGGACCC<br>TTCC | 60.0                             | 522                                           | DRR                                               | Ca_25059                            | J                     | --          |
| Ca6_P4_12335628  | Ca6                                     | 12335628                      | TGAAG/TG                                                      | GGAAGGGTGTGGTGT<br>GTTT    | TTGGTCACTAAGGGGG<br>TGAG | 59.7                             | 968                                           | DRR                                               | Ca_24849                            | --                    | --          |
| Ca6_P4_12509102  | Ca6                                     | 12509102                      | AT/A                                                          | TTCTCTCTTCTTCTCC<br>CAA    | AAAATGAAGGGCTCG<br>ATTT  | 58.8                             | 263                                           | DRR                                               | Ca_05029                            | A                     | --          |
| Ca6_P4_1257304   | Ca6                                     | 1257304                       | TTATATATATATATATAT/TTATAT<br>ATATATATATATATAT                 | GGTGAGGATTGGTTCA<br>CTCG   | ATGAGTGGGGATCGAT<br>CTTG | 60.5                             | 341                                           | DRR                                               | Ca_13331                            | --                    | NF-YB       |
| Ca6_P4_12775088  | Ca6                                     | 12775088                      | TTATATATATATATAT/TTATATATAT<br>ATATATAT                       | TGCTGCAAAGGTTTCA<br>ATTTT  | TGCAACAATTTCCCTTC<br>ACA | 59.8                             | 899                                           | DRR                                               | Ca_05050                            | O                     | C2H2        |
| Ca6_P4_12865354  | Ca6                                     | 12865354                      | CT/CTTAATT                                                    | CGCGTAACGTGGTGAA<br>TAAA   | CTTCCACCCATTATGC<br>CACT | 59.6                             | 428                                           | DRR                                               | Ca_05059                            | O                     | MYB_related |
| Ca6_P4_12865567  | Ca6                                     | 12865567                      | GAAAAAAAAA/GAAAAAAAAA                                         | CGCGTAACGTGGTGAA<br>TAAA   | CTTCCACCCATTATGC<br>CACT | 59.6                             | 428                                           | DRR                                               | Ca_05059                            | O                     | MYB_related |
| Ca6_P4_12866234  | Ca6                                     | 12866234                      | TAA/TAAA                                                      | GGGTGGAAGTCATCCT<br>TAGTGA | AAAGGGAGGGAATGCC<br>TTAG | 60.4                             | 603                                           | DRR                                               | Ca_05059                            | O                     | MYB_related |
| Ca6_P4_12908477  | Ca6                                     | 12908477                      | G/GGAATCCGAAT                                                 | AAATGATGAATGCAGT<br>GGCA   | GCAGAAGAAATGGAAT<br>GCAA | 60.1                             | 844                                           | DRR                                               | Ca_05064                            | T                     | bHLH        |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca6_P4_12910113  | Ca6                                     | 12910113                      | TTTAAAA/T                                                     | TGGACAGGTGAAGACC<br>AACA  | TTCTTCCTCCAATCAA<br>TGC    | 60.1                             | 696                                           | DRR                                               | Ca_05064                            | T                     | bHLH        |
| Ca6_P4_12939201  | Ca6                                     | 12939201                      | CAA/CA                                                        | GAGAATGGAGGCAACA<br>AAGC  | GCACGATGAAGTTGGG<br>TTCT   | 59.8                             | 496                                           | DRR                                               | Ca_05066                            | --                    | --          |
| Ca6_P4_12962499  | Ca6                                     | 12962499                      | TAAAAAAA/TAAAAAAA                                             | TTGAGAGGTCGTATCC<br>CCTG  | AAGAGACACATGGGGT<br>TTGC   | 60.1                             | 215                                           | DRR                                               | Ca_05068                            | --                    | MYB_related |
| Ca6_P4_1304145   | Ca6                                     | 1304145                       | ATTTTTTTTT/ATTTTTTTTT                                         | CCGTTCACTACTACC<br>CCAC   | GGGAACCAATTCGTG<br>AATC    | 59.3                             | 722                                           | DRR                                               | Ca_13336                            | T                     | --          |
| Ca6_P4_13118128  | Ca6                                     | 13118128                      | TAAAAAAAAA/TAAAAAAAAA                                         | TTTGCTGCTTCAACT<br>CTCA   | CTGCCAAACAACCA<br>CTTT     | 59.7                             | 655                                           | DRR                                               | Ca_05085                            | U                     | FAR1        |
| Ca6_P4_15456380  | Ca6                                     | 15456380                      | AAA/AAACAA                                                    | GCTGTGTATTTTCATGC<br>CTGC | GAGATGAGGTGGTAGC<br>GAGC   | 59.3                             | 913                                           | DRR                                               | Ca_05328                            | O                     | C2H2        |
| Ca6_P4_15508917  | Ca6                                     | 15508917                      | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATAT           | TGTTTGATTGGGTTGG<br>TTCA  | TGGGTGCTTTATTAAGA<br>TGGG  | 59.8                             | 849                                           | DRR                                               | Ca_05334                            | --                    | --          |
| Ca6_P4_15597965  | Ca6                                     | 15597965                      | TAAA/TAAAA                                                    | CAGTTTCCACACGCAC<br>AGAT  | TGGGAACAAGCATGGT<br>GTAA   | 59.8                             | 681                                           | DRR                                               | Ca_05341                            | --                    | bHLH        |
| Ca6_P4_15800387  | Ca6                                     | 15800387                      | TGAACCTCTTTA/TGAACCTCTTTAG<br>AACCTCTTTA                      | CGTGGTCAACAAAGTG<br>GAAA  | TTGAAGCATGTCCTCT<br>CTTGAA | 59.6                             | 598                                           | DRR                                               | Ca_22015                            | --                    | TALE        |
| Ca6_P4_15946706  | Ca6                                     | 15946706                      | GATATATATATATATAT/GATATATAT<br>ATATATATAT                     | TGTTGCAGTCATGCTT<br>TTGA  | TGAATTCTGCTATGCG<br>CAAC   | 59.0                             | 306                                           | DRR                                               | Ca_22027                            | C                     | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                        | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                                      |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca6_P4_1683094   | Ca6                                     | 1683094                       | TATTAAC/TATTAACCATTGATTAAC                                                                           | AATAAGTCCATCCGGC<br>TCCT   | TTGTGGATGGCGTTTG<br>ATAA  | 59.9                             | 276                                           | DRR                                               | Ca_10299                            | --                    | HB-other |
| Ca6_P4_1683226   | Ca6                                     | 1683226                       | CAA/CA                                                                                               | AATAAGTCCATCCGGC<br>TCCT   | TTGTGGATGGCGTTTG<br>ATAA  | 59.9                             | 276                                           | DRR                                               | Ca_10299                            | --                    | HB-other |
| Ca6_P4_1683327   | Ca6                                     | 1683327                       | AC/A                                                                                                 | TTATCAAACGCCATCC<br>ACAA   | CACTTGCGTGTGGTAG<br>TGCT  | 59.9                             | 504                                           | DRR                                               | Ca_10299                            | --                    | HB-other |
| Ca6_P4_1683470   | Ca6                                     | 1683470                       | C/CCAAAACAATCATAAC                                                                                   | TTATCAAACGCCATCC<br>ACAA   | CACTTGCGTGTGGTAG<br>TGCT  | 59.9                             | 504                                           | DRR                                               | Ca_10299                            | --                    | HB-other |
| Ca6_P4_17043003  | Ca6                                     | 17043003                      | CTTTTTTTTT/CTTTTTTTTTT                                                                               | CGAGATTTAAACAAAA<br>TTGGGA | TATCTTGGTGGGACTG<br>GGAG  | 59.4                             | 533                                           | DRR                                               | Ca_06325                            | --                    | --       |
| Ca6_P4_17044026  | Ca6                                     | 17044026                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAA/A<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAA | AATTGGGGCATGTGCT<br>ATTG   | TGCTGCTGCAATTGAT<br>TTC   | 60.7                             | 874                                           | DRR                                               | Ca_06325                            | --                    | --       |
| Ca6_P4_17092081  | Ca6                                     | 17092081                      | A/AG                                                                                                 | TGCACCCCTAATTTTAA<br>GCAA  | GGATTTTGGGGAGCTT<br>GAA   | 59.6                             | 468                                           | DRR                                               | Ca_06327                            | C                     | --       |
| Ca6_P4_17503727  | Ca6                                     | 17503727                      | GAAAAAAAA/GAAAAAAAA                                                                                  | GTAGGAAGTCGCCATT<br>TGGA   | TGTCTCGATTGACTGA<br>GCG   | 60.1                             | 808                                           | DRR                                               | Ca_06365                            | --                    | WOX      |
| Ca6_P4_17755625  | Ca6                                     | 17755625                      | CTGTGT/CTGT                                                                                          | ATCATCCACGATCCAC<br>CAAT   | ACGTGGGGTGAAAA<br>CATA    | 60.0                             | 821                                           | DRR                                               | Ca_06394                            | E                     | --       |
| Ca6_P4_17855203  | Ca6                                     | 17855203                      | CATTTATTTATTTATTTATTTAT<br>TTATTTATT/CATTTATTTATTTAT<br>ATTTATTTATTTATTTATTTATT                      | ATTTTGGCGAAATGGT<br>ATGC   | TTTGGGTTACGAATTTG<br>ATGA | 59.8                             | 527                                           | DRR                                               | Ca_06403                            | --                    | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)              | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                            |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_1831168   | Ca6                                     | 1831168                       | AATATA/AATATATAAATAAAAGATAT<br>A                                           | GGCAAAAGAACAAGGT<br>CCAA  | CCTGGATGAACCAAT<br>ACACAA   | 60.1                             | 354                                           | DRR                                               | Ca_10310                            | G                     | --  |
| Ca6_P4_1831390   | Ca6                                     | 1831390                       | GATT/GATTGGAAAAATT                                                         | GGCAAAAGAACAAGGT<br>CCAA  | TGTTAATCGGTGATGA<br>ATTTCG  | 60.1                             | 745                                           | DRR                                               | Ca_10310                            | G                     | --  |
| Ca6_P4_1831423   | Ca6                                     | 1831423                       | TAAAAA/TAAAAAA                                                             | GGCAAAAGAACAAGGT<br>CCAA  | TGTTAATCGGTGATGA<br>ATTTCG  | 60.1                             | 745                                           | DRR                                               | Ca_10310                            | G                     | --  |
| Ca6_P4_1832442   | Ca6                                     | 1832442                       | A/AC                                                                       | AAAGGTACGTGAGGTG<br>TGCC  | CGTAATTAATGATGGT<br>GGAGTGG | 60.0                             | 614                                           | DRR                                               | Ca_10310                            | G                     | --  |
| Ca6_P4_1847229   | Ca6                                     | 1847229                       | CGC/CGCAAGC                                                                | GAAAGGCCACATGCAA<br>GATT  | GGACGTGATCTTTTG<br>CAAT     | 60.1                             | 734                                           | DRR                                               | Ca_10312                            | R                     | --  |
| Ca6_P4_19172700  | Ca6                                     | 19172700                      | TTTTTAAATTAATTTTTATTTTAA/T<br>TTTTAAATTAATTTTTATTTTAAATT<br>AATTTTTATTTTAA | GTGGCACAGTAGACCC<br>CATT  | CGTGACATTAACTTG<br>GCCT     | 59.9                             | 712                                           | DRR                                               | Ca_06524                            | R                     | --  |
| Ca6_P4_19244093  | Ca6                                     | 19244093                      | TTAGAGTTTG/T                                                               | AAATGAACCAAAACCG<br>CAAG  | TCAAAATCCCCCAATAA<br>CCA    | 60.0                             | 325                                           | DRR                                               | Ca_06530                            | --                    | --  |
| Ca6_P4_19524549  | Ca6                                     | 19524549                      | GTTTTTTTTTT/GTTTTTTTTTTT                                                   | AAACTCGAAAAGCATG<br>GTGG  | GCCCCAAATTGCCTCT<br>ATGA    | 60.1                             | 623                                           | DRR                                               | Ca_06559                            | --                    | --  |
| Ca6_P4_1976018   | Ca6                                     | 1976018                       | AAT/AATAGAT                                                                | GAAC TAGATGCCGCAA<br>AAGC | GTACGTGGTCTTCCC<br>TGAA     | 60.0                             | 560                                           | DRR                                               | Ca_10322                            | --                    | --  |
| Ca6_P4_1976736   | Ca6                                     | 1976736                       | TC/TCCC                                                                    | TTATTCTCCATTGGGC<br>ATCC  | TCCTGCGGGTAATGAT<br>AAGC    | 59.7                             | 963                                           | DRR                                               | Ca_10322                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                       |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca6_P4_1977350   | Ca6                                     | 1977350                       | A/ACTT                                                                | GCTTATCATTACCCGC<br>AGGA  | TAGCATAGTCCAAGCG<br>GACC   | 60.1                             | 465                                           | DRR                                               | Ca_10322                            | --                    | --   |
| Ca6_P4_21396710  | Ca6                                     | 21396710                      | ATTTT/ATTTT                                                           | GGTTCGCAAAACAAGG<br>CTTA  | TTGAATCGCAAAACAAC<br>CAA   | 60.2                             | 867                                           | DRR                                               | Ca_19862                            | --                    | --   |
| Ca6_P4_21408015  | Ca6                                     | 21408015                      | ATTTTTTTT/ATTTTTTT                                                    | AGGCCTTTTATTTTCGT<br>GCC  | TTGAATCGCAAAACAAC<br>CAA   | 60.4                             | 897                                           | DRR                                               | Ca_19860                            | --                    | --   |
| Ca6_P4_21660027  | Ca6                                     | 21660027                      | CTTTTTTTTTT/CTTTTTTTTTT                                               | TCCTCGTTCGCTTCC<br>TTGT   | CTTTCAGCCTCCATCA<br>AGC    | 60.0                             | 934                                           | DRR                                               | Ca_11274                            | R                     | C2H2 |
| Ca6_P4_21777762  | Ca6                                     | 21777762                      | TCCTCT/TCCTCTTATAAGCCCCCTC<br>T                                       | GATTGTCAGCCCAAA<br>GAGC   | TGAGGAACGACAGATC<br>GAAA   | 59.8                             | 753                                           | DRR                                               | Ca_11261                            | --                    | ERF  |
| Ca6_P4_21777889  | Ca6                                     | 21777889                      | GTA/GTATA                                                             | AGCACCACCAATGGAT<br>GTTT  | GTCGTACGCGTTGTGT<br>ATGG   | 60.2                             | 966                                           | DRR                                               | Ca_11261                            | --                    | ERF  |
| Ca6_P4_21919231  | Ca6                                     | 21919231                      | TTA/TTAATA                                                            | CTTGCATGGGTACGTT<br>AGCA  | ACTTAGCACGGGCTCG<br>ATAC   | 59.8                             | 370                                           | DRR                                               | Ca_11246                            | O                     | --   |
| Ca6_P4_23295842  | Ca6                                     | 23295842                      | CAAA/CAAAA                                                            | GGCATCGAATTCAAAT<br>TTTGT | TTGTGGAACATGCAAA<br>AGGA   | 60.2                             | 654                                           | DRR                                               | Ca_11127                            | --                    | --   |
| Ca6_P4_2341889   | Ca6                                     | 2341889                       | AACA/AA                                                               | GTTTCCCGTAGCAAC<br>AATC   | CCCTCTTCAATCTTCT<br>CATTCA | 59.4                             | 448                                           | DRR                                               | Ca_10365                            | --                    | --   |
| Ca6_P4_23573771  | Ca6                                     | 23573771                      | ATATTATTATTATTATTATTATTA<br>TTATTA/ATATTATTATTATTATTATT<br>ATTATTATTA | CCCCCTAGTAAGAGGT<br>CGCT  | CTCGTTCAGAGGGCTA<br>GACG   | 59.7                             | 542                                           | DRR                                               | Ca_11098                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                       |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca6_P4_23995395  | Ca6                                     | 23995395                      | CTTTTTTTTT/CTTTTTTTTTT                                                | TGGGTTCTGGTTGTG<br>ATGA  | GCGGACATTCTCTCCA<br>GTTC  | 59.9                             | 177                                           | DRR                                               | Ca_11062                            | --                    | --          |
| Ca6_P4_24582806  | Ca6                                     | 24582806                      | CATATATATATATATATATATATA<br>TATAT/CATATATATATATATATAT<br>ATATATATATAT | TCGTTTTGTTTATTGGG<br>GGA | GTAAATGCGGGGTTT<br>ATCG   | 60.2                             | 565                                           | DRR                                               | Ca_24169                            | --                    | bHLH        |
| Ca6_P4_25130968  | Ca6                                     | 25130968                      | A/AATAAGCCT                                                           | CCAAAAAGGGTGGAGA<br>TTGA | CCTTTTACAGCGCTTTT<br>CCA  | 59.9                             | 275                                           | DRR                                               | Ca_26068                            | --                    | --          |
| Ca6_P4_2516180   | Ca6                                     | 2516180                       | GAAAA/GAAAAA                                                          | CGGAAAGGATACCAAC<br>TGGA | AAGAACCCATTGGTGA<br>CGAG  | 59.9                             | 771                                           | DRR                                               | Ca_10383                            | A                     | --          |
| Ca6_P4_2518811   | Ca6                                     | 2518811                       | TA/TAA                                                                | AATCTGGCTCAAAATG<br>CAGC | AATGCATTGCCTGACT<br>CAA   | 60.4                             | 723                                           | DRR                                               | Ca_10384                            | --                    | --          |
| Ca6_P4_2523036   | Ca6                                     | 2523036                       | GGTAAT/G                                                              | TTGGTCTCTTGGTTTG<br>AGGG | CATGCTAGCAAATGCC<br>ATACA | 60.1                             | 791                                           | DRR                                               | Ca_10385                            | --                    | --          |
| Ca6_P4_2523359   | Ca6                                     | 2523359                       | ATT/ATTT                                                              | TTGCATTTGTTTCAGCA<br>AGG | TTGCCATCATCAATTCA<br>TCC  | 59.8                             | 822                                           | DRR                                               | Ca_10385                            | --                    | --          |
| Ca6_P4_2545558   | Ca6                                     | 2545558                       | CTTTTTTT/CTTTTTTTT                                                    | AGCCCTTGAGGGATGT<br>TTCT | TACTGAAGTGGCATCT<br>CCCC  | 60.1                             | 570                                           | DRR                                               | Ca_10387                            | O                     | MYB_related |
| Ca6_P4_25959668  | Ca6                                     | 25959668                      | TACATCAAA/TACATCAAAATATGA<br>CATCAAA                                  | TGTCATCCCAACACG<br>TCAT  | TTTTCCCATGCAAGG<br>TTAG   | 59.8                             | 339                                           | DRR                                               | Ca_25499                            | R                     | C2H2        |
| Ca6_P4_26113844  | Ca6                                     | 26113844                      | TAAAAAAAAA/TAAAAAAAAAA                                                | AGTTTGGTTCTGTGCT<br>GCCT | TTGTAAGCCCATTCTCA<br>CACA | 59.9                             | 769                                           | DRR                                               | Ca_25504                            | R                     | C2H2        |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca6_P4_26354164  | Ca6                                     | 26354164                      | GT/GTT                                                        | TGTTGATTTGGGAAA<br>GAGG   | GGTGCCAACATCCAAC<br>TTCT    | 59.9                             | 650                                           | DRR                                               | Ca_16678                            | --                    | GRAS     |
| Ca6_P4_26668470  | Ca6                                     | 26668470                      | T/TCTATATTTTTTA                                               | CGACGCAATGCATTAA<br>GAGA  | CCTTAATCGCCGAAAAT<br>CAT    | 60.0                             | 490                                           | DRR                                               | Ca_16695                            | --                    | --       |
| Ca6_P4_26704842  | Ca6                                     | 26704842                      | GCC/GC                                                        | TTCAACTTGGCCTAACT<br>CCG  | ACATGGGAATCCCTTT<br>CACA    | 60.2                             | 580                                           | DRR                                               | Ca_16698                            | I                     | --       |
| Ca6_P4_26749884  | Ca6                                     | 26749884                      | ATTAAAAATTTAAAAA/ATTAAAAATT<br>TAAAAATTTAAAAA                 | ATGGAGTGAATGGAA<br>CCAA   | TTGCTTGCATTGTTTGG<br>CTA    | 60.2                             | 480                                           | DRR                                               | Ca_16705                            | B                     | --       |
| Ca6_P4_26811709  | Ca6                                     | 26811709                      | GTGTTATGTTA/GTGTTA                                            | TTGGAGGACACACATG<br>AGGA  | TCAAAGATCGAACATC<br>CGTTT   | 60.1                             | 641                                           | DRR                                               | Ca_16710                            | K                     | MYB      |
| Ca6_P4_27194999  | Ca6                                     | 27194999                      | CA/CAA                                                        | TCACCGATAGGATTCC<br>AACA  | GACCAATTAAGAGGTT<br>TGATGGA | 59.1                             | 538                                           | DRR                                               | Ca_14627                            | K                     | --       |
| Ca6_P4_28326755  | Ca6                                     | 28326755                      | AT/ATT                                                        | TTTGGGCTTGAAGATG<br>AAAA  | TTTAAAAGCAAGGGTG<br>GTGG    | 58.3                             | 336                                           | DRR                                               | Ca_25968                            | A                     | --       |
| Ca6_P4_28327723  | Ca6                                     | 28327723                      | CATATATATATATAT/CATATATATAT<br>AT                             | CAAGAGCATCGTGTC<br>AGGA   | GTCCTGGCGTGACAAG<br>AAAT    | 60.0                             | 424                                           | DRR                                               | Ca_25968                            | A                     | --       |
| Ca6_P4_28577470  | Ca6                                     | 28577470                      | GATATATATATATATAT/GATATAT<br>ATATATATATATAT                   | GGTGTGGAGTCATGT<br>CTTTGA | ATTGAACTAACCCGTG<br>CGTC    | 60.0                             | 235                                           | DRR                                               | Ca_17491                            | O                     | Trihelix |
| Ca6_P4_29085384  | Ca6                                     | 29085384                      | CAAAAAA/CAAAAAA                                               | CGCTAGCAACAGAATT<br>GCAG  | TTCGACCGATTGAAGA<br>AAGC    | 59.8                             | 300                                           | DRR                                               | Ca_17464                            | U                     | LSD      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                    | Forward primers (5'-3')        | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------|--------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                                  |                                |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca6_P4_30588229  | Ca6                                     | 30588229                      | AATCGC/A                                                                                         | GGACGTCTACAACATT<br>GGGG       | CCACATGAGTGTGTTG<br>AGGG | 60.2                             | 948                                           | DRR                                               | Ca_16461                            | --                    | SAP      |
| Ca6_P4_30869145  | Ca6                                     | 30869145                      | AATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATT/AATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATT | TGAAATTTTCTTAATTC<br>AAATCGTGA | CCGCTTCATTACCAAAA<br>GGA | 60.2                             | 735                                           | DRR                                               | Ca_16482                            | R                     | C2H2     |
| Ca6_P4_31255770  | Ca6                                     | 31255770                      | TAAGAAGAAGAAGAAGAAGAA<br>GAAGAAGAA/TAAGAAGAAGAAGAA<br>GAAGAAGAAGAAGAAGAAGAA                      | TTACAAGAGGGAGGGC<br>TTTTT      | ATCAAATGGATTGGAG<br>GCAG | 59.3                             | 780                                           | DRR                                               | Ca_15164                            | --                    | --       |
| Ca6_P4_31331884  | Ca6                                     | 31331884                      | TTATATATATATATATATATA/TTA<br>TATATATATATATATA                                                    | TGACATTGTGATTTTCG<br>TTGTTTT   | GTTTGTGAAATTGGG<br>GGTG  | 58.5                             | 874                                           | DRR                                               | Ca_15166                            | --                    | --       |
| Ca6_P4_31769480  | Ca6                                     | 31769480                      | A/AT                                                                                             | CGGGAGATACGTAGGA<br>GCAA       | TCGATTATGCGTAGGG<br>AAGG | 60.2                             | 250                                           | DRR                                               | Ca_15194                            | --                    | --       |
| Ca6_P4_32150554  | Ca6                                     | 32150554                      | ATTTTCCACTTTTCCACTTTTCCA/A<br>TTTTCCACTTTTCCA                                                    | ATTTGAAATCACATGG<br>GGGA       | CTGCATGTTTTCCATG<br>GTTG | 60.0                             | 292                                           | DRR                                               | Ca_15215                            | MW                    | --       |
| Ca6_P4_34570110  | Ca6                                     | 34570110                      | ATTTTTTTTTTTT/ATTTTTTT                                                                           | TGGTCGACAAGCAACT<br>GAAG       | AACAATCTCCCCCTTTT<br>TGG | 60.0                             | 583                                           | DRR                                               | Ca_15816                            | --                    | --       |
| Ca6_P4_3852175   | Ca6                                     | 3852175                       | T/TACTA                                                                                          | GCGGTATTGGTCCGTG<br>TAGT       | GTTCTGTGATCCCTGG<br>TGGT | 59.9                             | 479                                           | DRR                                               | Ca_05916                            | --                    | --       |
| Ca6_P4_39781733  | Ca6                                     | 39781733                      | CATATATATATATATATATATATA<br>TA/CATATATATATATATATATATA<br>TATATA                                  | TCTCCGCATAAGCTTT<br>CGAT       | TGCTTCGACACAGTAG<br>CACC | 59.9                             | 478                                           | DRR                                               | Ca_15927                            | --                    | --       |
| Ca6_P4_41118947  | Ca6                                     | 41118947                      | CA/CAA                                                                                           | AAGAGTCCAAGTCCGC<br>TGAG       | ACGCTCTAAAAGCAGA<br>CCCA | 59.6                             | 635                                           | DRR                                               | Ca_23143                            | --                    | Trihelix |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                      | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                                                                                    |                          |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca6_P4_41957220  | Ca6                                     | 41957220                      | CTATATATATAT/CTATATATAT                                                                                                            | TCCCAACTTTTGAATT<br>TGC  | TGCTTCAGTCAATGGG<br>ACAG     | 59.9                             | 877                                           | DRR                                               | Ca_21949                            | O                     | --          |
| Ca6_P4_4498664   | Ca6                                     | 4498664                       | TAAAA/TAA                                                                                                                          | TCAGCCACATTGTTTCA<br>AGC | AATAGTGTGACGCGGT<br>AGTTTT   | 59.8                             | 373                                           | DRR                                               | Ca_05852                            | --                    | BES1        |
| Ca6_P4_4503593   | Ca6                                     | 4503593                       | CTTTTTTTTTTTTT/CTTTTTTTTT<br>TTTT                                                                                                  | ACCCTCAACATACCT<br>GCAT  | GATTGCGTTACCAATT<br>TGATG    | 59.3                             | 413                                           | DRR                                               | Ca_05851                            | --                    | --          |
| Ca6_P4_46134674  | Ca6                                     | 46134674                      | TAAAAA/TAAAAA                                                                                                                      | CCTGAAATCCTAACG<br>CCAA  | GCAGCGAAAAATCACC<br>AAGT     | 60.1                             | 446                                           | DRR                                               | Ca_13879                            | --                    | MYB_related |
| Ca6_P4_4800175   | Ca6                                     | 4800175                       | A/ATGCATTAACATGG                                                                                                                   | ATGGGATTGCGCATC<br>TAAC  | GCATCCACTACCGCTG<br>AAAT     | 59.9                             | 704                                           | DRR                                               | Ca_05819                            | --                    | --          |
| Ca6_P4_48038283  | Ca6                                     | 48038283                      | AATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATT/AATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATT | GTGGGTAATCCGTGCG<br>TAAT | CCCAAAATTTGTTAAAG<br>AAGGC   | 59.7                             | 663                                           | DRR                                               | Ca_23440                            | --                    | bZIP        |
| Ca6_P4_48792073  | Ca6                                     | 48792073                      | TAAATTACAAATTACAAAT/TAAATTA<br>CAAAT                                                                                               | TTTGCAGCCACAAAAG<br>ACTG | GAACTCTGCCTTCCAG<br>CAAC     | 60.0                             | 906                                           | DRR                                               | Ca_20702                            | --                    | --          |
| Ca6_P4_48925     | Ca6                                     | 48925                         | ATTCTTCTTCTTCTTCTTCTTCT<br>T/ATTCTTCTTCTTCTTCTTCTTCT<br>TTCTT                                                                      | ATGTGTTTTCGTTCCTC<br>GGG | TCCATGGGTTATTGT<br>GGCT      | 60.0                             | 485                                           | DRR                                               | Ca_26378                            | --                    | --          |
| Ca6_P4_49140036  | Ca6                                     | 49140036                      | AA/AACA                                                                                                                            | AGAAGCATGCTGATCT<br>CACG | CAATGCACCTGAGCTT<br>TCAA     | 59.1                             | 945                                           | DRR                                               | Ca_20719                            | --                    | ERF         |
| Ca6_P4_4919152   | Ca6                                     | 4919152                       | GTTTTTTTT/GTTTTTTTTT                                                                                                               | AACGTGAGTGAAAAA<br>TGCC  | TCAGCTAAAATAAATGG<br>ACCAAAA | 60.0                             | 541                                           | DRR                                               | Ca_05801                            | C                     | --          |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca6_P4_50525240  | Ca6                                     | 50525240                      | A/AC                                                          | TGGTATGGGAGAGGGA<br>TGAG  | TCCCAAAGATGCATTC<br>CATT  | 59.9                             | 817                                           | DRR                                               | Ca_13457                            | --                    | NAC      |
| Ca6_P4_50867728  | Ca6                                     | 50867728                      | AAAAATAAATAAA/AAAAATAATA<br>AATAAATAAA                        | CCAAGAGTTATTGGGT<br>GGAGA | TGAATTCACCTTTTACG<br>ACGC | 59.0                             | 787                                           | DRR                                               | Ca_19198                            | --                    | Trihelix |
| Ca6_P4_50977476  | Ca6                                     | 50977476                      | TTAA/TA                                                       | TTACCTCTCACGTGCA<br>ATCG  | AAGGGAACGTTGTGT<br>ACCG   | 59.9                             | 593                                           | DRR                                               | Ca_19195                            | --                    | --       |
| Ca6_P4_51495570  | Ca6                                     | 51495570                      | CTATTATTATTATTATT/CTATTA<br>TTATTATTATT                       | GCAAGCGAACAAACAA<br>CTGA  | ACCTCAACCTAACCTG<br>CCCT  | 60.0                             | 837                                           | DRR                                               | Ca_19164                            | --                    | Nin-like |
| Ca6_P4_51504679  | Ca6                                     | 51504679                      | TCA/T                                                         | ACCAACGAACGTCCTG<br>AATC  | TTTCTGCTTAAATCGT<br>GGG   | 60.0                             | 342                                           | DRR                                               | Ca_19163                            | --                    | Nin-like |
| Ca6_P4_52075058  | Ca6                                     | 52075058                      | GTTATTATTATT/GTTATTATTATT<br>T                                | GCGTGTCTTATTGGAG<br>AGAGC | GGCTATCGCTTATGCA<br>GGAC  | 59.1                             | 782                                           | DRR                                               | Ca_17514                            | --                    | SAP      |
| Ca6_P4_52481848  | Ca6                                     | 52481848                      | ATTTTTTTTT/ATTTTTTTTTT                                        | GAGCCATGGAGTTTGG<br>TTGT  | TGTGGCAACACTGTTC<br>AGAAA | 60.0                             | 468                                           | DRR                                               | Ca_17538                            | --                    | --       |
| Ca6_P4_53237470  | Ca6                                     | 53237470                      | AATATATATATATATATATATAT<br>A/AATATATATATATATATATAT<br>ATATATA | TCTGACTTTGGAGTTT<br>CACG  | AGGGCACCTTCCTATT<br>CTCC  | 58.0                             | 628                                           | DRR                                               | Ca_22920                            | V                     | ERF      |
| Ca6_P4_53481690  | Ca6                                     | 53481690                      | ACT/ACTGCATCT                                                 | GCATGCAAGTTCGAGA<br>TCAA  | TAGACTTTGCGGGAGC<br>AACT  | 60.0                             | 733                                           | DRR                                               | Ca_18888                            | O                     | GRAS     |
| Ca6_P4_53481750  | Ca6                                     | 53481750                      | TAAAAAAAAAAAAA/TAAAAAAAAA<br>AAAA                             | GCATGCAAGTTCGAGA<br>TCAA  | TAGACTTTGCGGGAGC<br>AACT  | 60.0                             | 733                                           | DRR                                               | Ca_18888                            | O                     | GRAS     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                      | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                                    |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca6_P4_54152599  | Ca6                                     | 54152599                      | AT/ATGGTGTGCT                                                                      | CGGGCAACTCTTTTC<br>ACAT  | AGCCGCTTGTATCCT<br>CTAA  | 60.1                             | 151                                           | DRR                                               | Ca_16269                            | --                    | FAR1 |
| Ca6_P4_54354788  | Ca6                                     | 54354788                      | ATT/ATTT                                                                           | TGTCTGTCAGGGTTCC<br>ATTG | ATACCAAACACGCGCC<br>TAAA | 59.5                             | 786                                           | DRR                                               | Ca_16292                            | --                    | --   |
| Ca6_P4_54354857  | Ca6                                     | 54354857                      | AAT/A                                                                              | TGTCTGTCAGGGTTCC<br>ATTG | GCATGCCTATCTCCTT<br>CCAA | 59.5                             | 964                                           | DRR                                               | Ca_16292                            | --                    | --   |
| Ca6_P4_54933465  | Ca6                                     | 54933465                      | TTTTCT/TTTTCTTTCT                                                                  | TTTACCACTTGAGTT<br>GGGC  | TTGGTCGTTTGAGCCT<br>TTCT | 60.0                             | 248                                           | DRR                                               | Ca_21211                            | --                    | B3   |
| Ca6_P4_5546080   | Ca6                                     | 5546080                       | TTATATATATATATATAT/TTATAT<br>ATATATATATATATAT                                      | GAAGCGTCGATTCACT<br>ATTT | GGGGATTCATAGAAGT<br>CGCT | 60.1                             | 748                                           | DRR                                               | Ca_05744                            | L                     | C3H  |
| Ca6_P4_5613994   | Ca6                                     | 5613994                       | CTATATATATATATATATAT/CT<br>ATATATATATATATATATATAT                                  | ATCTCAGCGGAGCTGG<br>TAAA | CGGAATCATACACCTG<br>CCTT | 60.0                             | 771                                           | DRR                                               | Ca_05735                            | O                     | --   |
| Ca6_P4_563674    | Ca6                                     | 563674                        | AATATATATATATATATATATTTT<br>ATATATATATAT/AATATATATATATA<br>TATATATATTTATATATATATAT | GGATCAGATGGGTCGG<br>TAGA | ATGCACGTTTGGTATG<br>GTCA | 59.9                             | 441                                           | DRR                                               | Ca_13277                            | C                     | --   |
| Ca6_P4_56688837  | Ca6                                     | 56688837                      | GTTTT/GTTTTT                                                                       | TGTTGAGTCGTGGTTA<br>TGGG | TGAACATGCATTCCGA<br>AAAA | 59.4                             | 725                                           | DRR                                               | Ca_17406                            | --                    | --   |
| Ca6_P4_5729834   | Ca6                                     | 5729834                       | GAAAAAAAA/GAAAAAAAAA                                                               | TCTCCGCTCACCGATT<br>ACTT | ACAACCACCACGATCA<br>CTCA | 59.8                             | 630                                           | DRR                                               | Ca_05721                            | --                    | --   |
| Ca6_P4_57786688  | Ca6                                     | 57786688                      | ATTTTTTTTT/ATTTTTTTTTT                                                             | CCTTGAATGCGGGTTA<br>TGTT | GGGGTACTTGGGAGG<br>GATTA | 59.8                             | 777                                           | DRR                                               | Ca_13662                            | R                     | C3H  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca6_P4_57992954  | Ca6                                     | 57992954                      | TTATATATATATATATAT/TTATAT<br>ATATATATATATATAT                 | CTGATCCATCTCAAAG<br>GGGA     | GAGGAAGAAACCACGT<br>TTGAA   | 60.0                             | 434                                           | DRR                                               | Ca_13636                            | O                     | --   |
| Ca6_P4_58594670  | Ca6                                     | 58594670                      | TAAAA/TAAAA                                                   | GATGATGTGGCTGCTC<br>AAGA     | TTCATTGTCCGTTGAG<br>TGC     | 60.0                             | 490                                           | DRR                                               | Ca_15401                            | --                    | --   |
| Ca6_P4_58785175  | Ca6                                     | 58785175                      | TTCTCTCTCTCTCT/TTCTCTCTC<br>TCTCT                             | TCAAATATTGATGCGA<br>CAAAAA   | TTGTCAAATGCTGTTTG<br>CGT    | 58.2                             | 522                                           | DRR                                               | Ca_15422                            | K                     | MYB  |
| Ca6_P4_58785791  | Ca6                                     | 58785791                      | AAATAATAATAATAATAATAATA<br>ATA/AAATAATAATAATAATAATA           | CGTACGCAAAACAGCAT<br>TTGA    | AAGAGGTCGCATCTCA<br>AGGA    | 60.8                             | 791                                           | DRR                                               | Ca_15422                            | K                     | MYB  |
| Ca6_P4_58786039  | Ca6                                     | 58786039                      | TT/TTAT                                                       | GAATACGTCAAATTAA<br>TGCAGTTG | AAGAGGTCGCATCTCA<br>AGGA    | 59.1                             | 471                                           | DRR                                               | Ca_15422                            | K                     | MYB  |
| Ca6_P4_58787039  | Ca6                                     | 58787039                      | TAATAAATAAATAAATAAATAA/TAA<br>TAAATAAATAAATAAATAAATAA<br>AA   | GCAAAGCATCTAGGTG<br>TCCC     | GCCAATCGATGAGATC<br>CAGT    | 59.7                             | 233                                           | DRR                                               | Ca_15422                            | K                     | MYB  |
| Ca6_P4_58811254  | Ca6                                     | 58811254                      | GTTTTTTTTT/GTTTTTTTTT                                         | GAGTGGATTTCCGTTG<br>AGGA     | TTTGATTCTTGACATG<br>GATACTT | 60.1                             | 388                                           | DRR                                               | Ca_15423                            | K                     | GATA |
| Ca6_P4_58823708  | Ca6                                     | 58823708                      | GTAA/GTAAATAA                                                 | AATTTTAGATCACGTG<br>GCGT     | GCACTCATTAGCCGTT<br>CCAT    | 57.2                             | 830                                           | DRR                                               | Ca_15424                            | S                     | --   |
| Ca6_P4_58845180  | Ca6                                     | 58845180                      | AATATATATATATATATAT/AAAT<br>ATATATATATAT                      | CTTCGCATGATTGGTT<br>GTTG     | TTTCCCTCATGTTTGT<br>TCC     | 60.1                             | 375                                           | DRR                                               | Ca_15426                            | G                     | ERF  |
| Ca6_P4_59081987  | Ca6                                     | 59081987                      | TCG/T                                                         | TCTAATTGTGCACGCG<br>AGTC     | GATTCCCTTCAGTGGC<br>ATGT    | 60.0                             | 395                                           | DRR                                               | Ca_18866                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                        | Forward primers (5'-3')        | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------|--------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                                                                      |                                |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca6_P4_59096470  | Ca6                                     | 59096470                      | ACC/AC                                                                                               | TTTATTCGAGGTCCGC<br>ATTCT      | AGAGCCCTCCCACTGA<br>TTTT       | 60.0                             | 455                                           | DRR                                               | Ca_18864                            | --                    | --      |
| Ca6_P4_59254408  | Ca6                                     | 59254408                      | GTATATATATATATATATATAT/GT<br>ATATATATATATATATATATATATA<br>TATAT                                      | GTTGGGCACGGTTATC<br>TGTT       | TTTGATAACTTTAATTG<br>CATTTTCG  | 59.9                             | 851                                           | DRR                                               | Ca_18849                            | --                    | --      |
| Ca6_P4_59399550  | Ca6                                     | 59399550                      | GAGAAAGAAAGAAAGAAAGAAAGAA<br>AGAAAG/GAGAAAGAAAGAAAGAA<br>GAAAGAAAGAAAGAAAG                           | GGCTATCGCTTATGCA<br>GGAC       | TTGTCTGTCAAAGTTCC<br>CTCC      | 59.8                             | 326                                           | DRR                                               | Ca_18842                            | --                    | SAP     |
| Ca6_P4_595167    | Ca6                                     | 595167                        | AATATATATATATATATATGTATG<br>TATATATATATATATATAT/AAAT<br>ATATATATATATATATGTATGTAT<br>ATATATATATATATAT | TTTGCAATCATCAACCA<br>TTCA      | CCTCTGACCAGGATTT<br>TCAA       | 59.9                             | 948                                           | DRR                                               | Ca_13281                            | Z                     | --      |
| Ca6_P4_6163420   | Ca6                                     | 6163420                       | ATTTTTTTTT/ATTTTTTTTT                                                                                | CCGTCCCTTAGCAAAA<br>TTCA       | AAGCAACTATGGCAAA<br>TGCG       | 60.1                             | 443                                           | DRR                                               | Ca_05680                            | T                     | G2-like |
| Ca6_P4_6311158   | Ca6                                     | 6311158                       | GATATATATATATATATATATATA<br>T/GATATATATATATATATATATAT<br>ATAT                                        | TGATTGACATTTTCATCA<br>AGACATAA | TGAACACGATAAGAATT<br>GTGATAAAA | 58.6                             | 763                                           | DRR                                               | Ca_16901                            | --                    | --      |
| Ca6_P4_7295988   | Ca6                                     | 7295988                       | TTATATATATATATATATATATATA<br>TATA/TTATATATATATATATATAT<br>ATATATA                                    | CAATTCATGTTGCACC<br>CTTG       | GGTCTGAGCACATTTG<br>GGAG       | 60.0                             | 824                                           | DRR                                               | Ca_09652                            | --                    | --      |
| Ca6_P4_7321786   | Ca6                                     | 7321786                       | A/AC                                                                                                 | CACCCTGACCTACGGT<br>GATT       | CACCTCCAGTTGCTCT<br>CACA       | 59.8                             | 470                                           | DRR                                               | Ca_09649                            | O                     | TCP     |
| Ca6_P4_7336213   | Ca6                                     | 7336213                       | AGTTGTT/AGTT                                                                                         | TGTGTTTGTCAGTGTC<br>GGGT       | AACAGAATGCCTCACA<br>TCCA       | 60.0                             | 477                                           | DRR                                               | Ca_09646                            | --                    | --      |
| Ca6_P4_7373908   | Ca6                                     | 7373908                       | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATATAT                                                | GGAAAGGCTTCACAAA<br>GCTG       | TAGCCCCTCCTGCTCA<br>TAGA       | 60.0                             | 696                                           | DRR                                               | Ca_09643                            | Q                     | --      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                 |                            |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca6_P4_7436843   | Ca6                                     | 7436843                       | AA/AATTTCTTTTGTATATCCA                                          | TGCCAATATGAAACAAA<br>TCTCC | GTTATTTAGCTTCGCC<br>GTGC      | 58.9                             | 278                                           | DRR                                               | Ca_09637                            | O                     | --   |
| Ca6_P4_7579531   | Ca6                                     | 7579531                       | CTTTTTTT/CTTTTTTTTT                                             | AGCTCGTCTCACATTG<br>CCTT   | TCTTAACCTGGCCCC<br>TTCA       | 60.0                             | 298                                           | DRR                                               | Ca_09627                            | S                     | --   |
| Ca6_P4_7609224   | Ca6                                     | 7609224                       | C/CGATTATTACAG                                                  | TCCCTGTCTTGGTCTT<br>GGTC   | CCCGATATGTTGAGGG<br>ATTG      | 60.1                             | 366                                           | DRR                                               | Ca_09624                            | R                     | --   |
| Ca6_P4_7613784   | Ca6                                     | 7613784                       | TTTCTTCTTCTTCTTCTT/TTTCT<br>TCTTCTTCTTCTT                       | TGATGATGACGATACG<br>GTTGA  | AAGATGACATTTACAA<br>ATCAATCA  | 59.9                             | 435                                           | DRR                                               | Ca_09622                            | --                    | --   |
| Ca6_P4_7627660   | Ca6                                     | 7627660                       | T/TG                                                            | GGCCGCAAAATTGAAA<br>ATAA   | AAGTGTCGCAAACTT<br>TCTG       | 59.9                             | 376                                           | DRR                                               | Ca_09619                            | R                     | WOX  |
| Ca6_P4_7650831   | Ca6                                     | 7650831                       | T/TAA                                                           | ACCTGCACACTGAATT<br>GCAC   | GAAACCAAACTACTTC<br>CAAGTGAA  | 59.8                             | 738                                           | DRR                                               | Ca_09618                            | --                    | --   |
| Ca6_P4_7651653   | Ca6                                     | 7651653                       | ATCTT/ATCTTCTT                                                  | TTTAGCTAATTTTCGGT<br>TTTCG | AAAGTCCGTTTGTGTG<br>GATT      | 57.8                             | 355                                           | DRR                                               | Ca_09618                            | --                    | --   |
| Ca6_P4_7652212   | Ca6                                     | 7652212                       | TATAAATAAATAAATAAATAA/TATA<br>AATAAATAAATAAATAAATAAATAA<br>TAAA | AATCGACAACAAACGG<br>ACTTT  | TTTATTATTGAACCAAT<br>TAAACGCA | 58.6                             | 723                                           | DRR                                               | Ca_09617                            | J                     | FAR1 |
| Ca6_P4_7664765   | Ca6                                     | 7664765                       | ACCCC/ACCC                                                      | TGGACCCATACTTCAG<br>CTCC   | TCCCATACAAAGCTC<br>CGTC       | 60.1                             | 253                                           | DRR                                               | Ca_09615                            | J                     | FAR1 |
| Ca6_P4_7664932   | Ca6                                     | 7664932                       | TA/TAA                                                          | GGACCCATACTTCAGC<br>TCCA   | GATAACAATGCGGAGA<br>TGGG      | 60.1                             | 419                                           | DRR                                               | Ca_09615                            | J                     | FAR1 |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                          |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca6_P4_7665642   | Ca6                                     | 7665642                       | TACACACAC/TACACAC                                             | AAAGTCCTCCCTTCC<br>TTGA  | GGGAGACACATTATCC<br>GGTG      | 60.0                             | 254                                           | DRR                                               | Ca_09615                            | J                     | FAR1  |
| Ca6_P4_7700010   | Ca6                                     | 7700010                       | TA/T                                                          | CGGAGCGCTAAAGTTG<br>AATC | CACGATGTCACGCATT<br>AACC      | 60.0                             | 382                                           | DRR                                               | Ca_09611                            | --                    | --    |
| Ca6_P4_7705531   | Ca6                                     | 7705531                       | CTATTATTA/CTATTATTATTA                                        | CAGATGGGCCGTATGT<br>TCTT | CAACCGACAATCACAT<br>CACA      | 60.0                             | 511                                           | DRR                                               | Ca_09610                            | --                    | --    |
| Ca6_P4_7706133   | Ca6                                     | 7706133                       | TAAAAA/TAAAA                                                  | TGTGATGTGATTGTCG<br>GTTG | CGGTCGAATCTTTACC<br>CTCA      | 58.9                             | 664                                           | DRR                                               | Ca_09609                            | --                    | --    |
| Ca6_P4_7723583   | Ca6                                     | 7723583                       | TG/T                                                          | GCAATTTTCCTGGCTG<br>GTTA | TGCATGCCGAACCAT<br>ATAG       | 60.1                             | 431                                           | DRR                                               | Ca_09607                            | --                    | --    |
| Ca6_P4_7729316   | Ca6                                     | 7729316                       | GATATATATATA/GATATATATA                                       | TGAGATGGTCCGACAA<br>AGAA | GGGTATCAGGAAATGA<br>GCCA      | 59.2                             | 431                                           | DRR                                               | Ca_09605                            | K                     | NF-YB |
| Ca6_P4_7760430   | Ca6                                     | 7760430                       | CAAAAAAAAA/CAAAAAAAAA                                         | CAAGCATTTTGGTCC<br>CTGT  | TCCTTGGTGGAACAAA<br>ACATC     | 60.0                             | 291                                           | DRR                                               | Ca_09602                            | R                     | SBP   |
| Ca6_P4_7766962   | Ca6                                     | 7766962                       | ATT/ATTT                                                      | GGAAGCCATTATTGGG<br>GATT | CCCAGCAGAACATACA<br>GGGT      | 60.0                             | 505                                           | DRR                                               | Ca_09600                            | --                    | bZIP  |
| Ca6_P4_7826714   | Ca6                                     | 7826714                       | GT/GTGTTAAAT                                                  | CCAAACCTTGCGATC<br>AATAA | TCACACGCACATAAAT<br>GATTAAGTT | 60.0                             | 387                                           | DRR                                               | Ca_09596                            | --                    | --    |
| Ca6_P4_7839856   | Ca6                                     | 7839856                       | AATGAT/AAT                                                    | GTTCCCTCCCATTTCC<br>CTAA | TCCACGTGCTTTGACA<br>CATT      | 60.1                             | 341                                           | DRR                                               | Ca_09595                            | S                     | GRAS  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca6_P4_7847894   | Ca6                                     | 7847894                       | A/AG                                                          | TTGCCTTTCATTGCACT<br>CAG   | TTTTGTACCCGTTGT<br>GTCA      | 60.0                             | 461                                           | DRR                                               | Ca_09594                            | P                     | MIKC |
| Ca6_P4_7878598   | Ca6                                     | 7878598                       | GT/GTT                                                        | GTTGGCAGGTCGAAAG<br>AAAG   | GGGAATTTGCAATCAG<br>AGGA     | 59.9                             | 739                                           | DRR                                               | Ca_09589                            | --                    | NAC  |
| Ca6_P4_7892768   | Ca6                                     | 7892768                       | AG/A                                                          | GGTGTCTCCGTCACGA<br>GTTT   | TCCGCTTCAAAAGTTCA<br>ACA     | 60.2                             | 724                                           | DRR                                               | Ca_09586                            | I                     | --   |
| Ca6_P4_7893085   | Ca6                                     | 7893085                       | AAAGAA/AAA                                                    | CCTTACTTTGACGACTT<br>GTTGG | CAATCCGCTTCAAAAGT<br>TCA     | 58.8                             | 526                                           | DRR                                               | Ca_09586                            | I                     | --   |
| Ca6_P4_792792    | Ca6                                     | 792792                        | ATTTGTTTTGTTTTGTTT/ATTT<br>GTTTTGTTTTGTT                      | CGCAGCCCTTTTTGTT<br>TGTA   | CAATTGTTTTAAGGAAT<br>TCCAATG | 61.1                             | 421                                           | DRR                                               | Ca_13295                            | --                    | GRAS |
| Ca6_P4_7941617   | Ca6                                     | 7941617                       | CTAGT/CTAGTAGT                                                | TTGCTTCTAATGGGTC<br>GGTC   | ATAGGACTCGGTCACA<br>TGGC     | 60.1                             | 154                                           | DRR                                               | Ca_09580                            | --                    | --   |
| Ca6_P4_7947224   | Ca6                                     | 7947224                       | TATATAAAATAATATAAAATAAT/TAT<br>ATAAAATAAT                     | TGATCCTTCCGATGAT<br>AGCC   | ACGGCAATTGCGTTAA<br>AACT     | 60.0                             | 678                                           | DRR                                               | Ca_09579                            | J                     | --   |
| Ca6_P4_7948041   | Ca6                                     | 7948041                       | AA/AAATA                                                      | AATTGCCGTTGAAAGT<br>CGAG   | GCCTATGGCCAAATTG<br>CTTA     | 60.2                             | 906                                           | DRR                                               | Ca_09579                            | J                     | --   |
| Ca6_P4_7958310   | Ca6                                     | 7958310                       | AATATATATA/AATATATA                                           | CAAATTCAACCCAAACA<br>CCC   | AATACCACATTGCGAG<br>GCTT     | 60.1                             | 352                                           | DRR                                               | Ca_09578                            | --                    | ERF  |
| Ca6_P4_7958786   | Ca6                                     | 7958786                       | AAATAT/AAATATCGACAATAT                                        | AAGCCTCGCAATGTGG<br>TATT   | ATCCAACGGCGTCAAA<br>TAAA     | 59.6                             | 675                                           | DRR                                               | Ca_09578                            | --                    | ERF  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca6_P4_7998659   | Ca6                                     | 7998659                       | TATCATATTAT/TATCATATTATCAAT<br>CATATTAT                       | TGGTCCACGTGATACC<br>AAAA   | CCATTTAAACGCACAAC<br>CAA  | 59.8                             | 709                                           | DRR                                               | Ca_09575                            | --                    | --          |
| Ca6_P4_8061727   | Ca6                                     | 8061727                       | CTT/CTTCAATCCTTT                                              | TGTTTTGCAGGGATTT<br>GTGA   | GATGGATGGGAGACGA<br>AAGA  | 60.1                             | 631                                           | DRR                                               | Ca_09567                            | G                     | --          |
| Ca6_P4_8062172   | Ca6                                     | 8062172                       | T/TG                                                          | TTTCGTCTCCCATCCAT<br>CTC   | CGTCACCCAAAGCAAT<br>TGTA  | 60.0                             | 532                                           | DRR                                               | Ca_09567                            | G                     | --          |
| Ca6_P4_8062636   | Ca6                                     | 8062636                       | ATTTTTTTTT/ATTTTTTTT                                          | TACAATTGCTTTGGGT<br>GACG   | AGGCGCTAAATCTTA<br>CGGT   | 59.6                             | 774                                           | DRR                                               | Ca_09567                            | G                     | --          |
| Ca6_P4_8062787   | Ca6                                     | 8062787                       | CTTTT/CTTT                                                    | TACAATTGCTTTGGGT<br>GACG   | GAAGGGTACTGGGCAG<br>ATGA  | 59.6                             | 864                                           | DRR                                               | Ca_09567                            | G                     | --          |
| Ca6_P4_8066437   | Ca6                                     | 8066437                       | CTA/CTACCTAAAATA                                              | AAGTGGTTGGGATGAA<br>AAAGAA | TTGATTTTCGGTTTGGGA<br>AGC | 59.9                             | 567                                           | DRR                                               | Ca_09565                            | --                    | MYB_related |
| Ca6_P4_8078323   | Ca6                                     | 8078323                       | GATATATATATATATATATATAT/G<br>ATATATATATATATAT                 | ATGTTGGTTCTTGTGC<br>CCTC   | CCAAAAATCCACAATCAT<br>CCC | 60.0                             | 623                                           | DRR                                               | Ca_09564                            | U                     | Trihelix    |
| Ca6_P4_8093284   | Ca6                                     | 8093284                       | CTAT/CTATAT                                                   | GCCTTTTGACAGGTAAA<br>GCAA  | TCAACGCCCTGTATGA<br>ATGA  | 60.4                             | 571                                           | DRR                                               | Ca_09562                            | S                     | CAMTA       |
| Ca6_P4_8133267   | Ca6                                     | 8133267                       | T/TATTTTTTTTA                                                 | CATGCAGATCTGGTGG<br>TTGT   | TTGCAGCAGTTGCACT<br>TAGG  | 59.6                             | 466                                           | DRR                                               | Ca_09555                            | P                     | GRAS        |
| Ca6_P4_8174386   | Ca6                                     | 8174386                       | TG/T                                                          | AACTCACCGTTGACT<br>TTGC    | GAGTGGTGAGCATGCG<br>TTTA  | 60.2                             | 924                                           | DRR                                               | Ca_09552                            | K                     | --          |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                    | Forward primers (5'-3')         | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------|---------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                                                                  |                                 |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca6_P4_8594301   | Ca6                                     | 8594301                       | ATTATAT/A                                                                                        | AAGCACCATTGGCTA<br>CACC         | GCCTCAACCGTTTATT<br>TGG  | 60.0                             | 806                                           | DRR                                               | Ca_16779                            | --                    | --    |
| Ca6_P4_9060428   | Ca6                                     | 9060428                       | TTATAAACATATAAAA/TTATAAAA                                                                        | AAAGTACAATGAGTCA<br>AACAATTATCC | ATATGCTTCACTTGCCC<br>CAC | 58.2                             | 555                                           | DRR                                               | Ca_16733                            | E                     | --    |
| Ca6_P4_9203559   | Ca6                                     | 9203559                       | G/GTTATATT                                                                                       | TCGTGAAATAGTGGAC<br>GGTG        | TGAACATCAAAATGCC<br>CAAA | 59.6                             | 763                                           | DRR                                               | Ca_08676                            | OT                    | --    |
| Ca6_P4_9952396   | Ca6                                     | 9952396                       | ATTAATTTAATTTAATTTAATTTAATT<br>TAATTTAATTTA/ATTAATTTAATTTA<br>ATTTAATTTAATTTAATTTAATTTAAT<br>TTA | GGAGCACAGAAGAACT<br>CGGA        | TTGGAAATGGTTTGCTT<br>GAA | 60.3                             | 345                                           | DRR                                               | Ca_08595                            | --                    | --    |
| Ca7_P4_10049659  | Ca7                                     | 10049659                      | GTCTCTCTCTCTCT/GTCTCTCTCTC<br>T                                                                  | TGGATTTGTGTGTCGT<br>TGGT        | TATGCAGATGCCTCGT<br>TCAG | 59.9                             | 679                                           | DRR                                               | Ca_12768                            | --                    | --    |
| Ca7_P4_10690477  | Ca7                                     | 10690477                      | GTT/GTTTT                                                                                        | CCTGGCTTGCAACAT<br>ACAA         | CAGCCAAGTAACACGC<br>AAAA | 59.7                             | 897                                           | DRR                                               | Ca_12825                            | K                     | ARR-B |
| Ca7_P4_10757230  | Ca7                                     | 10757230                      | A/AT                                                                                             | GGTCTCATAGTTCTCA<br>TCGCGT      | TCGCTTGGACAATTCT<br>CGTT | 60.7                             | 533                                           | DRR                                               | Ca_12830                            | E                     | TALE  |
| Ca7_P4_10831556  | Ca7                                     | 10831556                      | GTTTTTTTT/GTTTTTTTT                                                                              | CACCTCCAAGTCCAAC<br>CAAT        | TGCAGCGTTTTGTTTTG<br>TTC | 59.8                             | 334                                           | DRR                                               | Ca_12836                            | S                     | --    |
| Ca7_P4_10877853  | Ca7                                     | 10877853                      | CTTTTT/CTTT                                                                                      | GATGCGGGTTCGGTCT<br>AGTA        | TTGCGTTGTGTTGTGA<br>TGTG | 60.1                             | 444                                           | DRR                                               | Ca_12842                            | R                     | CPP   |
| Ca7_P4_11106661  | Ca7                                     | 11106661                      | CAATTTTAAT/CAAT                                                                                  | AGTGTTTGGGAAATGC<br>TTGG        | TGAAATTATGCACGTGT<br>GGG | 60.0                             | 689                                           | DRR                                               | Ca_09376                            | G                     | --    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                 | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                                                               |                               |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_11697550  | Ca7                                     | 11697550                      | TAATAATAAATACTCTGAATAATAAT<br>AACTCTGAATAATAA/TAATAATAATA<br>ACTCTGAATAATAATACTCTGAATA<br>ATAATACTCTGAATAATAA | GGCTATCGCTTATGCA<br>GGAC      | TTCAGCGATTATTCAA<br>CGATTT | 59.8                             | 709                                           | DRR                                               | Ca_09328                            | --                    | SAP  |
| Ca7_P4_12465968  | Ca7                                     | 12465968                      | TTATATATATATATATATATATATATA<br>TATAT/TTATATATATATATATATATA<br>TATATATATATATATAT                               | TTATGAACTCGGTTGC<br>TTCG      | CAGATGTGAGTCAGTC<br>CGAGA  | 58.9                             | 331                                           | DRR                                               | Ca_09270                            | --                    | --   |
| Ca7_P4_12483012  | Ca7                                     | 12483012                      | T/TAAGGAG                                                                                                     | GCGCAAACGCAAGT<br>CATA        | CCTTTTCGGACAGGAA<br>ATCA   | 60.0                             | 723                                           | DRR                                               | Ca_09268                            | R                     | bHLH |
| Ca7_P4_12940315  | Ca7                                     | 12940315                      | AA/AATA                                                                                                       | TTCTTCCCTCCCTCT<br>CATT       | TTTCATCTAGCGAACC<br>CCTC   | 60.0                             | 671                                           | DRR                                               | Ca_09227                            | --                    | --   |
| Ca7_P4_13555513  | Ca7                                     | 13555513                      | C/CGTAAT                                                                                                      | TTTCTAATCAGTGGCC<br>TGGTC     | TCAACGAGCATGTGGA<br>AAAG   | 59.2                             | 554                                           | DRR                                               | Ca_16040                            | --                    | bZIP |
| Ca7_P4_13958576  | Ca7                                     | 13958576                      | GTTATTTATTTATTTATTTAT/TG<br>TTATTTATTTATTTATTTAT                                                              | TACATTGGCAACTCAT<br>CCCA      | TTTTAATTTGGTGTGG<br>CCT    | 59.9                             | 668                                           | DRR                                               | Ca_16068                            | --                    | --   |
| Ca7_P4_1420274   | Ca7                                     | 1420274                       | TAAAAAAAAA/TAAAAAAAAA                                                                                         | TTAGATTAATGTTTTCT<br>TTTTGTTG | TCTAAAAGACTCATCGC<br>GGC   | 57.4                             | 466                                           | DRR                                               | Ca_03326                            | --                    | --   |
| Ca7_P4_14529836  | Ca7                                     | 14529836                      | TAAAAAAAAA/TAAAAAAAAA                                                                                         | TAACCAACGCAATTT<br>GATG       | ACGTCGAGGGGTGTGA<br>ATAG   | 59.4                             | 317                                           | DRR                                               | Ca_09990                            | Q                     | B3   |
| Ca7_P4_14904978  | Ca7                                     | 14904978                      | GCCCC/GCCCCC                                                                                                  | AGAATGAAGAGGAGCG<br>ACCA      | TTTAACTGGACCGAAA<br>CCG    | 60.0                             | 534                                           | DRR                                               | Ca_09960                            | O                     | bZIP |
| Ca7_P4_16548666  | Ca7                                     | 16548666                      | TG/T                                                                                                          | TCCCTTCTACTTGGTG<br>GTGG      | GTGATTCATGCTCCAA<br>GGCT   | 60.0                             | 624                                           | DRR                                               | Ca_20555                            | R                     | --   |

[illegible]

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_2047396   | Ca7                                     | 2047396                       | TTATATATATATATATATATATATATATATAT<br>T                         | ATGGGACTAGGCAACA<br>CGTC   | TTTCAACCGTAAATCAT<br>ACTTGG | 60.0                             | 630                                           | DRR                                               | Ca_03268                            | GC                    | HSF  |
| Ca7_P4_20494272  | Ca7                                     | 20494272                      | CAA/CAAA                                                      | AGACGTGTCGATCGAG<br>CTTT   | AGCTGAATGCAAACCC<br>TTGA    | 60.0                             | 497                                           | DRR                                               | Ca_12400                            | --                    | AP2  |
| Ca7_P4_20525384  | Ca7                                     | 20525384                      | TAAAAAAAAA/TAAAAAAAAA                                         | TGTTCACTGCCAACT<br>CTGC    | GGAAATAGTGATAGCG<br>GCCA    | 60.0                             | 640                                           | DRR                                               | Ca_12401                            | --                    | --   |
| Ca7_P4_20539386  | Ca7                                     | 20539386                      | CAAAAAAAAA/CAAAAAAAAA                                         | TTCTTCCTTGATGAAT<br>GGC    | GTAAGTCACCGACAAG<br>GGGA    | 60.0                             | 335                                           | DRR                                               | Ca_12403                            | --                    | C2H2 |
| Ca7_P4_20557114  | Ca7                                     | 20557114                      | ATCACTCA/ATCACTCACTCA                                         | TACTTTGCCGCTCTG<br>CTAT    | CAACGCGCAGATCAG<br>TAAA     | 60.0                             | 589                                           | DRR                                               | Ca_12405                            | K                     | --   |
| Ca7_P4_20571099  | Ca7                                     | 20571099                      | AAAA/AAAATAAA                                                 | TCCCAAATAATGAGG<br>GCAA    | ACAGACGGCGAAAATT<br>GTTT    | 60.3                             | 381                                           | DRR                                               | Ca_12407                            | --                    | --   |
| Ca7_P4_20600329  | Ca7                                     | 20600329                      | GAAAAAAAAA/GAAAAAAAAA                                         | TGGTGCAGAGTAAAGA<br>ATGGAA | GTCCCCCATAAACATTC<br>ACG    | 59.7                             | 579                                           | DRR                                               | Ca_12410                            | --                    | bHLH |
| Ca7_P4_20604250  | Ca7                                     | 20604250                      | CTAATATAATATAATA/CTAATATAAT<br>ATAATATAATA                    | ACCATTTCCTTTTCGA<br>TTT    | TGCTTTGTCAATTGCT<br>TGC     | 59.6                             | 589                                           | DRR                                               | Ca_12412                            | YU                    | --   |
| Ca7_P4_21743270  | Ca7                                     | 21743270                      | CAA/CA                                                        | TTGCCCCCTCTAAATTC<br>TGG   | TCCCTCGTATTTAGCC<br>CTCA    | 59.2                             | 686                                           | DRR                                               | Ca_14521                            | --                    | --   |
| Ca7_P4_21743482  | Ca7                                     | 21743482                      | TGGCTAAATATGAGGGCTAAATAT<br>GGCTAAATA                         | TCGAAGCATAAGGTTG<br>ATCC   | GGGATTGAGCGCCTAT<br>ACAA    | 57.8                             | 500                                           | DRR                                               | Ca_14521                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_21743627  | Ca7                                     | 21743627                      | ATTTTTTT/ATTTTTTTT                                            | TGAGGGCTAAATACGA<br>GGGA | GGGATTGAGCGCCTAT<br>ACAA   | 59.7                             | 461                                           | DRR                                               | Ca_14521                            | --                    | --   |
| Ca7_P4_21743947  | Ca7                                     | 21743947                      | AA/AAATA                                                      | CCTGGTGTGCATTGAA<br>AAGA | AATTGCGGTTTTGGTT<br>CAAG   | 59.7                             | 410                                           | DRR                                               | Ca_14521                            | --                    | --   |
| Ca7_P4_21876016  | Ca7                                     | 21876016                      | GTTTTTTT/GTTTTTTT                                             | GTTTGGGGTTTTGGGT<br>TCTT | CCACCATTGTTATGTG<br>GACG   | 60.1                             | 593                                           | DRR                                               | Ca_14530                            | S                     | --   |
| Ca7_P4_22327481  | Ca7                                     | 22327481                      | TC/T                                                          | GATTCATCGCAGCTCA<br>AACA | GATCAAACCGGGAA<br>AAAT     | 60.0                             | 638                                           | DRR                                               | Ca_14548                            | --                    | --   |
| Ca7_P4_22362135  | Ca7                                     | 22362135                      | AG/A                                                          | TGTCAGTACCCACCCA<br>CTCA | CAAGGGAGGCTGTTGT<br>GAAT   | 60.0                             | 914                                           | DRR                                               | Ca_14551                            | --                    | SAP  |
| Ca7_P4_22554279  | Ca7                                     | 22554279                      | TC/TCCAAC                                                     | AGTGGAGGCAAACCAT<br>AACG | CACCCACCCACCAATA<br>GTGT   | 60.0                             | 578                                           | DRR                                               | Ca_19538                            | T                     | FAR1 |
| Ca7_P4_23667025  | Ca7                                     | 23667025                      | AAATAATAATAATAATA/AAATAA<br>TAATAATAATAATAATA                 | ACACTGATTTCCCAAAA<br>CGC | TTTCCTTCCCTTCTCAT<br>TGC   | 60.0                             | 728                                           | DRR                                               | Ca_26877                            | G                     | FAR1 |
| Ca7_P4_23851009  | Ca7                                     | 23851009                      | G/GCA                                                         | TAACGTTCCCACGGCT<br>TAAC | AAGGATGCGACGAAAT<br>TGAG   | 60.0                             | 593                                           | DRR                                               | Ca_26881                            | --                    | --   |
| Ca7_P4_24786712  | Ca7                                     | 24786712                      | AATATATATATATATATATATATAT/A<br>ATATATATATATATATATATATATAT     | ACAGACCCGACCAAGT<br>CAAC | TCAAACATTTAACGATC<br>ACCAT | 60.0                             | 447                                           | DRR                                               | Ca_19894                            | GC                    | HSF  |
| Ca7_P4_25118793  | Ca7                                     | 25118793                      | AGG/AG                                                        | CTCTACCCAAGAAGA<br>TCGC  | CCCTGTGACAAACACA<br>ATCG   | 60.0                             | 608                                           | DRR                                               | Ca_23601                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_25984688  | Ca7                                     | 25984688                      | CTTTTTTTTT/CTTTTTTTTT                                         | GCCATTTATGGCAGAG<br>GTTT   | TTTGATGTTGTTGGAG<br>ATGAAAA | 59.0                             | 571                                           | DRR                                               | Ca_23636                            | --                    | NAC  |
| Ca7_P4_26700837  | Ca7                                     | 26700837                      | C/CTT                                                         | ACTATCCGTTCTGTGG<br>TGCC   | CAGTGGCTTGGTTAAG<br>GGAA    | 60.0                             | 835                                           | DRR                                               | Ca_16249                            | --                    | --   |
| Ca7_P4_26701106  | Ca7                                     | 26701106                      | A/ACTAGGAATTACTCCC                                            | CAATAGGGCGAGTCGA<br>ATGT   | AAGTCCAGTAGCCGAA<br>AGCA    | 60.1                             | 838                                           | DRR                                               | Ca_16249                            | --                    | --   |
| Ca7_P4_26701534  | Ca7                                     | 26701534                      | C/CG                                                          | AAGCTTCATCCTGGTC<br>ATGG   | AAGTCCAGTAGCCGAA<br>AGCA    | 60.1                             | 381                                           | DRR                                               | Ca_16249                            | --                    | --   |
| Ca7_P4_2831340   | Ca7                                     | 2831340                       | TAAAAAAAA/TAAAAAAAA                                           | TGATAATCTCGCGGA<br>TAGG    | GAATTGCCGAAAAATG<br>ATTGA   | 60.0                             | 465                                           | DRR                                               | Ca_03193                            | K                     | GATA |
| Ca7_P4_29038300  | Ca7                                     | 29038300                      | TAAAAAAAA/TAAAAAAAA                                           | TTCGAAATCTTAATGTG<br>CTCAA | GGGTAAATCGATTAGT<br>CCGGT   | 58.9                             | 646                                           | DRR                                               | Ca_11800                            | --                    | --   |
| Ca7_P4_29433568  | Ca7                                     | 29433568                      | T/TG                                                          | AGGCATGATTCAAGGT<br>ACGG   | CAGGTGAAGGTCCATT<br>TCGT    | 60.0                             | 278                                           | DRR                                               | Ca_11776                            | --                    | --   |
| Ca7_P4_29446201  | Ca7                                     | 29446201                      | ATTTTTTTTT/ATTTTTTTTTT                                        | CGTTGCGCATGTGTAA<br>TTTG   | TCATTCCCAACATTATT<br>TCGTG  | 61.1                             | 639                                           | DRR                                               | Ca_11775                            | R                     | --   |
| Ca7_P4_29610109  | Ca7                                     | 29610109                      | T/TTC                                                         | AACAGAAAGAAGGCCG<br>TTTG   | TGAGTTAAGCCCCGCT<br>AGAA    | 59.4                             | 134                                           | DRR                                               | Ca_11764                            | --                    | --   |
| Ca7_P4_30036720  | Ca7                                     | 30036720                      | TCTACTA/TCTA                                                  | CACCTTTGCCAACCAC<br>TTTT   | ACCACATTTCATGTGCTT<br>GGA   | 60.0                             | 638                                           | DRR                                               | Ca_11724                            | O                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca7_P4_30102864  | Ca7                                     | 30102864                      | GA/G                                                          | TAAACTGGGGCAATCA<br>CACA  | TGATTATGCAGCAACC<br>AAAA | 60.0                             | 585                                           | DRR                                               | Ca_11717                            | --                    | bZIP        |
| Ca7_P4_30166196  | Ca7                                     | 30166196                      | CAA/CTTAAA                                                    | TGAGCCCATAATGTGC<br>AGAA  | CTTTTGTAAAGGGCAT<br>CAGC | 60.2                             | 520                                           | DRR                                               | Ca_11711                            | Q                     | B3          |
| Ca7_P4_30220020  | Ca7                                     | 30220020                      | CA/C                                                          | CGCTCTAGCGCAAACT<br>AAGG  | AACACCGACACCGAAT<br>TCAT | 60.3                             | 163                                           | DRR                                               | Ca_11705                            | GC                    | HSF         |
| Ca7_P4_30232337  | Ca7                                     | 30232337                      | ATTTTT/ATTTTT                                                 | GGAGCACAGATCACT<br>CATGTC | TTCGGGAGTCGACTAT<br>ACGC | 59.7                             | 245                                           | DRR                                               | Ca_11704                            | GC                    | HSF         |
| Ca7_P4_30233283  | Ca7                                     | 30233283                      | CT/CTAAT                                                      | CCATTATGCACCCCTTT<br>CAC  | GGAAGATGGATCCTCC<br>ACAA | 60.2                             | 420                                           | DRR                                               | Ca_11704                            | GC                    | HSF         |
| Ca7_P4_30424399  | Ca7                                     | 30424399                      | AT/ATT                                                        | TCATCTTCGATGCAAA<br>CCA   | TCGTTACGACTGATG<br>TTGA  | 60.2                             | 938                                           | DRR                                               | Ca_11688                            | --                    | MYB_related |
| Ca7_P4_30874290  | Ca7                                     | 30874290                      | TAA/TAAA                                                      | TTGTCTCAACAATCTCC<br>CCC  | ACCACCTCACTGCCCT<br>ACAC | 59.9                             | 734                                           | DRR                                               | Ca_23317                            | --                    | --          |
| Ca7_P4_30930614  | Ca7                                     | 30930614                      | TCC/TC                                                        | CCACTCAAGGCCAGTG<br>ATTT  | ATGAGCAGCACCAACA<br>TCAA | 60.1                             | 222                                           | DRR                                               | Ca_23314                            | --                    | --          |
| Ca7_P4_30967683  | Ca7                                     | 30967683                      | ATTTT/ATTTT                                                   | CCCCATGATCTTCCT<br>TTTT   | GCAACAAACCTATGGC<br>AGGT | 60.1                             | 355                                           | DRR                                               | Ca_23312                            | --                    | --          |
| Ca7_P4_31186109  | Ca7                                     | 31186109                      | T/TG                                                          | CACTTTTGAGAGACCC<br>GGAA  | GAGCAAATCCCTTACC<br>CACA | 60.2                             | 320                                           | DRR                                               | Ca_10140                            | T                     | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca7_P4_31196032  | Ca7                                     | 31196032                      | ATTTT/ATT                                                     | CAACCAAGATTTTGAT<br>GAGTCG | TTGTTCACGGTGGTAA<br>TTTTT  | 59.6                             | 287                                           | DRR                                               | Ca_10139                            | K                     | NAC      |
| Ca7_P4_31196582  | Ca7                                     | 31196582                      | TTTTATATT/TTTTATATTATATT                                      | AAAAATTACCACCGTG<br>AACAA  | TGTTCTTAACCTAGCTG<br>GCGA  | 57.1                             | 897                                           | DRR                                               | Ca_10138                            | --                    | --       |
| Ca7_P4_31197530  | Ca7                                     | 31197530                      | A/AGTGACACG                                                   | CCTTCGTTTAACTTGT<br>GACACC | GTGGCAGGTGCAGGTA<br>AAGT   | 60.0                             | 602                                           | DRR                                               | Ca_10138                            | --                    | --       |
| Ca7_P4_31210939  | Ca7                                     | 31210939                      | CTC/CTCAATC                                                   | CCTTTCTCAGCCCATAT<br>CCA   | TCAACAATGCAAACGAA<br>GGA   | 60.0                             | 306                                           | DRR                                               | Ca_10136                            | --                    | ARF      |
| Ca7_P4_31215378  | Ca7                                     | 31215378                      | GAAAAAAAA/GAAAAAAAAA                                          | GTTGTGCCGCTTAAGT<br>TGGT   | ATGGGACCACTTGGTG<br>GTAA   | 60.2                             | 854                                           | DRR                                               | Ca_10135                            | G                     | --       |
| Ca7_P4_31216107  | Ca7                                     | 31216107                      | TC/T                                                          | TTACCACCAAGTGGTC<br>CCAT   | CGAAATTTTAAAGGTC<br>GCCA   | 60.1                             | 741                                           | DRR                                               | Ca_10135                            | G                     | --       |
| Ca7_P4_32230923  | Ca7                                     | 32230923                      | TACA/TA                                                       | CTGGGCAAGGGATCTG<br>AATA   | ATTGCCCACCCATAATT<br>TCA   | 60.0                             | 540                                           | DRR                                               | Ca_10050                            | --                    | Trihelix |
| Ca7_P4_32901214  | Ca7                                     | 32901214                      | AATTTTTTATTTTTATTTTTTA/A<br>ATTTTTTATTTTTTA                   | GTAGTGCAAACCTGG<br>TGCT    | GTCGCTGGTGTGACTG<br>AAAA   | 60.2                             | 462                                           | DRR                                               | Ca_10009                            | --                    | bZIP     |
| Ca7_P4_33060172  | Ca7                                     | 33060172                      | GTTTTTTTTT/GTTTTTTTTTTT                                       | TGAATTGTTGAAGGGG<br>CCTA   | TGGGAATTTGGATCTTT<br>TTGTC | 60.4                             | 635                                           | DRR                                               | Ca_09996                            | --                    | --       |
| Ca7_P4_33060237  | Ca7                                     | 33060237                      | ATTTTTTT/ATTTTTT                                              | TGAATTGTTGAAGGGG<br>CCTA   | TGGGAATTTGGATCTTT<br>TTGTC | 60.4                             | 635                                           | DRR                                               | Ca_09996                            | --                    | --       |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca7_P4_33159162  | Ca7                                     | 33159162                      | CT/C                                                          | TGTTCCAACTTCCAAC<br>CTCC  | GACAAATGATGCTTCT<br>GGCA     | 59.9                             | 207                                           | DRR                                               | Ca_16147                            | --                    | --      |
| Ca7_P4_33230823  | Ca7                                     | 33230823                      | TTATATATA/TTATATATATA                                         | CCAAATTCTCCACACG<br>GTCT  | GAATTATGTCGATGGTT<br>TTTGACA | 60.0                             | 622                                           | DRR                                               | Ca_16150                            | --                    | --      |
| Ca7_P4_33243964  | Ca7                                     | 33243964                      | GA/GAA                                                        | CAACGGTGCAGAGTGA<br>AAAA  | TGTTTCATAACTGAAGG<br>GGGA    | 59.9                             | 624                                           | DRR                                               | Ca_16151                            | --                    | --      |
| Ca7_P4_33244102  | Ca7                                     | 33244102                      | TT/TTTTAT                                                     | CGAATGTGGAACAATT<br>CATGT | TGTTTCATAACTGAAGG<br>GGGA    | 58.3                             | 547                                           | DRR                                               | Ca_16151                            | --                    | --      |
| Ca7_P4_33258061  | Ca7                                     | 33258061                      | TTC/T                                                         | CCTGTGGGGGACACTT<br>TCTA  | ACTCCATCTGTTCCCC<br>AATG     | 60.0                             | 333                                           | DRR                                               | Ca_16153                            | S                     | --      |
| Ca7_P4_33258253  | Ca7                                     | 33258253                      | TAATGA/TAATGATCATTTAATAAAAT<br>GA                             | CCTGTGGGGGACACTT<br>TCTA  | ACTCCATCTGTTCCCC<br>AATG     | 60.0                             | 333                                           | DRR                                               | Ca_16153                            | S                     | --      |
| Ca7_P4_33336366  | Ca7                                     | 33336366                      | T/TA                                                          | AAGCCAGGCGATTTAT<br>GATG  | ATCGGCAAATATCCGA<br>GAAA     | 60.1                             | 510                                           | DRR                                               | Ca_16158                            | R                     | G2-like |
| Ca7_P4_33336445  | Ca7                                     | 33336445                      | TTG/TTGCTTGATTATG                                             | AAGCCAGGCGATTTAT<br>GATG  | ATCGGCAAATATCCGA<br>GAAA     | 60.1                             | 510                                           | DRR                                               | Ca_16158                            | R                     | G2-like |
| Ca7_P4_33361035  | Ca7                                     | 33361035                      | GATATATATATATATATA/GATATATA<br>TATATATATATATA                 | TGCACGACGCTAATTC<br>AGTC  | TCCATGTACACTGGCA<br>CTCC     | 60.0                             | 410                                           | DRR                                               | Ca_16161                            | YU                    | --      |
| Ca7_P4_33367476  | Ca7                                     | 33367476                      | CT/CTT                                                        | GGGGGATGATCATATC<br>TTGTG | CACGGAGACCAACGAA<br>ACTT     | 59.1                             | 677                                           | DRR                                               | Ca_16162                            | YU                    | --      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33367558  | Ca7                                     | 33367558                      | ATTTTTTTT/ATTTTTTT                                            | GGGGGATGATCATATC<br>TTGTG   | CACGGAGACCAACGAA<br>ACTT  | 59.1                             | 677                                           | DRR                                               | Ca_16162                            | YU                    | --  |
| Ca7_P4_33367648  | Ca7                                     | 33367648                      | TTATATAT/TTATAT                                               | CCCTATTAAGCATGAA<br>CATGGA  | CACGGAGACCAACGAA<br>ACTT  | 59.0                             | 507                                           | DRR                                               | Ca_16162                            | YU                    | --  |
| Ca7_P4_33382900  | Ca7                                     | 33382900                      | TCC/TC                                                        | TGACGTGACACATCTA<br>ACAAACA | TGAAAGCATCATGCAA<br>AAAGA | 59.2                             | 379                                           | DRR                                               | Ca_16163                            | --                    | --  |
| Ca7_P4_33409151  | Ca7                                     | 33409151                      | TA/TAAATAACAA                                                 | GCATCATGAGTTTGAG<br>GGGA    | TATCATGCGTCCATGC<br>ACTT  | 61.0                             | 430                                           | DRR                                               | Ca_16164                            | --                    | C3H |
| Ca7_P4_33409928  | Ca7                                     | 33409928                      | CAAAAA/CAAAA                                                  | CCGAAAGAATTGGAT<br>CATCA    | TTCTTGCATGATTGG<br>GACA   | 59.9                             | 405                                           | DRR                                               | Ca_16164                            | --                    | C3H |
| Ca7_P4_33483669  | Ca7                                     | 33483669                      | TTATATA/TTATA                                                 | ATTCAGTGGGCAACAG<br>AACC    | CATGACTGTGCCAAAC<br>TGCT  | 60.0                             | 731                                           | DRR                                               | Ca_16169                            | --                    | --  |
| Ca7_P4_33537677  | Ca7                                     | 33537677                      | CA/C                                                          | GTCAATGTTGTGGGAG<br>GTGA    | ATTTTGCCAATCCAG<br>CTAA   | 59.4                             | 337                                           | DRR                                               | Ca_16173                            | --                    | --  |
| Ca7_P4_33538151  | Ca7                                     | 33538151                      | AAAAAA/AAAAAGAAAAA                                            | TTAGCTGGATTGGCCA<br>AAAT    | GGTCCATGGATGAGCT<br>TGTT  | 59.5                             | 396                                           | DRR                                               | Ca_16173                            | --                    | --  |
| Ca7_P4_33560601  | Ca7                                     | 33560601                      | TGG/TGGG                                                      | TCTTGAGATCTTGGGC<br>TTTGA   | AAGGGAAAGGGGAGTA<br>CACG  | 59.9                             | 337                                           | DRR                                               | Ca_16175                            | QI                    | B3  |
| Ca7_P4_33575183  | Ca7                                     | 33575183                      | TAAAAAAAAA/TAAAAAAAAA                                         | CAAATTGCATTTTCCTC<br>CCT    | TTGTTGGTGAGTGCTC<br>TTGG  | 59.0                             | 691                                           | DRR                                               | Ca_16178                            | I                     | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_33576122  | Ca7                                     | 33576122                      | GTTTTTTTTT/GTTTTTTTTT                                         | TAATTTAACGAACGCG<br>CGAG   | TTGGGTGACTCATGGT<br>GAGA | 60.1                             | 410                                           | DRR                                               | Ca_16178                            | I                     | --   |
| Ca7_P4_33639029  | Ca7                                     | 33639029                      | TAAAAAAAAA/TAAAAAAAAA                                         | TCAGAGCTTTGCAGTT<br>ATGTGA | GCACATGGTTTCGAAT<br>GTTG | 58.7                             | 555                                           | DRR                                               | Ca_16180                            | --                    | ERF  |
| Ca7_P4_33640029  | Ca7                                     | 33640029                      | TTA/T                                                         | CCAAATCGTCGGTGTG<br>AATA   | TTTTGGAGGAGATGTT<br>TGGG | 59.4                             | 526                                           | DRR                                               | Ca_16180                            | --                    | ERF  |
| Ca7_P4_33640082  | Ca7                                     | 33640082                      | TAA/TAAA                                                      | CCAAATCGTCGGTGTG<br>AATA   | CCTTTGTTTGCTGGGA<br>TCAT | 59.4                             | 614                                           | DRR                                               | Ca_16180                            | --                    | ERF  |
| Ca7_P4_33640133  | Ca7                                     | 33640133                      | CAAA/CAAAAATAAAA                                              | CCAAATCGTCGGTGTG<br>AATA   | CCTTTGTTTGCTGGGA<br>TCAT | 59.4                             | 614                                           | DRR                                               | Ca_16180                            | --                    | ERF  |
| Ca7_P4_33746470  | Ca7                                     | 33746470                      | T/TAA                                                         | CAAAATTAATGGCAC<br>AGGG    | TTTCCCAATCCACCACT<br>CTC | 59.4                             | 332                                           | DRR                                               | Ca_16182                            | --                    | --   |
| Ca7_P4_33758707  | Ca7                                     | 33758707                      | ACC/AC                                                        | CGAATTCAACTCGGG<br>TCAT    | ACAATTTGGCGGTGAG<br>AAAC | 59.9                             | 452                                           | DRR                                               | Ca_16184                            | --                    | B3   |
| Ca7_P4_33802472  | Ca7                                     | 33802472                      | TTATATATATTCAT/TTATATATATTC<br>ATATATATATTCAT                 | TACTGACCTCTATCGC<br>CGGT   | CGTATGCGACTCATCC<br>ATTG | 59.7                             | 612                                           | DRR                                               | Ca_16188                            | P                     | GRAS |
| Ca7_P4_33802677  | Ca7                                     | 33802677                      | CT/CTT                                                        | TCATCCAATGAAATGG<br>GTTTT  | CGTATGCGACTCATCC<br>ATTG | 59.1                             | 201                                           | DRR                                               | Ca_16188                            | P                     | GRAS |
| Ca7_P4_33802690  | Ca7                                     | 33802690                      | GAATAAATAAATAAATA/GAATAAAT<br>AAATAAATAAATA                   | TCATCCAATGAAATGG<br>GTTTT  | CGTATGCGACTCATCC<br>ATTG | 59.1                             | 201                                           | DRR                                               | Ca_16188                            | P                     | GRAS |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_33803105  | Ca7                                     | 33803105                      | CTTTTT/CTTTT                                                  | ACATCAATGGATGAGT<br>CGCA   | CTTTGGTTTCACATTGG<br>GCT  | 60.1                             | 767                                           | DRR                                               | Ca_16188                            | P                     | GRAS |
| Ca7_P4_33803283  | Ca7                                     | 33803283                      | TTTA/T                                                        | TGAGGATGGAATGGGT<br>TTTG   | CTTTGGTTTCACATTGG<br>GCT  | 60.7                             | 555                                           | DRR                                               | Ca_16188                            | P                     | GRAS |
| Ca7_P4_33803390  | Ca7                                     | 33803390                      | TACAC/TAC                                                     | TGAGGATGGAATGGGT<br>TTTG   | CTTTGGTTTCACATTGG<br>GCT  | 60.7                             | 555                                           | DRR                                               | Ca_16188                            | P                     | GRAS |
| Ca7_P4_33812222  | Ca7                                     | 33812222                      | ATT/AT                                                        | TGGATGAAAGAGACAA<br>GCAAAA | AGTGTACCCATGTGAG<br>GTGCT | 59.9                             | 543                                           | DRR                                               | Ca_16189                            | --                    | C3H  |
| Ca7_P4_33812418  | Ca7                                     | 33812418                      | TC/T                                                          | TTGGATGAAAGAGACA<br>AGCAAA | GTATCCATGAATTGGG<br>GGTG  | 59.9                             | 687                                           | DRR                                               | Ca_16189                            | --                    | C3H  |
| Ca7_P4_33812533  | Ca7                                     | 33812533                      | CTTTTT/CTTTT                                                  | TTGGATGAAAGAGACA<br>AGCAAA | GTATCCATGAATTGGG<br>GGTG  | 59.9                             | 687                                           | DRR                                               | Ca_16189                            | --                    | C3H  |
| Ca7_P4_33815491  | Ca7                                     | 33815491                      | GT/GTT                                                        | TTTGTTTTTCATGCATGT<br>GTCC | TCTGCATGGCAGTGAA<br>TAGC  | 59.4                             | 162                                           | DRR                                               | Ca_16190                            | E                     | --   |
| Ca7_P4_33815769  | Ca7                                     | 33815769                      | TAAA/TA                                                       | ATGGCTATTCAGTGCC<br>ATGC   | ATCATCCTTGGTCCCG<br>AATA  | 61.0                             | 434                                           | DRR                                               | Ca_16190                            | E                     | --   |
| Ca7_P4_33843751  | Ca7                                     | 33843751                      | TTTCTATTTTCTCCTCT/TT                                          | TAGAGCATGGCATTTC<br>ACCA   | GGCCTTTAAATTGGGC<br>TTTC  | 60.2                             | 229                                           | DRR                                               | Ca_16192                            | --                    | NAC  |
| Ca7_P4_33881339  | Ca7                                     | 33881339                      | GTT/GAATT                                                     | TTCTCTCATTTGGGT<br>CTGA    | TCCTCTCTCTAAGGGA<br>CCAT  | 58.2                             | 172                                           | DRR                                               | Ca_16194                            | O                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_33890873  | Ca7                                     | 33890873                      | ATTT/ATTTT                                                    | ATTGTTTCCCATCGTT<br>CCA    | TTGCTATGGATGGCTA<br>AGGG   | 60.2                             | 537                                           | DRR                                               | Ca_16196                            | O                     | TCP  |
| Ca7_P4_34183842  | Ca7                                     | 34183842                      | GC/GCC                                                        | TCCCAAGAATGTCCAC<br>ACAA   | GGACGAATTTTCGGAG<br>TGAA   | 59.9                             | 628                                           | DRR                                               | Ca_21005                            | --                    | --   |
| Ca7_P4_34189529  | Ca7                                     | 34189529                      | CTTT/CTTCTTTATTTT                                             | TGTGCATCGTATTAC<br>CTCG    | GGGAAACAAATGCCTG<br>AATG   | 60.7                             | 511                                           | DRR                                               | Ca_21004                            | S                     | --   |
| Ca7_P4_34189939  | Ca7                                     | 34189939                      | ATTTTTTT/ATTTTTT                                              | CATTCAGGCATTTGTT<br>CCC    | TTGGTCTTTTGCATCT<br>TCG    | 60.3                             | 700                                           | DRR                                               | Ca_21004                            | S                     | --   |
| Ca7_P4_34190282  | Ca7                                     | 34190282                      | GTTTTTTTT/GTTTTTTTTT                                          | AACAATCGAACTACTT<br>GCGTGA | TTGGTCTTTTGCATCT<br>TCG    | 59.8                             | 564                                           | DRR                                               | Ca_21004                            | S                     | --   |
| Ca7_P4_34190333  | Ca7                                     | 34190333                      | AAG/AAGAG                                                     | TCGAACTACTTGCCTG<br>AGAA   | TTGGTCTTTTGCATCT<br>TCG    | 57.2                             | 559                                           | DRR                                               | Ca_21004                            | S                     | --   |
| Ca7_P4_34190508  | Ca7                                     | 34190508                      | AT/A                                                          | TCGAAGATGCAAAAGA<br>ACCA   | AAAGGTGACACATCCT<br>TTGCTT | 59.4                             | 189                                           | DRR                                               | Ca_21004                            | S                     | --   |
| Ca7_P4_34195712  | Ca7                                     | 34195712                      | AT/ATTT                                                       | GAGGCTCCATATTGCG<br>AAAA   | AGGCTAACACCATTGC<br>CAAC   | 60.2                             | 189                                           | DRR                                               | Ca_21002                            | --                    | WRKY |
| Ca7_P4_34195793  | Ca7                                     | 34195793                      | TAAAAAAAAA/TAAAAAAAAA                                         | GAGGCTCCATATTGCG<br>AAAA   | AGGCTAACACCATTGC<br>CAAC   | 60.2                             | 189                                           | DRR                                               | Ca_21003                            | O                     | FAR1 |
| Ca7_P4_34196242  | Ca7                                     | 34196242                      | GTTT/GTT                                                      | GTTGGCAATGGTGTTA<br>GCCT   | TTGAGGGTTGCTTTTG<br>TTGTT  | 60.0                             | 771                                           | DRR                                               | Ca_21002                            | --                    | WRKY |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca7_P4_34206613  | Ca7                                     | 34206613                      | GTTTTTTTTT/GTTTTTTTTT                                         | ACCAACATCATAAAG<br>CGGC   | TGCAACCTTTATGTCAA<br>CGC | 60.0                             | 831                                           | DRR                                               | Ca_21001                            | A                     | --     |
| Ca7_P4_34216629  | Ca7                                     | 34216629                      | GTTTTTTTTT/GTTTTTTTTT                                         | TTTGTCCCTCCCAAGA<br>AATG  | ATCTCACCCCTGGTTG<br>TCTG | 59.9                             | 427                                           | DRR                                               | Ca_20999                            | L                     | --     |
| Ca7_P4_34256619  | Ca7                                     | 34256619                      | TCA/TCACA                                                     | CGGAGTGGACTCTAAC<br>CCAA  | TTAGGTGATTCTATGC<br>GCCC | 60.1                             | 532                                           | DRR                                               | Ca_20996                            | S                     | --     |
| Ca7_P4_34274392  | Ca7                                     | 34274392                      | TAAAA/TAAA                                                    | ACCACCGAGTCATCAG<br>CTCT  | AGCCCGTTTGCTACCT<br>TTTT | 59.9                             | 552                                           | DRR                                               | Ca_20991                            | --                    | M-type |
| Ca7_P4_34283808  | Ca7                                     | 34283808                      | CTTTTTTTTT/CTTTTTTTTT                                         | CATAACCCATATGCGA<br>GCAA  | TCCATGAATTTGTCAAC<br>CGA | 59.5                             | 662                                           | DRR                                               | Ca_20990                            | A                     | --     |
| Ca7_P4_34283992  | Ca7                                     | 34283992                      | GAAAAAAAA/GAAAAAAAA                                           | CATAACCCATATGCGA<br>GCAA  | TCCATGAATTTGTCAAC<br>CGA | 59.5                             | 662                                           | DRR                                               | Ca_20990                            | A                     | --     |
| Ca7_P4_34303984  | Ca7                                     | 34303984                      | A/ATT                                                         | AGGACAGTGACTTGGG<br>ATGG  | TCTTCATCTGTGGGAC<br>GAAA | 60.0                             | 649                                           | DRR                                               | Ca_20988                            | --                    | NAC    |
| Ca7_P4_34324551  | Ca7                                     | 34324551                      | CT/CTGATT                                                     | TCGCAATTGTGTGTGA<br>GATTC | ACCGATGAGAAAGCTT<br>TGGA | 59.7                             | 977                                           | DRR                                               | Ca_20987                            | R                     | NAC    |
| Ca7_P4_34347433  | Ca7                                     | 34347433                      | CTTT/CTTTT                                                    | CCATCAAATCTCAATG<br>CGTG  | AGAAACCAGCCGCTAA<br>ATGA | 60.1                             | 515                                           | DRR                                               | Ca_20986                            | C                     | --     |
| Ca7_P4_34347667  | Ca7                                     | 34347667                      | A/AC                                                          | TCATTTAGCGGCTGGT<br>TTCT  | TGCCGCAATAAAATGA<br>AACA | 59.8                             | 643                                           | DRR                                               | Ca_20986                            | C                     | --     |

[illegible]

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca7_P4_35333033  | Ca7                                     | 35333033                      | C/CT                                                          | TGCAAAGCACCAATT<br>GTAG  | CTTTCCATGCCACGG<br>TACT  | 59.7                             | 974                                           | DRR                                               | Ca_17647                            | BK                    | FAR1     |
| Ca7_P4_3535267   | Ca7                                     | 3535267                       | CCATCATCA/CCATCA                                              | CGTGCGAGTTTGACAC<br>CTAA | AATGGCAATGGAAGGA<br>AATG | 59.9                             | 222                                           | DRR                                               | Ca_03115                            | S                     | --       |
| Ca7_P4_35369159  | Ca7                                     | 35369159                      | CAAAAAAAAA/CAAAAAAAAA                                         | CCAAAGGCATTGAGG<br>ATTC  | TTGCCATTCTTTGACAC<br>ACA | 59.5                             | 308                                           | DRR                                               | Ca_17651                            | --                    | --       |
| Ca7_P4_35370294  | Ca7                                     | 35370294                      | TCTAC/TCTACTAC                                                | ATAATTTGAGCCATGA<br>CGGG | TCTTGACAGGTTTGGT<br>TGGA | 59.8                             | 128                                           | DRR                                               | Ca_17651                            | --                    | --       |
| Ca7_P4_3544380   | Ca7                                     | 3544380                       | T/TA                                                          | TGAAGCATGAAGAGAC<br>ACGG | AATGGCAAGATCACCC<br>AAAG | 60.0                             | 160                                           | DRR                                               | Ca_03114                            | S                     | --       |
| Ca7_P4_3567820   | Ca7                                     | 3567820                       | AATATATATAT/AATATATAT                                         | CGCGCTAACACATAA<br>AGCA  | TGATGATGTGACGTGC<br>AATG | 60.0                             | 448                                           | DRR                                               | Ca_03112                            | U                     | MYB      |
| Ca7_P4_3598965   | Ca7                                     | 3598965                       | GAAAAATAATTAATAA/GAAAA                                        | CACCTGCTAGCCTAAC<br>CACA | TCCAATGGGATGGACA<br>AAGT | 58.9                             | 743                                           | DRR                                               | Ca_03108                            | --                    | NAC      |
| Ca7_P4_36117059  | Ca7                                     | 36117059                      | CTTTA/CTTTTCTTTATTTTA                                         | TGGATTGGGCTTTCCA<br>ATAA | TGCCTTAACGTACCCA<br>AACA | 60.3                             | 435                                           | DRR                                               | Ca_13721                            | G                     | Trihelix |
| Ca7_P4_3638430   | Ca7                                     | 3638430                       | TTAT/TTATAT                                                   | AGGGCACATAAGCCAC<br>AAGT | TAATGTCGTTGCCGCC<br>TATT | 59.6                             | 619                                           | DRR                                               | Ca_03105                            | --                    | --       |
| Ca7_P4_3638546   | Ca7                                     | 3638546                       | TAAAAAA/TAAAAAA                                               | AGGGCACATAAGCCAC<br>AAGT | TAATGTCGTTGCCGCC<br>TATT | 59.6                             | 619                                           | DRR                                               | Ca_03105                            | --                    | --       |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_3643180   | Ca7                                     | 3643180                       | GTTTT/GT                                                      | GTTGCCCAATAACGTA<br>ACCG     | TTTTCGCCCAAATGAAA<br>AAG    | 60.2                             | 525                                           | DRR                                               | Ca_03104                            | --                    | ERF |
| Ca7_P4_3649235   | Ca7                                     | 3649235                       | GAATCCAATATCTA/GAATCCAATAT<br>CTAAAATCCAATATCTA               | GTCCGAGTCCTAACAG<br>CAGC     | TCATGGTGAGATTGGC<br>AAAA    | 60.0                             | 722                                           | DRR                                               | Ca_03103                            | U                     | LBD |
| Ca7_P4_36548120  | Ca7                                     | 36548120                      | TAAAA/TAAAAAA                                                 | ACAACCAAGCGTGTGC<br>TGTA     | TGTTTGTGGAGAAAT<br>GCCA     | 60.2                             | 213                                           | DRR                                               | Ca_13744                            | O                     | --  |
| Ca7_P4_36603437  | Ca7                                     | 36603437                      | ATTTTTTTTT/ATTTTTTTT                                          | AGCCAGTCAGCCAGTC<br>ATCT     | GGACCAATCGTGAAT<br>GCTT     | 60.0                             | 684                                           | DRR                                               | Ca_13749                            | --                    | --  |
| Ca7_P4_3670558   | Ca7                                     | 3670558                       | A/AT                                                          | AAGGCAATAGGTGATG<br>GTGG     | TCACTATTCACACGCG<br>GAAG    | 59.8                             | 717                                           | DRR                                               | Ca_03102                            | TU                    | --  |
| Ca7_P4_36717770  | Ca7                                     | 36717770                      | AATATATATATATATA/AATATATA<br>TATATATATATA                     | TGCCTTTAACAATAATC<br>GAGAATG | TGGTTTGGTTCCATCA<br>GGTT    | 59.6                             | 803                                           | DRR                                               | Ca_13757                            | S                     | --  |
| Ca7_P4_3672046   | Ca7                                     | 3672046                       | AT/A                                                          | ACATAGGTCGGCATA<br>TCGG      | TACAGTTTCAGCCTGG<br>GTCC    | 60.0                             | 330                                           | DRR                                               | Ca_03102                            | TU                    | --  |
| Ca7_P4_3683029   | Ca7                                     | 3683029                       | A/AGAAAAG                                                     | ATTGAGGCTACTTGAG<br>GGCA     | GAAGCCAAAAAGTCTG<br>CATAGAA | 59.8                             | 532                                           | DRR                                               | Ca_03101                            | --                    | --  |
| Ca7_P4_3683088   | Ca7                                     | 3683088                       | T/TA                                                          | ATTGAGGCTACTTGAG<br>GGCA     | GAAGCCAAAAAGTCTG<br>CATAGAA | 59.8                             | 532                                           | DRR                                               | Ca_03101                            | --                    | --  |
| Ca7_P4_3683696   | Ca7                                     | 3683696                       | TA/T                                                          | CCATGAAATCACCTTAA<br>ATGACA  | CCGACAAGGCGACAAG<br>TAAT    | 58.9                             | 451                                           | DRR                                               | Ca_03101                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca7_P4_3684559   | Ca7                                     | 3684559                       | CAAAA/CAAA                                                    | AAAATTGAAACTGGAA<br>TGGTACA | GGTTGGCGCATATAA<br>ACAG   | 58.9                             | 472                                           | DRR                                               | Ca_03101                            | --                    | --       |
| Ca7_P4_36871436  | Ca7                                     | 36871436                      | AAGAGAGAGAGAGAGAGAGAGA<br>/AAGAGAGAGAGAGAGAGAGAG<br>AGA       | TGAGCTGAAACAACAT<br>GCGT    | TGTCGGGAACCATTC<br>CTTA   | 60.5                             | 893                                           | DRR                                               | Ca_13774                            | R                     | --       |
| Ca7_P4_3689131   | Ca7                                     | 3689131                       | CATAT/CAT                                                     | AACCAATGACCATCGA<br>GAATC   | TGGGATTCTCTTGAC<br>CTCACA | 58.9                             | 513                                           | DRR                                               | Ca_03100                            | S                     | --       |
| Ca7_P4_3689211   | Ca7                                     | 3689211                       | CTTTTT/CTTTTTT                                                | AACCAATGACCATCGA<br>GAATC   | TGGGATTCTCTTGAC<br>CTCACA | 58.9                             | 513                                           | DRR                                               | Ca_03100                            | S                     | --       |
| Ca7_P4_3689317   | Ca7                                     | 3689317                       | ATTTT/ATTT                                                    | AACCAATGACCATCGA<br>GAATC   | ACTCCTCTCCCCCTA<br>CCAT   | 58.9                             | 640                                           | DRR                                               | Ca_03100                            | S                     | --       |
| Ca7_P4_3689798   | Ca7                                     | 3689798                       | TAGAGAG/TAGAG                                                 | ATGGTAGGGGAAGA<br>GGAGT     | CTTTTCGTTTGGCCAAT<br>GTT  | 58.9                             | 381                                           | DRR                                               | Ca_03100                            | S                     | --       |
| Ca7_P4_37047318  | Ca7                                     | 37047318                      | ATTTTTTTTTT/ATTTTTTTTTT                                       | GAAAAAGCGCTGTAAG<br>TGGC    | CATCCTCCTCTCTGGC<br>TTTG  | 59.9                             | 714                                           | DRR                                               | Ca_13788                            | --                    | Trihelix |
| Ca7_P4_37154177  | Ca7                                     | 37154177                      | TTATATATATATATA/TTATATATATA<br>TATATA                         | TGTCATCAAAATGGGT<br>CACAA   | TCAAAGGTTTTCTGCCA<br>TCC  | 59.8                             | 693                                           | DRR                                               | Ca_13797                            | --                    | --       |
| Ca7_P4_37711486  | Ca7                                     | 37711486                      | TG/T                                                          | TACCCTGTGGATGGGA<br>ATGT    | TTGTCGATCCGAAATG<br>TGAA  | 60.1                             | 870                                           | DRR                                               | Ca_22800                            | --                    | --       |
| Ca7_P4_3782917   | Ca7                                     | 3782917                       | CATATATATATATAT/CATATAT                                       | TGGGGACAAGCCTTAT<br>TTTG    | GATTGAAGCCACCCAA<br>CATT  | 59.9                             | 668                                           | DRR                                               | Ca_03087                            | O                     | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca7_P4_3785579   | Ca7                                     | 3785579                       | TAAAAA/TAAAA                                                  | CCGGTTCAACCTCCGT<br>ACTA | ATTCTTGTGCGCTTTC<br>GTTT    | 60.0                             | 302                                           | DRR                                               | Ca_03086                            | --                    | --      |
| Ca7_P4_38333257  | Ca7                                     | 38333257                      | AAGA/AA                                                       | GTCATGGACGCAAGTC<br>CTTT | TTAGATTTTCCGCCTTG<br>GTG    | 60.1                             | 585                                           | DRR                                               | Ca_16409                            | P                     | --      |
| Ca7_P4_38757753  | Ca7                                     | 38757753                      | TAAAAAAAAA/TAAAAAAAAA                                         | GCCATCTTTATTCCAAC<br>CGA | TTTGATGAATTTGATGT<br>TGTTGG | 59.9                             | 776                                           | DRR                                               | Ca_16426                            | --                    | SBP     |
| Ca7_P4_39361236  | Ca7                                     | 39361236                      | CAA/CAAAA                                                     | CGATTGCAGAGTGAAA<br>ATCC | CCTAATGCGCTGACAC<br>AGAC    | 58.3                             | 464                                           | DRR                                               | Ca_19590                            | --                    | BBR-BPC |
| Ca7_P4_39397852  | Ca7                                     | 39397852                      | TCACAGAGGTAC/TC                                               | CCTCCCTTTCAAATCG<br>ATCA | CAGTACCATTGCGCA<br>GGTT     | 60.0                             | 401                                           | DRR                                               | Ca_19592                            | --                    | --      |
| Ca7_P4_39830592  | Ca7                                     | 39830592                      | AGGGGGGG/AGGGGGG                                              | CCTGCTCAAAGCACAC<br>GTTA | TAATCATCCTCGGGTT<br>GAGG    | 60.1                             | 636                                           | DRR                                               | Ca_25100                            | --                    | --      |
| Ca7_P4_40304518  | Ca7                                     | 40304518                      | CAAA/CAA                                                      | CACCAATGATATTGGG<br>CAAA | AGTCGGTCAACGGTCA<br>AAAC    | 59.2                             | 592                                           | DRR                                               | Ca_20249                            | S                     | --      |
| Ca7_P4_4224423   | Ca7                                     | 4224423                       | CCGCGC/CCGC                                                   | CAGTGGCATAGCTCCA<br>GACA | CAGAGACAAACCAAG<br>GGAG     | 60.0                             | 419                                           | DRR                                               | Ca_03038                            | --                    | --      |
| Ca7_P4_42270355  | Ca7                                     | 42270355                      | CTTTTTTTTT/CTTTTTTTTT                                         | TTAGGCGAAGGCTAGG<br>TTGA | TTTTGGGAAAAACAAGT<br>TCGAT  | 60.0                             | 422                                           | DRR                                               | Ca_17965                            | G                     | --      |
| Ca7_P4_42337005  | Ca7                                     | 42337005                      | GAAAAAAAAA/GAAAAAAAAA                                         | CCAAACAAAATTGCCT<br>CGAT | TGATCAGCGAGATGGA<br>CAAG    | 59.9                             | 704                                           | DRR                                               | Ca_17962                            | --                    | --      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')   | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|---------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                                               |                           |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca7_P4_44150096  | Ca7                                     | 44150096                      | T/TTTA                                                                        | AGTCTTACCAGCGCCA<br>CACT  | TCCCAACTACAACGAG<br>GACC       | 59.9                             | 567                                           | DRR                                               | Ca_21366                            | O                     | --     |
| Ca7_P4_44150736  | Ca7                                     | 44150736                      | TAAAAA/TAAAAAA                                                                | GGTCCTCGTTGTAGTT<br>GGGA  | CCAAGGCATCAGCTCA<br>CATA       | 60.0                             | 467                                           | DRR                                               | Ca_21366                            | O                     | --     |
| Ca7_P4_44372091  | Ca7                                     | 44372091                      | GAATAATAATAATAATAATAATA<br>ATA/GAATAATAATAATAATAATA<br>ATAATAATA              | CGGAGAGTTGATTTCA<br>CACAA | CGTCAAAGACGTTCTT<br>CAATCA     | 58.8                             | 498                                           | DRR                                               | Ca_21371                            | --                    | --     |
| Ca7_P4_4439880   | Ca7                                     | 4439880                       | ATTTTTTTTTT/ATTTTTTTTTT                                                       | TGCCTTGTGTGAAA<br>TGGA    | TGGACGCTCCAATTAA<br>GCAG       | 60.1                             | 753                                           | DRR                                               | Ca_03014                            | R                     | --     |
| Ca7_P4_44885868  | Ca7                                     | 44885868                      | CA/CAGAAAAATA                                                                 | TTTGGTTCAAACAAGG<br>GGAG  | ACGAAAATGTCAAAAAC<br>CGC       | 59.9                             | 373                                           | DRR                                               | Ca_15709                            | --                    | FAR1   |
| Ca7_P4_45248869  | Ca7                                     | 45248869                      | AATATATATATATATATATATAT<br>ATATATAT/AATATATATATATATA<br>TATATATATATATATATATAT | GTTATCGCAATTGGG<br>GATG   | TCAAAGTTAACGTGTTT<br>GAGTAGATG | 60.2                             | 576                                           | DRR                                               | Ca_15725                            | I                     | bHLH   |
| Ca7_P4_45731609  | Ca7                                     | 45731609                      | AATTTATATTTA/AATTTA                                                           | TTTGCAGCCACAAAAG<br>TCTG  | TTGTGTGTTTAATTTTG<br>CGTTTG    | 60.0                             | 625                                           | DRR                                               | Ca_15750                            | --                    | --     |
| Ca7_P4_45762039  | Ca7                                     | 45762039                      | ATTTGT/ATTACTAGTTATTTGTTG<br>T                                                | TTTTAAGCGTGTTTTT<br>GGG   | TCAACAAGTCACAGGC<br>GATT       | 60.0                             | 893                                           | DRR                                               | Ca_15751                            | J                     | --     |
| Ca7_P4_4592459   | Ca7                                     | 4592459                       | TA/T                                                                          | CGGATACGGTCTGGTC<br>AAGT  | CACATCACACCAAATCA<br>ACACA     | 60.0                             | 517                                           | DRR                                               | Ca_02993                            | U                     | GATA   |
| Ca7_P4_45933626  | Ca7                                     | 45933626                      | GAAAAAAAAA/GAAAAAAAAA                                                         | GCACATGCGTGTGTCT<br>TCTC  | TCTTTGGAGTATTTCAAG<br>TGGAGG   | 60.5                             | 455                                           | DRR                                               | Ca_15757                            | T                     | E2F/DP |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca7_P4_47208313  | Ca7                                     | 47208313                      | ATTTTTTTTT/ATTTTTTTTT                                         | TTCTGCAATGTGGAT<br>CATTG | GCAGGCCAACCATAGT<br>TCTG | 59.5                             | 524                                           | DRR                                               | Ca_19491                            | G                     | E2F/DP      |
| Ca7_P4_47551388  | Ca7                                     | 47551388                      | C/CCA                                                         | TGGCATTGATGATGGC<br>TTTA | CCAGGATAAACAGCC<br>CAGA  | 60.0                             | 622                                           | DRR                                               | Ca_19500                            | O                     | MYB_related |
| Ca7_P4_47551645  | Ca7                                     | 47551645                      | ATTCTAGAACGGTTTTCTA/ATTCTA<br>GAACGGTTTTCTAGAACGGTTTTCT<br>A  | GCAATTTTGTGAAGGA<br>GGGA | CCAGGATAAACAGCC<br>CAGA  | 60.1                             | 497                                           | DRR                                               | Ca_19500                            | O                     | MYB_related |
| Ca7_P4_48703820  | Ca7                                     | 48703820                      | CAAAAAAAAA/CAAAAAAAAA                                         | TCAGTCAAACGCACAC<br>AAAA | TTCGGTTTGAGGGAAG<br>TCAC | 58.9                             | 496                                           | DRR                                               | Ca_26166                            | --                    | --          |
| Ca7_P4_5254880   | Ca7                                     | 5254880                       | CTTTT/CTTT                                                    | TGGGCTGGACTATACA<br>AGGG | CACGGCCATTTTCATCT<br>CTT | 59.9                             | 705                                           | DRR                                               | Ca_06846                            | C                     | --          |
| Ca7_P4_5379802   | Ca7                                     | 5379802                       | CAAAAAAAAA/CAAAAAAAAA                                         | TGGTCAGGATCACGCT<br>AACA | AACGAATGGCCAACTT<br>CAAT | 60.3                             | 688                                           | DRR                                               | Ca_06834                            | A                     | --          |
| Ca7_P4_5379954   | Ca7                                     | 5379954                       | CAAA/CAA                                                      | TCGTTTTGTGTCAAT<br>GACTC | GAACCGAATTGGGCTA<br>CAAA | 58.6                             | 904                                           | DRR                                               | Ca_06834                            | A                     | --          |
| Ca7_P4_5380199   | Ca7                                     | 5380199                       | TAAAAAA/TAAAAAA                                               | ATTGAAGTTGCCATT<br>CGTT  | TGTTGCCACGTGTAC<br>CTTA  | 59.4                             | 554                                           | DRR                                               | Ca_06834                            | A                     | --          |
| Ca7_P4_5396891   | Ca7                                     | 5396891                       | CAAAA/CAAA                                                    | CGGGGCAACAAATTAT<br>CAAG | TCCACTTGACAATGTT<br>CGG  | 60.3                             | 737                                           | DRR                                               | Ca_06831                            | R                     | --          |
| Ca7_P4_5416537   | Ca7                                     | 5416537                       | TA/TAA                                                        | TGCAGGCACAATCTCT<br>TTTG | ATTTTCCTCCGGTTTGC<br>TTT | 60.0                             | 925                                           | DRR                                               | Ca_06827                            | T                     | WRKY        |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca7_P4_5418013   | Ca7                                     | 5418013                       | ACTA/ACTAATGTATAATCTA                                         | TGTGAAGCTCACGTTTC<br>ACCA | GGGACCTTCTACTTAC<br>CCGC     | 58.7                             | 517                                           | DRR                                               | Ca_06827                            | T                     | WRKY        |
| Ca7_P4_5434792   | Ca7                                     | 5434792                       | CTTTT/CTTT                                                    | GAAAGAGGATCAACCC<br>GACA  | CATGGTCCACTTCGAG<br>GAAT     | 60.1                             | 466                                           | DRR                                               | Ca_06825                            | --                    | --          |
| Ca7_P4_5436143   | Ca7                                     | 5436143                       | AAA/AAATATCACAA                                               | TGTTTAGATGTGGTGG<br>TGCTG | CAAGCAGGTATGTGAG<br>GGGT     | 59.6                             | 721                                           | DRR                                               | Ca_06825                            | --                    | --          |
| Ca7_P4_5464695   | Ca7                                     | 5464695                       | TTATATATATATATATATATA/TTA<br>TATATATATATATATATA               | TTTTGTGGCTGCATTC<br>TCTG  | GCTGCTGAGGCTGTTA<br>TTCC     | 60.0                             | 656                                           | DRR                                               | Ca_06820                            | --                    | --          |
| Ca7_P4_5513596   | Ca7                                     | 5513596                       | TTATATATATAT/TTATATATAT                                       | AGGCTGCTGTAGGAGA<br>TGGA  | AATCAACCTTGAATG<br>GTGC      | 60.0                             | 504                                           | DRR                                               | Ca_06816                            | BK                    | G2-like     |
| Ca7_P4_5517542   | Ca7                                     | 5517542                       | GAAA/GAA                                                      | TGCAGCCTACCAAATT<br>CAAA  | TTGTTGGTGGTCTTTC<br>CTGA     | 59.3                             | 709                                           | DRR                                               | Ca_06815                            | R                     | MYB_related |
| Ca7_P4_5524205   | Ca7                                     | 5524205                       | CATGGAAAAATGAAAAATG/CATG<br>GAAAAATG                          | AGGCCTGAACACAGTG<br>GAAC  | AAGGAACCGTGTGAAC<br>CAAG     | 60.2                             | 248                                           | DRR                                               | Ca_06814                            | --                    | TCP         |
| Ca7_P4_5525422   | Ca7                                     | 5525422                       | T/TG                                                          | AATGTCAAGGGCATT<br>GGTC   | TGTTTAGAGTTTGTAGCA<br>GCCACA | 59.8                             | 337                                           | DRR                                               | Ca_06814                            | --                    | TCP         |
| Ca7_P4_5540435   | Ca7                                     | 5540435                       | TTTAACAATATT/TTTAACAATATTAA<br>ATTAACAATATT                   | GCATCCAACTCCAAAG<br>TGCT  | TGCACAACTCCAACAT<br>TGA      | 60.3                             | 711                                           | DRR                                               | Ca_06810                            | R                     | G2-like     |
| Ca7_P4_5540728   | Ca7                                     | 5540728                       | TC/T                                                          | TCAATGTTGGAGTTTG<br>TGCAT | CGCATATCAAACATTGC<br>AGC     | 59.0                             | 569                                           | DRR                                               | Ca_06810                            | R                     | G2-like     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca7_P4_5549714   | Ca7                                     | 5549714                       | ACTCT/ACT                                                     | TCTGTGACTGCTTTGA<br>TGCC  | TCATGATGGTTAAGGG<br>CAAA | 60.0                             | 672                                           | DRR                                               | Ca_06809                            | --                    | --          |
| Ca7_P4_5562230   | Ca7                                     | 5562230                       | TTATATATA/TTATATATATA                                         | ACACCGTTTGAAGCAA<br>ATCC  | AGCTGAGACTTGTGGT<br>GGCT | 60.0                             | 833                                           | DRR                                               | Ca_06807                            | E                     | MYB_related |
| Ca7_P4_5567293   | Ca7                                     | 5567293                       | TC/T                                                          | GCACCATAGTGTTAC<br>CAAAAA | TCTGATCCTCTCCAC<br>CAAC  | 59.9                             | 585                                           | DRR                                               | Ca_06806                            | --                    | --          |
| Ca7_P4_5567501   | Ca7                                     | 5567501                       | TAAAAAAAA/TAAAAAAAAA                                          | TCATGAAATGTCATTG<br>GTTG  | TTTTTGGCCTGAAAA<br>CAAG  | 59.4                             | 200                                           | DRR                                               | Ca_06806                            | --                    | --          |
| Ca7_P4_5578208   | Ca7                                     | 5578208                       | AG/AGAATGAATG                                                 | ATGGGAAATTGTGAAT<br>GGGA  | TGCCCGTTAGTCAATG<br>TTTG | 60.0                             | 435                                           | DRR                                               | Ca_06805                            | --                    | --          |
| Ca7_P4_5633058   | Ca7                                     | 5633058                       | T/TAAG                                                        | GCAAGCCAAACCACAA<br>AAAT  | ACAGGCGCTTCCTTCT<br>TGTA | 60.0                             | 386                                           | DRR                                               | Ca_06796                            | GC                    | HSF         |
| Ca7_P4_5658376   | Ca7                                     | 5658376                       | CATAT/CATATAT                                                 | CTGCTGGATCTGGGAA<br>ATGT  | TCTTGCTATTGGCTGC<br>AGTG | 60.1                             | 334                                           | DRR                                               | Ca_06792                            | GC                    | HSF         |
| Ca7_P4_5658804   | Ca7                                     | 5658804                       | TTTTATTTA/T                                                   | CACTGCAGCCAATAGC<br>AAGA  | TCGTTTTCAACCTAAAC<br>CCA | 60.2                             | 495                                           | DRR                                               | Ca_06792                            | GC                    | HSF         |
| Ca7_P4_5671646   | Ca7                                     | 5671646                       | CAAAA/CAAAAA                                                  | TTTAAATGACACTGGG<br>CGTG  | TGGTGTAATATGGCA<br>GCGA  | 59.6                             | 612                                           | DRR                                               | Ca_06790                            | --                    | C2H2        |
| Ca7_P4_5671743   | Ca7                                     | 5671743                       | ATT/AT                                                        | TTTAAATGACACTGGG<br>CGTG  | TGGTGTAATATGGCA<br>GCGA  | 59.6                             | 612                                           | DRR                                               | Ca_06790                            | --                    | C2H2        |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_5683344   | Ca7                                     | 5683344                       | TGC/T                                                         | TTTATTTGATGGGTGG<br>GGAA    | CAGACAGCAGTTGGAG<br>TGGA   | 60.0                             | 795                                           | DRR                                               | Ca_06788                            | Q                     | --   |
| Ca7_P4_5684253   | Ca7                                     | 5684253                       | ATTTTTTTTT/ATTTTTTTTT                                         | TGGAAGTGAAGCATCT<br>GACG    | TTTGTTCCTTGCATGTG<br>GGA   | 60.0                             | 830                                           | DRR                                               | Ca_06789                            | K                     | --   |
| Ca7_P4_5685708   | Ca7                                     | 5685708                       | T/TG                                                          | TTCGGTTTTAGCAGTTT<br>GGG    | GCGTCACACTGAGACT<br>GGAA   | 60.1                             | 788                                           | DRR                                               | Ca_06789                            | K                     | --   |
| Ca7_P4_5686029   | Ca7                                     | 5686029                       | CAA/CA                                                        | AACCGCTTGTTTTGAA<br>CTCC    | GCGTCACACTGAGACT<br>GGAA   | 59.2                             | 365                                           | DRR                                               | Ca_06789                            | K                     | --   |
| Ca7_P4_5713279   | Ca7                                     | 5713279                       | CAAAA/CAAA                                                    | GCCTGGTTGCTCCAAT<br>TAAA    | GGGCTTCAGAAGTTGC<br>TCAC   | 60.1                             | 488                                           | DRR                                               | Ca_06787                            | Q                     | --   |
| Ca7_P4_5729677   | Ca7                                     | 5729677                       | AT/ATGCTT                                                     | TCAGCTGGAGCTTTTC<br>AACA    | CGTCGACATAGAGCAA<br>CCAA   | 59.7                             | 355                                           | DRR                                               | Ca_06785                            | R                     | FAR1 |
| Ca7_P4_5790699   | Ca7                                     | 5790699                       | CAATTTAA/CAA                                                  | TTTGGCAGTGTGACCA<br>ACAT    | ATCGAAGAGCCTTAAA<br>ATGTGT | 60.0                             | 575                                           | DRR                                               | Ca_06779                            | S                     | --   |
| Ca7_P4_5791015   | Ca7                                     | 5791015                       | CTTTTTTT/CTTTTTTTTT                                           | TTTCGGTGGAATTTGA<br>GTTTTT  | CATGTGCGTGTAACCT<br>CTGGA  | 59.9                             | 861                                           | DRR                                               | Ca_06779                            | S                     | --   |
| Ca7_P4_5791147   | Ca7                                     | 5791147                       | AATTTTAAAGT/AATTTTAAAGTAATA<br>ATATTTTAAAGT                   | CGACATGAATAAATTG<br>AGGATGA | TGATCTGGTTGGTGT<br>GTCC    | 59.0                             | 988                                           | DRR                                               | Ca_06779                            | S                     | --   |
| Ca7_P4_5799703   | Ca7                                     | 5799703                       | CAAAAAAAAA/CAAAAAAAAA                                         | CCATCATACCCCTAGC<br>GAAA    | CATCACCATATGAATGC<br>ACCA  | 59.9                             | 666                                           | DRR                                               | Ca_06778                            | R                     | --   |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5799756   | Ca7                                     | 5799756                       | TGAGA/TGAGAGA                                                 | CCATCATACCCCTAGC<br>GAAA | CAGCCTATGTTTGAA<br>ACCC    | 59.9                             | 730                                           | DRR                                               | Ca_06778                            | R                     | --  |
| Ca7_P4_5800832   | Ca7                                     | 5800832                       | TTTCTT/TTT                                                    | AAAAGCGGGCCATTCT<br>AGTT | TTCTAGCATTGTGGCT<br>GTGC   | 60.1                             | 375                                           | DRR                                               | Ca_06778                            | R                     | --  |
| Ca7_P4_5841713   | Ca7                                     | 5841713                       | CAA/CA                                                        | TTTTACCGGACTACGG<br>TTGC | TGCCATTGTTTTTCCAA<br>GTTT  | 60.0                             | 918                                           | DRR                                               | Ca_06775                            | --                    | --  |
| Ca7_P4_5841891   | Ca7                                     | 5841891                       | CTTT/CTTTT                                                    | TGCAACTTTGAAGGTG<br>CTTG | CAACAAAGCCACAAAA<br>GCAA   | 60.0                             | 731                                           | DRR                                               | Ca_06775                            | --                    | --  |
| Ca7_P4_5842196   | Ca7                                     | 5842196                       | T/TG                                                          | TTGTTTCGAACCAAT<br>GGA   | CAACAAAGCCACAAAA<br>GCAA   | 59.9                             | 511                                           | DRR                                               | Ca_06775                            | --                    | --  |
| Ca7_P4_5842517   | Ca7                                     | 5842517                       | GA/GAAA                                                       | TTGCTTTTGTGGCTTT<br>GTTG | ATTAATTGCGCCGTCA<br>AAGA   | 59.9                             | 487                                           | DRR                                               | Ca_06775                            | --                    | --  |
| Ca7_P4_5842987   | Ca7                                     | 5842987                       | TAAAA/TAAAAA                                                  | TCATCGTTGACAGACC<br>TGGA | TTTAGGCAATTTTGCCC<br>TTG   | 60.2                             | 352                                           | DRR                                               | Ca_06775                            | --                    | --  |
| Ca7_P4_585059    | Ca7                                     | 585059                        | TAAA/TAA                                                      | GTTTAGGCCGCCACAA<br>AATA | GAACCTGCTTCCAG<br>CAAC     | 60.0                             | 871                                           | DRR                                               | Ca_24416                            | --                    | --  |
| Ca7_P4_5850631   | Ca7                                     | 5850631                       | ATGTGT/ATGT                                                   | CAATTCGGACGTGAAC<br>TTGA | TGTTCCCACTTTTTCAT<br>TCTTG | 59.7                             | 290                                           | DRR                                               | Ca_06773                            | O                     | --  |
| Ca7_P4_5850664   | Ca7                                     | 5850664                       | AATA/AA                                                       | CAATTCGGACGTGAAC<br>TTGA | TGTTCCCACTTTTTCAT<br>TCTTG | 59.7                             | 290                                           | DRR                                               | Ca_06773                            | O                     | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_5850863   | Ca7                                     | 5850863                       | TAAA/TAA                                                      | CAATTCGGACGTGAAC<br>TTGA | AAGTATCTCCAGGCG<br>CAAA    | 59.7                             | 819                                           | DRR                                               | Ca_06773                            | O                     | --   |
| Ca7_P4_5852220   | Ca7                                     | 5852220                       | CTTGAATTTTGAATTTT/CTTGAATTT<br>TGAATTTTGAATTTT                | TTGCTGCGAGCGTTAC<br>TCTA | TTCTGGGTATTGAACTC<br>GGC   | 59.9                             | 527                                           | DRR                                               | Ca_06773                            | O                     | --   |
| Ca7_P4_5867187   | Ca7                                     | 5867187                       | ATATTATTATTATTAT/ATATTAT<br>TATTATTATTATTAT                   | ACAACAGATGATGGCT<br>GCTG | AATGTACGCACTCCAC<br>CACA   | 59.9                             | 606                                           | DRR                                               | Ca_06771                            | P                     | --   |
| Ca7_P4_5867216   | Ca7                                     | 5867216                       | TGTAGTAGTAGTAGTA/TGTAGTAGT<br>AGTAGTAGTA                      | ACAACAGATGATGGCT<br>GCTG | AATGTACGCACTCCAC<br>CACA   | 59.9                             | 606                                           | DRR                                               | Ca_06771                            | P                     | --   |
| Ca7_P4_5867639   | Ca7                                     | 5867639                       | CAAAAA/CAAAAAAAAA                                             | TGTGGTGGAGTGCCTA<br>CATT | TGAACATTCAATCGTTC<br>CCA   | 60.0                             | 321                                           | DRR                                               | Ca_06771                            | P                     | --   |
| Ca7_P4_5868409   | Ca7                                     | 5868409                       | AATATATAT/AATATAT                                             | ACTGTTGAACCAGCTG<br>AGGC | TGGTGAGACAATGGGA<br>TGAA   | 60.5                             | 673                                           | DRR                                               | Ca_06771                            | P                     | --   |
| Ca7_P4_586986    | Ca7                                     | 586986                        | AACA/AATTACA                                                  | TTCCATTTCTCCACAA<br>AGC  | CAACCGCATTGTCATC<br>ATTC   | 60.1                             | 531                                           | DRR                                               | Ca_24415                            | --                    | --   |
| Ca7_P4_5889222   | Ca7                                     | 5889222                       | CTTT/CTT                                                      | ATTGGCAAGAGTGTTA<br>CGGG | GTGTGACTTTGGCCAC<br>CTTA   | 60.0                             | 520                                           | DRR                                               | Ca_06769                            | O                     | --   |
| Ca7_P4_5890416   | Ca7                                     | 5890416                       | TAAAAA/TAAAAA                                                 | TCGCACTCTCAAATGA<br>CCAC | TCAAAATATCACCCGTA<br>TCAAA | 59.8                             | 630                                           | DRR                                               | Ca_06769                            | O                     | --   |
| Ca7_P4_5945202   | Ca7                                     | 5945202                       | AGGTTGGGTTG/AGGTTG                                            | CACCGCAAGTTCTTCC<br>AAAT | GCGAGAAAGGCGTGT<br>GTAT    | 60.1                             | 534                                           | DRR                                               | Ca_06763                            | S                     | C2H2 |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_5978218   | Ca7                                     | 5978218                       | GGAAGATGAT/GGAAGATGATGAAG<br>ATGAT                            | AAATCCGTGCAACAC<br>ACG     | ACTGATGGGGCAAGT<br>ACAC     | 60.6                             | 448                                           | DRR                                               | Ca_06760                            | --                    | --   |
| Ca7_P4_6010128   | Ca7                                     | 6010128                       | CTTTGAGCTTTGTAGTAT/CTTTGAG<br>CTTTGTAGTATTTGAGCTTTGTAGT<br>AT | ATGTGCGTTAAGGGAA<br>CTGG   | TTGGAGACCCACGTTC<br>TACC    | 60.0                             | 260                                           | DRR                                               | Ca_06759                            | --                    | --   |
| Ca7_P4_6020433   | Ca7                                     | 6020433                       | TAAAAAA/TAAAAAA                                               | AATCCGTTGAGATTGG<br>GATG   | TTTTTGTTCATTGGTG<br>TTATTTT | 59.8                             | 677                                           | DRR                                               | Ca_06757                            | R                     | --   |
| Ca7_P4_6034341   | Ca7                                     | 6034341                       | ATTTT/ATTTT                                                   | AACATGGAAATTGTTG<br>GCA    | TTTTCGAAGGCAATTGA<br>ACC    | 58.9                             | 638                                           | DRR                                               | Ca_06755                            | A                     | --   |
| Ca7_P4_6063507   | Ca7                                     | 6063507                       | ATT/ATT                                                       | GCACGAGCTAAACTA<br>TAGGCG  | ATTGGTCATTTTCCAC<br>GAA     | 60.4                             | 660                                           | DRR                                               | Ca_06754                            | K                     | TALE |
| Ca7_P4_6065107   | Ca7                                     | 6065107                       | ATTTTTTTTT/ATTTTTTTT                                          | CCATGAAATATCCTC<br>GTGCT   | TGCTCAGTGCTCACGA<br>GTCT    | 59.1                             | 948                                           | DRR                                               | Ca_06752                            | T                     | bZIP |
| Ca7_P4_6065331   | Ca7                                     | 6065331                       | TAAAA/TAAAA                                                   | TTGTCCACCAAAGTTTC<br>ATTTC | ATCATGCTTTTTCCCGT<br>CTG    | 59.0                             | 492                                           | DRR                                               | Ca_06752                            | T                     | bZIP |
| Ca7_P4_6065402   | Ca7                                     | 6065402                       | ATTTT/ATTTT                                                   | TTGTCCACCAAAGTTTC<br>ATTTC | ATCATGCTTTTTCCCGT<br>CTG    | 59.0                             | 492                                           | DRR                                               | Ca_06752                            | T                     | bZIP |
| Ca7_P4_6089737   | Ca7                                     | 6089737                       | ATTTTTTTTT/ATTTTTTTT                                          | AGGATCAGCAAGAGAA<br>GCCA   | CGGCTTGATCCTACAA<br>GAGG    | 60.1                             | 324                                           | DRR                                               | Ca_06750                            | O                     | --   |
| Ca7_P4_6106620   | Ca7                                     | 6106620                       | TA/T                                                          | TTAGGGCATGTCTCCA<br>GCTT   | ACTTTCGACCACCACTT<br>CCA    | 59.8                             | 553                                           | DRR                                               | Ca_06747                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_6107206   | Ca7                                     | 6107206                       | AA/AACAATA                                                    | TGGAAGTGGTGGTCGA<br>AAGT   | TGAAAATGGTGAAAGT<br>GGAACA | 60.5                             | 647                                           | DRR                                               | Ca_06747                            | --                    | --  |
| Ca7_P4_6126281   | Ca7                                     | 6126281                       | TAAAAA/TAAAA                                                  | TTTCTGCCTAGAAAAGT<br>TCCAT | TGTAGCCACGTAAGGA<br>AACCT  | 57.2                             | 246                                           | DRR                                               | Ca_06744                            | O                     | --  |
| Ca7_P4_6126376   | Ca7                                     | 6126376                       | TAAATAAAT/TAAATAAATAAAAA<br>TAAAT                             | CGGTCATTTTCAACG<br>TATTTT  | TGTAGCCACGTAAGGA<br>AACCT  | 58.1                             | 151                                           | DRR                                               | Ca_06744                            | O                     | --  |
| Ca7_P4_6145585   | Ca7                                     | 6145585                       | ATTTTTTT/ATTTTTTTT                                            | AAGGATCGTGCCAAAA<br>CAAC   | AAAATTCATCGGATCAA<br>CGG   | 60.0                             | 316                                           | DRR                                               | Ca_06742                            | --                    | --  |
| Ca7_P4_6146295   | Ca7                                     | 6146295                       | GAAAAAA/GAAAAAA                                               | CAAGAGAAACCAAAT<br>CGCC    | TCCCCATAAGCTCTTC<br>CCT    | 59.7                             | 341                                           | DRR                                               | Ca_06742                            | --                    | --  |
| Ca7_P4_6154870   | Ca7                                     | 6154870                       | TT/TTGAT                                                      | CCCTTCAGAGTCCCAT<br>GCTA   | TGTCATGTGCTGAGTC<br>GTCA   | 60.2                             | 625                                           | DRR                                               | Ca_06741                            | --                    | --  |
| Ca7_P4_6195527   | Ca7                                     | 6195527                       | GTATATATATATATATAT/GTATAT<br>ATATATATATATATAT                 | GATCTAACGGCTGAGC<br>GAAC   | CAGAAGCTCCAAGAAC<br>TGCC   | 60.0                             | 156                                           | DRR                                               | Ca_06738                            | --                    | --  |
| Ca7_P4_760350    | Ca7                                     | 760350                        | T/TGTA                                                        | TCTAGCGACGGTCTG<br>ATCT    | CAAATGCCAACAAGCG<br>TTTA   | 60.0                             | 365                                           | DRR                                               | Ca_03403                            | R                     | --  |
| Ca7_P4_760856    | Ca7                                     | 760856                        | GTTGAAGATTG/GTTGAAGATTGAA<br>GATTG                            | TAAACGCTTGTTGGCA<br>TTTG   | AGTTCGACGGCTCTGT<br>TGTT   | 59.7                             | 445                                           | DRR                                               | Ca_03403                            | R                     | --  |
| Ca7_P4_7685716   | Ca7                                     | 7685716                       | AATATATATATATATATATAT/AAT<br>ATATATATATATATATATATAT           | ACTCACAGAGAATCTC<br>CGGC   | TTACGATGCTGACGCC<br>ATAG   | 59.4                             | 360                                           | DRR                                               | Ca_06591                            | J                     | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                      | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                                                                                    |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca7_P4_7751929   | Ca7                                     | 7751929                       | G/GT                                                                                                                                               | AAGGTATCCCTTCCC<br>AAGA     | TTGTTCCGCAATTGATT<br>TGA  | 59.8                             | 821                                           | DRR                                               | Ca_13244                            | --                    | --       |
| Ca7_P4_8096374   | Ca7                                     | 8096374                       | ATATTATTATTATTATTAT/ATAT<br>TATTATTATTATTATTATTAT                                                                                                  | GCTTGGGACCTGAGAT<br>CCTT    | TCGGTGTGTCATTATT<br>TTGTG | 60.6                             | 650                                           | DRR                                               | Ca_13206                            | L                     | NAC      |
| Ca7_P4_8097200   | Ca7                                     | 8097200                       | AATTATTATTATTATTATTATT<br>TATTATT/AATTATTATTATTATT<br>ATTATTATTATT                                                                                 | CAACTCTGTTGAAAG<br>AAGATCAA | TGTTGTCGTAGAACCG<br>GTGA  | 59.9                             | 556                                           | DRR                                               | Ca_13206                            | L                     | NAC      |
| Ca7_P4_816979    | Ca7                                     | 816979                        | AAATAAAATTAATAAAAT/AAATAA<br>AAATTAATAAAATTAATAAAAT                                                                                                | CGACCAATGTTTTCTT<br>CTTCA   | CAGATCATGGCACGTG<br>AAAG  | 59.2                             | 496                                           | DRR                                               | Ca_03396                            | --                    | --       |
| Ca7_P4_977714    | Ca7                                     | 977714                        | GGAAGAAGAAGAAGAAGAAGA<br>AGAAGAAGAAGAAGAAGAAGA<br>AGAAGAAGAAGAAGAAGAAGA<br>AGAAGAAGAAGAAGAAGAAGA<br>AGAAGAAGAAGAAGAAGAAGA<br>AGAAGAAGAAGAAGAAGAAGA | GTCGAAGAGGCAAGAA<br>AACG    | GTCCCTCTCCATCTCC<br>TTCC  | 60.0                             | 255                                           | DRR                                               | Ca_03380                            | --                    | ERF      |
| Ca7_P4_9828006   | Ca7                                     | 9828006                       | CTATATATATATATATATATATAT<br>ATAT/CTATATATATATATATATAT<br>ATATATATAT                                                                                | TTTAGAGGGAGGGAGG<br>GAAA    | AGGACGCAAGGAAGA<br>CAGA   | 60.0                             | 264                                           | DRR                                               | Ca_12748                            | U                     | --       |
| Ca8_P4_10301817  | Ca8                                     | 10301817                      | TTAATAATAATAATAATA/TTAATAA<br>TAATAATAA                                                                                                            | ACTGGGGAAGTTGGCT<br>TTTT    | ACGAGGTGTCAGATTT<br>TGGC  | 60.0                             | 689                                           | DRR                                               | Ca_18422                            | R                     | Trihelix |
| Ca8_P4_10509590  | Ca8                                     | 10509590                      | GA/GAA                                                                                                                                             | GCCATGTCAACCGAAG<br>AGAT    | ATGCCAAGCGTTTCAC<br>TTTT  | 60.1                             | 596                                           | DRR                                               | Ca_18435                            | --                    | --       |
| Ca8_P4_10934374  | Ca8                                     | 10934374                      | AT/ATT                                                                                                                                             | TCCGATTCATCCTCTT<br>GGTC    | AATGAAAAAGCGGGGA<br>AACT  | 60.0                             | 368                                           | DRR                                               | Ca_19747                            | R                     | NAC      |
| Ca8_P4_11124508  | Ca8                                     | 11124508                      | CATAT/CAT                                                                                                                                          | CAGTGGGAAAAGTCAA<br>CGGT    | GGTTCGACATCACAG<br>GAGT   | 60.0                             | 536                                           | DRR                                               | Ca_16840                            | --                    | WRKY     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_11449628  | Ca8                                     | 11449628                      | ATT/ATTT                                                      | GAAAGGGGAAAATGG<br>TGAT       | TGGTCAAACAACATAA<br>GCCG   | 60.0                             | 833                                           | DRR                                               | Ca_16817                            | --                    | NAC |
| Ca8_P4_11536143  | Ca8                                     | 11536143                      | CATTATTATTATTATTATT/CATTATT<br>ATTATTATTATTATT                | TCTTACACTGCAGCAA<br>TAAAAATCA | TGGTTGATGCCCAAGT<br>ACAA   | 60.2                             | 576                                           | DRR                                               | Ca_16812                            | R                     | MYB |
| Ca8_P4_13993624  | Ca8                                     | 13993624                      | TTG/T                                                         | GCACAATTTGGCAAGA<br>ACAA      | TTGGGATTGAGGTTGA<br>GGAG   | 59.7                             | 455                                           | DRR                                               | Ca_22739                            | K                     | --  |
| Ca8_P4_13993907  | Ca8                                     | 13993907                      | GTTTTT/GTTTT                                                  | CTCCTCAACCTCAATC<br>CCAA      | TCACCGGTCAATCAATT<br>AAAAA | 60.0                             | 228                                           | DRR                                               | Ca_22739                            | K                     | --  |
| Ca8_P4_14077330  | Ca8                                     | 14077330                      | TAGAGAAAAGAAGAGAAA/TAGAGA<br>AA                               | TTGATATGTCATCCCC<br>GGTT      | TTCTTTCCCACTTCT<br>TCC     | 60.0                             | 696                                           | DRR                                               | Ca_22744                            | U                     | --  |
| Ca8_P4_14077398  | Ca8                                     | 14077398                      | GA/GAAA                                                       | TTGATATGTCATCCCC<br>GGTT      | AGCTGCATCTTCCACG<br>ATTT   | 60.0                             | 940                                           | DRR                                               | Ca_22744                            | U                     | --  |
| Ca8_P4_14138599  | Ca8                                     | 14138599                      | AA/AACACA                                                     | TTGAAATCCACAAAATT<br>CCAAA    | TTCATTTTCATCCTCTC<br>GGC   | 59.3                             | 730                                           | DRR                                               | Ca_13046                            | O                     | --  |
| Ca8_P4_14138805  | Ca8                                     | 14138805                      | TAAAAAAA/TAAAAAAA                                             | CAAAGAAAAGGAAGAA<br>CCCACA    | TTCATTTTCATCCTCTC<br>GGC   | 60.5                             | 290                                           | DRR                                               | Ca_13046                            | O                     | --  |
| Ca8_P4_14143645  | Ca8                                     | 14143645                      | ATTTTTTTT/ATTTTTTTTT                                          | ATGCATGTGAAAGGGA<br>CACA      | AAGGGCCCCACTATCA<br>CTTC   | 60.0                             | 497                                           | DRR                                               | Ca_13045                            | --                    | --  |
| Ca8_P4_14248630  | Ca8                                     | 14248630                      | TAAAAAAA/TAAAAAAA                                             | ATGCTTCCAAACAATT<br>CCG       | TTCCCTTGTTTCTATG<br>CCAA   | 59.9                             | 797                                           | DRR                                               | Ca_13039                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca8_P4_14248780  | Ca8                                     | 14248780                      | ATTTTTTTTT/ATTTTTTTTTTT                                       | ATGCTTCCAAACAATT<br>CCG    | TTCCCTTGTTTTCTATG<br>CCAA | 59.9                             | 797                                           | DRR                                               | Ca_13039                            | --                    | --          |
| Ca8_P4_14257165  | Ca8                                     | 14257165                      | GTT/GTTCAGACCTTT                                              | AGGCCGCAGATGAACT<br>GTAT   | TGGTTTGCTTTTAAGC<br>GAGG  | 59.7                             | 824                                           | DRR                                               | Ca_13038                            | --                    | --          |
| Ca8_P4_14257769  | Ca8                                     | 14257769                      | AG/A                                                          | CCTCGCTTAAAGCAA<br>ACCA    | GAGTGGCGAAACCCTA<br>ATGA  | 60.4                             | 437                                           | DRR                                               | Ca_13037                            | O                     | MYB_related |
| Ca8_P4_14279667  | Ca8                                     | 14279667                      | CAAAAAA/CAAAAAA                                               | CAAGTCTCCCAACTTC<br>CCAA   | ACGAGCCCGTCTTTAG<br>TTGA  | 60.1                             | 533                                           | DRR                                               | Ca_13036                            | S                     | --          |
| Ca8_P4_14320669  | Ca8                                     | 14320669                      | A/AG                                                          | CAATGGCAGTAACATG<br>CAGC   | TCCCAACAACCTCAATT<br>CCA  | 60.3                             | 700                                           | DRR                                               | Ca_13032                            | Z                     | MYB_related |
| Ca8_P4_14320978  | Ca8                                     | 14320978                      | TG/T                                                          | TGATGCTTTGGTTTCAT<br>GTCA  | TCCCAACAACCTCAATT<br>CCA  | 60.1                             | 359                                           | DRR                                               | Ca_13032                            | Z                     | MYB_related |
| Ca8_P4_14574261  | Ca8                                     | 14574261                      | AGTG/AGTGTG                                                   | GTGGAATGGTGTGAAA<br>GGGT   | TAGCCAGAGAACAACC<br>CTCC  | 59.7                             | 520                                           | DRR                                               | Ca_13010                            | --                    | --          |
| Ca8_P4_14576894  | Ca8                                     | 14576894                      | ATTTTTTT/ATTTTTTT                                             | TTTTGTTTGGTGGTTG<br>ATCATT | AGCAGCTCCAGAATTG<br>ACTTG | 59.2                             | 923                                           | DRR                                               | Ca_13009                            | Z                     | MYB_related |
| Ca8_P4_14577677  | Ca8                                     | 14577677                      | AATA/AA                                                       | CAAGTCAATTCTGGAG<br>CTGCTA | AAAGACGAAGAAATCG<br>AGCG  | 59.7                             | 620                                           | DRR                                               | Ca_13009                            | Z                     | MYB_related |
| Ca8_P4_14603641  | Ca8                                     | 14603641                      | GCA/GCACTATACCA                                               | AATGCCGTTAAGTTGA<br>TGGG   | CGTATTGCGGAACAAC<br>AATG  | 59.8                             | 268                                           | DRR                                               | Ca_13007                            | C                     | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_14615758  | Ca8                                     | 14615758                      | GACAC/GAC                                                     | CCCGCATCAAAGATCA<br>AACT | GGTGCAGCAATTGTTG<br>AGAA  | 60.1                             | 324                                           | DRR                                               | Ca_13006                            | K                     | C3H |
| Ca8_P4_14615814  | Ca8                                     | 14615814                      | TAAA/TAAAA                                                    | CCCGCATCAAAGATCA<br>AACT | GGTGCAGCAATTGTTG<br>AGAA  | 60.1                             | 324                                           | DRR                                               | Ca_13006                            | K                     | C3H |
| Ca8_P4_14617513  | Ca8                                     | 14617513                      | AT/A                                                          | GCTCCAACCGTAAAC<br>CAAA  | GTGAGGACGGAGAGG<br>AGACA  | 60.0                             | 598                                           | DRR                                               | Ca_13006                            | K                     | C3H |
| Ca8_P4_14623977  | Ca8                                     | 14623977                      | TAAAAA/TAAAAAAA                                               | GCAATTGTGCATTGT<br>CCAC  | GTGAATGTAAATGGTG<br>GGGG  | 60.0                             | 695                                           | DRR                                               | Ca_13005                            | U                     | --  |
| Ca8_P4_14625060  | Ca8                                     | 14625060                      | CAAAAAA/CAAAAAA                                               | GCGTCAACACTTCCAA<br>CACA | CACTCCAACGAACCCA<br>GTTT  | 60.8                             | 426                                           | DRR                                               | Ca_13005                            | U                     | --  |
| Ca8_P4_14625324  | Ca8                                     | 14625324                      | TC/T                                                          | GCGTCAACACTTCCAA<br>CACA | TAAGGACTGGACGTAA<br>CCCG  | 60.8                             | 682                                           | DRR                                               | Ca_13005                            | U                     | --  |
| Ca8_P4_14625350  | Ca8                                     | 14625350                      | CTTTTTTT/CTTTTTTTT                                            | AACTGGGTTTCGTTGG<br>AGTG | TAAGGACTGGACGTAA<br>CCCG  | 60.0                             | 276                                           | DRR                                               | Ca_13005                            | U                     | --  |
| Ca8_P4_14643292  | Ca8                                     | 14643292                      | TCCC/TCCCC                                                    | AGCAAATCTTGAAGG<br>GACG  | CAATGGGAGTTTGTGG<br>TG TG | 59.3                             | 638                                           | DRR                                               | Ca_13004                            | --                    | --  |
| Ca8_P4_14652708  | Ca8                                     | 14652708                      | GGA/G                                                         | CCCTAATTACAGCCC<br>TCAA  | TGGTGTTAGCTTGTT<br>GGTG   | 60.0                             | 152                                           | DRR                                               | Ca_13003                            | --                    | --  |
| Ca8_P4_14693755  | Ca8                                     | 14693755                      | TAATTAGAAT/TAATTAGAATTAGAA<br>T                               | TCAAATCACCGTTGAT<br>GGTC | ATCATGGGAATGGTTG<br>AGGA  | 59.3                             | 515                                           | DRR                                               | Ca_13001                            | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                                                           |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca8_P4_1469473   | Ca8                                     | 1469473                       | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATAT                                         | ACCAACCGGATTGTT<br>TCAG  | AAAAACACATTGGTTGA<br>GATGC  | 59.8                             | 570                                           | DRR                                               | Ca_15025                            | D                     | --    |
| Ca8_P4_14698427  | Ca8                                     | 14698427                      | CATTATTATTATTATTATTATTAT<br>TATTATTAT/CATTATTATTATTATTA<br>TTATTATTATTATTATTAT            | GGCAGTTTCATCCCTC<br>AAGA | TTATGGGACCAACCCA<br>GGTA    | 60.2                             | 886                                           | DRR                                               | Ca_13000                            | --                    | --    |
| Ca8_P4_14751499  | Ca8                                     | 14751499                      | TGG/TG                                                                                    | ATGAAGACCAACCAAG<br>TGCC | ACAAAGCTCGTTTGCT<br>CACA    | 60.0                             | 189                                           | DRR                                               | Ca_12994                            | --                    | --    |
| Ca8_P4_14757174  | Ca8                                     | 14757174                      | TAAAAAAAA/TAAAAAAAA                                                                       | CATGGAATCCAAATCG<br>ATGA | ACCTCCCTCCAACA<br>AATC      | 59.3                             | 477                                           | DRR                                               | Ca_12993                            | O                     | --    |
| Ca8_P4_14768319  | Ca8                                     | 14768319                      | ATTTTTT/ATTTTTT                                                                           | TAATCGATCACCCGAC<br>CATT | TTGGGACTGGTGAAAG<br>GGTA    | 60.2                             | 621                                           | DRR                                               | Ca_12991                            | O                     | SRS   |
| Ca8_P4_14821171  | Ca8                                     | 14821171                      | GAAAAAAAA/GAAAAAAAA                                                                       | ACATCCGTGATGGTCA<br>CACA | GATCAGCTGCAGACAT<br>TGGA    | 60.9                             | 657                                           | DRR                                               | Ca_12987                            | D                     | bHLH  |
| Ca8_P4_1568214   | Ca8                                     | 1568214                       | AATATATATATATATATATA/AA<br>TATATATATATATATATATA                                           | TGGATCACTTGGCATT<br>GGTA | AAGTAAAAGTTTGCCA<br>GCCG    | 59.9                             | 561                                           | DRR                                               | Ca_15013                            | T                     | FAR1  |
| Ca8_P4_15821014  | Ca8                                     | 15821014                      | CAAAAAAAAA/CAAAAAAAAA                                                                     | GTCGCGATCAAGAAA<br>ACAA  | TCAAGTGACAAAGAAA<br>GGGAGTT | 58.9                             | 500                                           | DRR                                               | Ca_17863                            | --                    | NF-YB |
| Ca8_P4_15862033  | Ca8                                     | 15862033                      | GTATATATATATATATATATAT<br>ATATATATATATATATATAT/GT<br>ATATATATATATATATATATA<br>TATATATATAT | AGGGAATCAATGGCAT<br>CTTG | CTCACAGGCAACTCCA<br>AACA    | 59.9                             | 856                                           | DRR                                               | Ca_17858                            | T                     | --    |
| Ca8_P4_16132504  | Ca8                                     | 16132504                      | AATATATATATATATATATAT/A<br>ATATATATATATATATATAT                                           | CGTGGCGAGCATTATT<br>TCAT | CTGGCTGGACTGACAT<br>AGCA    | 61.0                             | 681                                           | DRR                                               | Ca_15525                            | J                     | --    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                 | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca8_P4_16135891  | Ca8                                     | 16135891                      | GAAAAAAAAA/GAAAAAAAAAA<br>A                                                                   | TGTTGTGGTTCGGATT<br>TTTG     | TGCACATGCATCCAAAT<br>TTTA   | 59.4                             | 484                                           | DRR                                               | Ca_15526                            | Q                     | --   |
| Ca8_P4_1631334   | Ca8                                     | 1631334                       | AA/ATAATAATAATA                                                                               | GCGGCTAACCTAACCA<br>AATTC    | TGCTGATTGGCTTCAC<br>TTTTT   | 60.0                             | 407                                           | DRR                                               | Ca_02445                            | --                    | WRKY |
| Ca8_P4_1777813   | Ca8                                     | 1777813                       | AATTATTATTATTATT/AATTATTATT<br>ATTATTATT                                                      | TCAATTGATTTTCGGTA<br>TCCTTC  | AGGCAAATGACCAATT<br>GAGG    | 59.3                             | 698                                           | DRR                                               | Ca_02430                            | --                    | GRF  |
| Ca8_P4_1881652   | Ca8                                     | 1881652                       | ATGTGTGTGTGTGTGTGTGT/AT<br>GTGTGTGTGTGTGTGTGTGTGT                                             | TGAAAAGTTTTGAATGA<br>AAAGTGG | CCATCCAAATTACACAT<br>GCCT   | 59.6                             | 549                                           | DRR                                               | Ca_02414                            | T                     | NAC  |
| Ca8_P4_1993541   | Ca8                                     | 1993541                       | A/AGGGAATAATAAT                                                                               | ATTCATCCCCAACCG<br>TGTA      | GGACTCCAAAGGAAAT<br>GCAA    | 60.1                             | 666                                           | DRR                                               | Ca_02403                            | R                     | --   |
| Ca8_P4_2289033   | Ca8                                     | 2289033                       | CTATATATATATATATATATAT/CT<br>ATATATATATATATATATATATAT                                         | TGAGCTGCTCGTGAAT<br>ATGG     | TTCCAAATACACCCCTC<br>ACG    | 60.0                             | 786                                           | DRR                                               | Ca_02360                            | F                     | bHLH |
| Ca8_P4_2325798   | Ca8                                     | 2325798                       | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATA<br>TATATAT                             | TTTTTGAGCGAGCCAT<br>TTCT     | TTGTTGTTCTCCTAAGG<br>TTTTGC | 60.0                             | 695                                           | DRR                                               | Ca_02357                            | C                     | --   |
| Ca8_P4_2521414   | Ca8                                     | 2521414                       | ATGG/ATGGTGG                                                                                  | TGAAGCACACTGGCAA<br>AGTC     | ATCCAAATTCCTGGCTT<br>GC     | 60.0                             | 613                                           | DRR                                               | Ca_02333                            | L                     | --   |
| Ca8_P4_2522963   | Ca8                                     | 2522963                       | ATTTTTTTTT/ATTTTTTTTTT                                                                        | ACCAATGGGAGGTTT<br>TCAT      | CTCAGTGACTTTCATT<br>GGCA    | 60.4                             | 332                                           | DRR                                               | Ca_02333                            | L                     | --   |
| Ca8_P4_3565360   | Ca8                                     | 3565360                       | TTATATATATATATATATATATATA<br>TATATATATATA/TTATATATATATAT<br>ATATATATATATATATATATATATA<br>TATA | CGAGAATAAGAAATGA<br>AGCCTGA  | GGTCAATTTTGTGTG<br>GCCT     | 59.9                             | 539                                           | DRR                                               | Ca_02220                            | P                     | GRAS |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                          | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                                                                                        |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca8_P4_3804574   | Ca8                                     | 3804574                       | T/TC                                                                                                                   | AATGTTTGGGCACACA<br>TGAA  | GATTTTCCTTCCCCACC<br>AAT    | 59.8                             | 337                                           | DRR                                               | Ca_02194                            | K                     | --      |
| Ca8_P4_4307029   | Ca8                                     | 4307029                       | GTTTATTTATTTATTTATTTATTTATTT<br>T/GTTTATTTATTTATTTATTTATTTA<br>TTTATTT                                                 | AACACTGCCTCGGTGT<br>TTCT  | CCGTCCTTGTAGCCCA<br>TTGT    | 59.8                             | 576                                           | DRR                                               | Ca_02136                            | --                    | bZIP    |
| Ca8_P4_4439470   | Ca8                                     | 4439470                       | GAAAAAAAAA/GAAAAAAAAA                                                                                                  | GAGGAATTGTGTGTG<br>CTGC   | TTGAAGTGAAGTGAAG<br>CTGGAA  | 59.3                             | 518                                           | DRR                                               | Ca_02122                            | --                    | G2-like |
| Ca8_P4_4983898   | Ca8                                     | 4983898                       | AATATATATATAT/AATATATATAT                                                                                              | TATGTTCTCTCTGCAT<br>GGC   | TTGGAATGAGCAAATA<br>GGCA    | 59.8                             | 594                                           | DRR                                               | Ca_02055                            | Q                     | GeBP    |
| Ca8_P4_5033226   | Ca8                                     | 5033226                       | ATATATTTATTTATTTATTTATTTA<br>TATTT/ATATATTTATTTATTTATTTA<br>TATTTATTTATTTATTT                                          | GCCCATTCATCACCC<br>ATCA   | GACGGAGCATCTCTCA<br>CACA    | 60.7                             | 857                                           | DRR                                               | Ca_02051                            | QI                    | bHLH    |
| Ca8_P4_5467804   | Ca8                                     | 5467804                       | CATATATATATATATATATATATA<br>TA/CATATATATATATATATATATA<br>TA                                                            | TCCATATATTTACGCT<br>GATCG | TCCTCCATTCCTTCAA<br>TCG     | 60.0                             | 847                                           | DRR                                               | Ca_01997                            | T                     | --      |
| Ca8_P4_6311569   | Ca8                                     | 6311569                       | CAATAATA/CAATA                                                                                                         | TTTTTGGCCTAGTACCT<br>GCAT | CCAGGCCAAGCCATAA<br>GTAG    | 58.8                             | 143                                           | DRR                                               | Ca_23580                            | BK                    | --      |
| Ca8_P4_6775686   | Ca8                                     | 6775686                       | TTATATATATATATA/TTATATATATA<br>TA                                                                                      | GATCCATCCTGACATG<br>GCTT  | CAACATGCACGCTTCT<br>TCAT    | 59.9                             | 272                                           | DRR                                               | Ca_10705                            | D                     | --      |
| Ca8_P4_7455373   | Ca8                                     | 7455373                       | AATTATTATTATTATTATTATTATT<br>TATTATTATTATTATTATTATTATT/A<br>ATTATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATTATT | ACTCTATTTGGGGGAG<br>CGAT  | TCAATTGATTTTCGGTA<br>TCCTTC | 59.9                             | 584                                           | DRR                                               | Ca_10646                            | K                     | C3H     |
| Ca8_P4_7560262   | Ca8                                     | 7560262                       | TAAAAA/TAAAAA                                                                                                          | GGGGGTTGAATAGGGA<br>TTTT  | TGGAAGTAGCCATCTT<br>TGGG    | 59.0                             | 194                                           | DRR                                               | Ca_10632                            | --                    | --      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca8_P4_7798966   | Ca8                                     | 7798966                       | CATATATATATATATATATATA/CA<br>TATATATATATATATATATA             | CCAAACATTGGCTGCA<br>AAAT   | AGGGGATAAGCATACC<br>GTCC | 60.9                             | 734                                           | DRR                                               | Ca_10605                            | --                    | M-type  |
| Ca8_P4_7927288   | Ca8                                     | 7927288                       | CAAA/CAAAA                                                    | AGGACCGTGCAAATGT<br>TTCT   | TGGCCTACTTATGGTC<br>TGCC | 59.6                             | 349                                           | DRR                                               | Ca_11431                            | J                     | --      |
| Ca8_P4_7927539   | Ca8                                     | 7927539                       | GTATTGCTTTTAT/GTATTGCTTTTA<br>TTGCTTTTAT                      | GCCAGACCATAAGTAG<br>GCCA   | GCAACTGGATTGCTGG<br>ATTT | 60.1                             | 509                                           | DRR                                               | Ca_11430                            | J                     | --      |
| Ca8_P4_7927639   | Ca8                                     | 7927639                       | ATT/AT                                                        | GCCAGACCATAAGTAG<br>GCCA   | GCAACTGGATTGCTGG<br>ATTT | 60.1                             | 509                                           | DRR                                               | Ca_11430                            | J                     | --      |
| Ca8_P4_7956165   | Ca8                                     | 7956165                       | GTTATATAATATTA/GTTATATAATAT<br>TATTATATAATATTA                | TTGATTGTCTAGAAG<br>CAGCACA | CACTTCTGGCTGAGT<br>TGGA  | 60.1                             | 476                                           | DRR                                               | Ca_11432                            | --                    | G2-like |
| Ca8_P4_7979395   | Ca8                                     | 7979395                       | TTTAATAATAATTATTTTATTA/TTTA                                   | CACCTGAACCGTTTCG<br>TAAT   | CCCCGTTTCATAGCAG<br>ATGT | 59.9                             | 291                                           | DRR                                               | Ca_11434                            | --                    | --      |
| Ca8_P4_7987942   | Ca8                                     | 7987942                       | AATATATATATATATATATATA/AA<br>TATATATATATATATATATA             | TTTATGTTTGCATTTGC<br>GGA   | ATTGCACACGTGTAA<br>GCCA  | 60.1                             | 701                                           | DRR                                               | Ca_11437                            | I                     | G2-like |
| Ca8_P4_799203    | Ca8                                     | 799203                        | ATT/A                                                         | AGTGTCTCGACCGTCA<br>TGAAT  | GCAACTTGTGCTGTCT<br>GCAT | 59.6                             | 836                                           | DRR                                               | Ca_11842                            | I                     | --      |
| Ca8_P4_8287736   | Ca8                                     | 8287736                       | ATTTTTTTTT/ATTTTTTTT                                          | AACAAGCCATTCCATT<br>CAGG   | TCGACGCTTTGCTTCT<br>GTG  | 59.9                             | 308                                           | DRR                                               | Ca_11462                            | J                     | --      |
| Ca8_P4_8290043   | Ca8                                     | 8290043                       | A/ACTCTCGGCAT                                                 | CAATGTGGCATGGAGA<br>TGAC   | GTCGTGGTGTGGAAG<br>GACT  | 59.9                             | 448                                           | DRR                                               | Ca_11461                            | J                     | --      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca8_P4_8366370   | Ca8                                     | 8366370                       | ATTTTTTTTT/ATTTTTTTT                                          | AACAGTCGTATTGTAT<br>GGGCCT | GTTTCAGGGTTGGTGC<br>TTGT    | 59.8                             | 705                                           | DRR                                               | Ca_11470                            | --                    | HD-ZIP |
| Ca8_P4_8774111   | Ca8                                     | 8774111                       | TA/TAGCGAA                                                    | CCACATGAGTGTGTG<br>AGGG    | CGCTAATAATGACACAT<br>TCGCT  | 60.0                             | 655                                           | DRR                                               | Ca_11507                            | --                    | SAP    |
| Ca8_P4_8854983   | Ca8                                     | 8854983                       | TAAAG/TAAAGGAAAAATAAG                                         | GCCATATCCGGCTTAC<br>CTTT   | CCCTTGACCAATTCCA<br>GAGA    | 60.3                             | 475                                           | DRR                                               | Ca_11515                            | --                    | --     |
| Ca8_P4_8882090   | Ca8                                     | 8882090                       | T/TTCCAAAC                                                    | ATCATTCCACGGATTTT<br>CCA   | TGAAAACAAACAAGAA<br>ACAGAAA | 60.1                             | 108                                           | DRR                                               | Ca_11519                            | --                    | --     |
| Ca8_P4_8885241   | Ca8                                     | 8885241                       | TTTGTCACATTGT/TTTGTCACATTG<br>TCACATTGT                       | GTGTGGAAGCACGAGA<br>CAGA   | AAAGGAACATTGTTGG<br>ACCG    | 60.0                             | 723                                           | DRR                                               | Ca_11520                            | C                     | --     |
| Ca8_P4_8894265   | Ca8                                     | 8894265                       | ATTTTTTTTT/ATTTTTTTT                                          | GAGGCCCAAAATGAAT<br>AGCA   | TTGTGACGTCCTCGG<br>TATT     | 60.0                             | 485                                           | DRR                                               | Ca_11521                            | G                     | --     |
| Ca8_P4_8909443   | Ca8                                     | 8909443                       | TATATATATACA/TA                                               | TTGCAAGAGCATGAAG<br>AACG   | TCATGGGATGGTGAAT<br>GCTA    | 60.1                             | 457                                           | DRR                                               | Ca_11522                            | --                    | --     |
| Ca8_P4_8922765   | Ca8                                     | 8922765                       | ATCT/ATCTACTCT                                                | GATTCGATAGGGGTGC<br>AAGA   | GGCAAGTGCCTGGAAG<br>TTAG    | 60.0                             | 335                                           | DRR                                               | Ca_11523                            | --                    | --     |
| Ca8_P4_9057136   | Ca8                                     | 9057136                       | TAAAAAAA/TAAAAAAA                                             | GCGGAGACGCAACTAC<br>TGTT   | TGGCTTTGTGAAGTCC<br>AAGA    | 60.5                             | 599                                           | DRR                                               | Ca_11528                            | --                    | --     |
| Ca8_P4_9101623   | Ca8                                     | 9101623                       | CT/CTTT                                                       | CAAGGTTCTCCAGAAA<br>CCCA   | ACACGTGTGCGCTCAA<br>AATA    | 60.1                             | 671                                           | DRR                                               | Ca_11533                            | --                    | C2H2   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca8_P4_9101771   | Ca8                                     | 9101771                       | ATTTTTTTT/ATTTTTTTT                                           | TCATGTTTTGAACGTA<br>GGGGA   | TACACGTGTGCGCTCA<br>AAAT  | 60.4                             | 526                                           | DRR                                               | Ca_11533                            | --                    | C2H2 |
| Ca8_P4_9102845   | Ca8                                     | 9102845                       | CTTTT/CTTTT                                                   | TTGTTTGCATATTGGAA<br>ATTTTG | AAAGTGTCTCGATTTC<br>AATGC | 58.9                             | 523                                           | DRR                                               | Ca_11533                            | --                    | C2H2 |
| Ca8_P4_9102997   | Ca8                                     | 9102997                       | TTAAGT/TTAAGTAAGT                                             | TTCGAAAACGGAAAA<br>TTTGA    | AGAATTGCTCCTTGCC<br>AAAA  | 59.6                             | 633                                           | DRR                                               | Ca_11533                            | --                    | C2H2 |
| Ca8_P4_9103038   | Ca8                                     | 9103038                       | CAAAA/CAAAAA                                                  | TTCGAAAACGGAAAA<br>TTTGA    | AGAATTGCTCCTTGCC<br>AAAA  | 59.6                             | 633                                           | DRR                                               | Ca_11533                            | --                    | C2H2 |
| Ca8_P4_9103229   | Ca8                                     | 9103229                       | GA/GATAAAAA                                                   | TTCGAAAACGGAAAA<br>TTTGA    | AGAATTGCTCCTTGCC<br>AAAA  | 59.6                             | 633                                           | DRR                                               | Ca_11533                            | --                    | C2H2 |
| Ca8_P4_9110561   | Ca8                                     | 9110561                       | TCTTATTTGCA/T                                                 | ACGTGGAACGTAACCT<br>TGCC    | TCATCTCAGATCTCCAA<br>TCCG | 60.0                             | 558                                           | DRR                                               | Ca_11534                            | --                    | --   |
| Ca8_P4_9151161   | Ca8                                     | 9151161                       | CAAAA/CAAA                                                    | ACAAATGGGGTTTCGA<br>TATG    | TTCCGTGTCTTCACGT<br>CTTG  | 59.5                             | 288                                           | DRR                                               | Ca_11539                            | O                     | --   |
| Ca8_P4_9151647   | Ca8                                     | 9151647                       | AAAAA/AAAAAGCAAAA                                             | CAAGACGTGAAGACAC<br>GGAA    | CAGACACAATGGCCTG<br>ATTG  | 59.9                             | 363                                           | DRR                                               | Ca_11539                            | O                     | --   |
| Ca8_P4_9220067   | Ca8                                     | 9220067                       | C/CTA                                                         | AAAATTAGGGGAACA<br>CAGGA    | GTATGTGTGGTGCCAT<br>TTGC  | 59.7                             | 909                                           | DRR                                               | Ca_11542                            | --                    | --   |
| Ca8_P4_9220216   | Ca8                                     | 9220216                       | CTTTTT/CTTTTT                                                 | ACCATTCAAGTAGCCG<br>ACCA    | GTATGTGTGGTGCCAT<br>TTGC  | 60.5                             | 368                                           | DRR                                               | Ca_11542                            | --                    | --   |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                        |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca8_P4_9220602         | Ca8                                     | 9220602                       | TAA/TAAA                                                      | GCAAATGGCACCACAC<br>ATAC    | GGCATCACCTCGAAA<br>ACTA    | 59.9                             | 303                                           | DRR                                               | Ca_11542                            | --                    | --       |
| Ca8_P4_9323319         | Ca8                                     | 9323319                       | ATCAAT/ATCAATCAAACACTTTCAA<br>T                               | CAGTGGTTGAGACGAG<br>CGTA    | TTTAATTTCTTGAAACG<br>GTTGG | 60.0                             | 585                                           | DRR                                               | Ca_11553                            | --                    | Dof      |
| Ca8_P4_9951759         | Ca8                                     | 9951759                       | TTATAT/TTATATAT                                               | TGGAGGTCATGTGGAT<br>CAAA    | ACTTGTGACGTGGAAT<br>GCTG   | 59.9                             | 438                                           | DRR                                               | Ca_18394                            | --                    | --       |
| Ca8_P4_9953316         | Ca8                                     | 9953316                       | TTGTGT/TTGTGTGT                                               | AGCAGCAACAACCGTC<br>TTTT    | AAAAATCGATCGGGTG<br>CATA   | 59.9                             | 312                                           | DRR                                               | Ca_18394                            | --                    | --       |
| scaffold10_P4_15748    | scaffold10                              | 15748                         | TAAAAAAA/TAAAAAA                                              | CCTCCCGTTGGTGTTA<br>AAAA    | CAAGGACTGGTTCGGT<br>TCAT   | 59.8                             | 478                                           | DRR                                               | Ca_27293                            | --                    | --       |
| scaffold1003_P4_13636  | scaffold1003                            | 13636                         | GAAGTAAAG/GAAG                                                | TGCCACTATCGGGCTA<br>ATTT    | ATTTTCGCATCCAATTA<br>CCG   | 59.6                             | 885                                           | DRR                                               | Ca_27802                            | QR                    | B3       |
| scaffold1006_P4_520865 | scaffold1006                            | 520865                        | ATTTTTT/ATTTTTTT                                              | TGGAGTGTGCCAAAA<br>GTTG     | CAACCTCCCTTTGTTTT<br>GCT   | 59.7                             | 567                                           | DRR                                               | Ca_18036                            | M                     | HB-other |
| scaffold1006_P4_582985 | scaffold1006                            | 582985                        | GC/G                                                          | TCTGCTCCAAAGGGA<br>GAAA     | TGATCCCTCCTTGCTT<br>TGG    | 59.9                             | 197                                           | DRR                                               | Ca_18042                            | --                    | --       |
| scaffold1047_P4_53093  | scaffold1047                            | 53093                         | AT/A                                                          | CAATTAGCGCATTGTT<br>TTAGTTT | TTGATTTGCGTATTGG<br>AATTG  | 58.9                             | 608                                           | DRR                                               | Ca_17175                            | R                     | Trihelix |
| scaffold1055_P4_202942 | scaffold1055                            | 202942                        | GA/G                                                          | GAGGCATATGGACTGC<br>CATT    | CGATACTCACCCCTCG<br>TTGT   | 59.9                             | 400                                           | DRR                                               | Ca_25313                            | --                    | --       |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                        |                                         |                               |                                                                   |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| scaffold1067_P4_203101 | scaffold1067                            | 203101                        | ATTTTTTTT/AATTTTTTTT                                              | TGAAACTGGGAGGAGG<br>AAGA   | CAGTGCGATGGAGAAA<br>TCAA | 59.8                             | 418                                           | DRR                                               | Ca_24425                            | --                    | --       |
| scaffold1109_P4_148572 | scaffold1109                            | 148572                        | CAATTAATTAATTAAT/CAATTAATTA<br>ATTAATTAAT                         | TGGGTGGTTGTTTGAG<br>TGAC   | GCGCTGTAAATGTGC<br>AAAA  | 59.4                             | 849                                           | DRR                                               | Ca_25534                            | --                    | --       |
| scaffold1114_P4_55938  | scaffold1114                            | 55938                         | TT/TTAATAT                                                        | ACGAGAGCGAAAATGG<br>AGAA   | AGGTGGGAGGAAATGA<br>GGTT | 60.0                             | 592                                           | DRR                                               | Ca_27287                            | --                    | --       |
| scaffold1131_P4_12797  | scaffold1131                            | 12797                         | CAAAAAAAAAA/CAAAAAAAAAAA<br>AA                                    | AAAATGGTTATTGCCA<br>GCTTTT | TTCCAAAGGCATAGTTT<br>GGC | 59.1                             | 331                                           | DRR                                               | Ca_25661                            | K                     | --       |
| scaffold1153_P4_24313  | scaffold1153                            | 24313                         | AAAGAAGAAGAAGAAGAA/AAA<br>GAAGAAGAAGAAGAAGAA                      | GAAGGAGGGAGGGAA<br>TCAAG   | ACACTGAATCCAATGG<br>CACA | 60.0                             | 215                                           | DRR                                               | Ca_27057                            | --                    | --       |
| scaffold1180_P4_36749  | scaffold1180                            | 36749                         | CTATTTATTTATTTATTTATTTATTTA<br>TTT/CTATTTATTTATTTATTTATTTA<br>TTT | TACGGTTCGATCTCAT<br>GCAA   | TGCCTCTCCCTGTTT<br>CTA   | 60.2                             | 419                                           | DRR                                               | Ca_25737                            | --                    | G2-like  |
| scaffold1196_P4_165815 | scaffold1196                            | 165815                        | TTATATATATATAT/TTATATATATAT<br>ATAT                               | CCACCTTGGAGTGTTT<br>CGAT   | ATGCCTCGCCTTCTCA<br>CATA | 60.0                             | 705                                           | DRR                                               | Ca_26185                            | V                     | --       |
| scaffold12_P4_101779   | scaffold12                              | 101779                        | TAAAAAAAAA/TAAAAAAAAAAAAA                                         | CTGGGCAAGGGATCTG<br>AATA   | AAGCGTTGTAAATGC<br>CCAC  | 60.0                             | 628                                           | DRR                                               | Ca_22971                            | --                    | Trihelix |
| scaffold1202_P4_177461 | scaffold1202                            | 177461                        | AG/ATTTAGAGG                                                      | CAGGCCTGGGTAATCT<br>TTGA   | CACACTTGGGTGTCCC<br>TCTT | 60.1                             | 397                                           | DRR                                               | Ca_24666                            | --                    | --       |
| scaffold1202_P4_6534   | scaffold1202                            | 6534                          | TAAAAAAA/TAAAAAA                                                  | AGTGCCCTCGTCAAAC<br>AAAC   | TTACAGCGCGTGTGA<br>AAAG  | 60.2                             | 824                                           | DRR                                               | Ca_24658                            | --                    | --       |



| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                        |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| scaffold1240_P4_120572 | scaffold1240                            | 120572                        | CATATATATATATATATATATA/CA<br>TATATATATATATATATATATA           | CACTGCAGCACTACCT<br>CCAA  | GCAGATAGCGTTGTGG<br>TCAA | 60.0                             | 499                                           | DRR                                               | Ca_26525                            | I                     | --   |
| scaffold127_P4_111345  | scaffold127                             | 111345                        | GAAAAAAAAA/GAAAAAAAAA                                         | TCATTGCTCCCCCGTA<br>ATAG  | CGACACTCGCTTCACC<br>AATA | 59.9                             | 504                                           | DRR                                               | Ca_26797                            | --                    | --   |
| scaffold1278_P4_34631  | scaffold1278                            | 34631                         | GA/GAA                                                        | TGTTCCAAGCAATATGT<br>TCCA | TGCCTTAAGTACAAA<br>GGGG  | 59.0                             | 433                                           | DRR                                               | Ca_27224                            | --                    | --   |
| scaffold128_P4_363869  | scaffold128                             | 363869                        | AGGG/AGG                                                      | TTGTCAATGGCAAAATT<br>GGA  | TAAGGCAAGTAGGAGG<br>TGCC | 59.9                             | 535                                           | DRR                                               | Ca_21442                            | --                    | --   |
| scaffold128_P4_7129    | scaffold128                             | 7129                          | TAAAAAAAAA/TAAAAAAAAA                                         | TTCAATTTGACATGTA<br>CGGG  | ATAATTCATGCGGAG<br>CCAA  | 58.4                             | 690                                           | DRR                                               | Ca_21428                            | K                     | --   |
| scaffold1309_P4_58470  | scaffold1309                            | 58470                         | CTTTT/CTTTT                                                   | TGGGTAACGTAACCTA<br>CGGC  | ATCCGGTAAAAATCTCC<br>GCT | 59.9                             | 951                                           | DRR                                               | Ca_26763                            | --                    | --   |
| scaffold1309_P4_58539  | scaffold1309                            | 58539                         | A/ACCAT                                                       | CAGCTTGTCGTCGGT<br>AAAT   | TTGGAAGGAGCCCTTA<br>CCTT | 60.1                             | 875                                           | DRR                                               | Ca_26763                            | --                    | --   |
| scaffold1316_P4_13036  | scaffold1316                            | 13036                         | AATTTATTTATTTATTTATTT/AA<br>TTTATTTATTTATTTATTTATTT           | ACATGCACAGAGAATG<br>CCAA  | GTGCCAGTCGATTGCC<br>TAAT | 60.3                             | 631                                           | DRR                                               | Ca_28021                            | --                    | --   |
| scaffold1324_P4_279339 | scaffold1324                            | 279339                        | ATTTT/ATTT                                                    | CATCATGAATTCGACC<br>ATGC  | ATAGTTGCACCACTTTG<br>GGC | 59.9                             | 722                                           | DRR                                               | Ca_19767                            | --                    | BES1 |
| scaffold1324_P4_49560  | scaffold1324                            | 49560                         | AT/ATT                                                        | ATTTTTCGGTTTGAA<br>GCAA   | CGATCAAGATTCGTTTC<br>CTG | 59.6                             | 602                                           | DRR                                               | Ca_19753                            | P                     | --   |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                       |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| scaffold1324_P4_49921 | scaffold1324                            | 49921                         | AAAGAGAA/AAA                                                  | GATCGATGCCAGTTGT<br>TTATGA | GCAACCTCAACTGGGT<br>GAAT   | 60.0                             | 468                                           | DRR                                               | Ca_19753                            | P                     | --       |
| scaffold1331_P4_31763 | scaffold1331                            | 31763                         | ATTTTTTT/ATTTTTTTT                                            | TTGTCACAAAGCGGTC<br>TCAC   | GTGACCCTTGCCTCAA<br>CACT   | 59.9                             | 149                                           | DRR                                               | Ca_26940                            | --                    | --       |
| scaffold1335_P4_45191 | scaffold1335                            | 45191                         | AAGCTAGCTA/AAGCTA                                             | TGAAGAGTTGCACGAG<br>ATGG   | ATGCCTCATTTCCCAAC<br>AAG   | 60.0                             | 198                                           | DRR                                               | Ca_28106                            | S                     | --       |
| scaffold1335_P4_46035 | scaffold1335                            | 46035                         | G/GC                                                          | TTGACCTCCTAGCATT<br>GGCT   | GGTTAAAGTGGGGT<br>CGTT     | 59.8                             | 411                                           | DRR                                               | Ca_28106                            | S                     | --       |
| scaffold1335_P4_46272 | scaffold1335                            | 46272                         | TC/T                                                          | TTCGTGCAACTGACGC<br>TAAC   | CCATTTGGATTAAAAAG<br>AAGCC | 60.1                             | 345                                           | DRR                                               | Ca_28106                            | S                     | --       |
| scaffold1359_P4_74272 | scaffold1359                            | 74272                         | T/TC                                                          | CCAATTTGAATTGTCC<br>GTCC   | TTAAAGAGATTCGCTG<br>CGGT   | 60.2                             | 663                                           | DRR                                               | Ca_26683                            | KR                    | G2-like  |
| scaffold1359_P4_74591 | scaffold1359                            | 74591                         | ATTTTTTTT/ATTTTTTTTTT                                         | TGGGTGGGAGTAATTT<br>TTCG   | TTAAAGAGATTCGCTG<br>CGGT   | 59.8                             | 297                                           | DRR                                               | Ca_26683                            | KR                    | G2-like  |
| scaffold1365_P4_4805  | scaffold1365                            | 4805                          | GTTTTTTTT/GTTTTTTTTT                                          | TGCATTTTACAGCGTTT<br>TCG   | TGGTGGATGAAAATGA<br>CCAA   | 59.9                             | 367                                           | DRR                                               | Ca_27716                            | --                    | Trihelix |
| scaffold1418_P4_31681 | scaffold1418                            | 31681                         | G/GT                                                          | GTCGCAATTTTGTCC<br>CCTA    | TTTCTTCCGATTGGT<br>TCITT   | 59.9                             | 733                                           | DRR                                               | Ca_25262                            | S                     | --       |
| scaffold1418_P4_33272 | scaffold1418                            | 33272                         | TAAAAAAA/TAAAAAA                                              | TCTTTGTGATTGTGTC<br>AGGT   | CCAAATGCAAAATTTAA<br>CATGG | 59.4                             | 798                                           | DRR                                               | Ca_25262                            | S                     | --       |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                            | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                        |                                         |                               |                                                                                          |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| scaffold1419_P4_17488  | scaffold1419                            | 17488                         | A/ATATATAT                                                                               | TGAATGAAATCGATTG<br>GCTG | TAAACACATGCGCTTC<br>CAAA | 59.6                             | 570                                           | DRR                                               | Ca_26980                            | --                    | --          |
| scaffold1448_P4_99427  | scaffold1448                            | 99427                         | GAATTTAATATAAATTAATTTAATAT<br>AAATT/GAATTTAATATAAAATTAATTT<br>AATATAAATTAATTTAATATAAAATT | CCAGGAAATGACCCCC<br>TATT | TTTATTTTAGCGCGGT<br>GTCC | 60.0                             | 774                                           | DRR                                               | Ca_26688                            | --                    | --          |
| scaffold1455_P4_19091  | scaffold1455                            | 19091                         | CG/C                                                                                     | TATTGGGTGCACCGTT<br>TACA | TTAGGTGGTACGGAAA<br>TCGC | 59.8                             | 438                                           | DRR                                               | Ca_27725                            | --                    | --          |
| scaffold1467_P4_11911  | scaffold1467                            | 11911                         | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATAT<br>TAT                           | TCGCAGCTGTGATGCT<br>AAGT | ATGGGAGGTCTTGTGC<br>AGTT | 59.8                             | 359                                           | DRR                                               | Ca_26807                            | Q                     | GeBP        |
| scaffold1483_P4_54945  | scaffold1483                            | 54945                         | CTTTT/CTTTT                                                                              | GCCAGTTCAATCATTC<br>CCAT | GCAAAAAGGGCAAAAG<br>AGAG | 59.8                             | 142                                           | DRR                                               | Ca_26255                            | R                     | MIKC        |
| scaffold1504_P4_227426 | scaffold1504                            | 227426                        | TA/TAA                                                                                   | ATGCAGGGTTGGTAGA<br>TGCT | GGTTTGATATATGGCC<br>GGTG | 59.6                             | 571                                           | DRR                                               | Ca_24095                            | O                     | MYB_related |
| scaffold1504_P4_314477 | scaffold1504                            | 314477                        | GAGCATCAA/GAGCATCAAAGCATC<br>AA                                                          | GGAGGGTCAGAGGAT<br>GTGAA | TCTGGGAGATGGAGTT<br>GTCC | 60.0                             | 615                                           | DRR                                               | Ca_24100                            | --                    | Dof         |
| scaffold1504_P4_391760 | scaffold1504                            | 391760                        | CTATATATATATATA/CTATATATA<br>TATATATATATATATA                                            | ATCTGAGGACTCTCCA<br>GGCA | CCCCTTTGTCAGTTAA<br>GGCA | 59.9                             | 488                                           | DRR                                               | Ca_24103                            | --                    | --          |
| scaffold151_P4_111639  | scaffold151                             | 111639                        | CTTTTTTTTT/CTTTTTTTTTT                                                                   | TTCAAATTTTGTGGG<br>GGA   | TTCATCCATTCTGGTTG<br>CAC | 60.1                             | 654                                           | DRR                                               | Ca_25625                            | --                    | --          |
| scaffold1511_P4_116957 | scaffold1511                            | 116957                        | TAAAAA/TAAAAA                                                                            | AATTTGCATTGTCGACA<br>CCA | TCCAAGAACTGCACA<br>TCCA  | 60.0                             | 159                                           | DRR                                               | Ca_25145                            | --                    | --          |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                        |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| scaffold1511_P4_127158 | scaffold1511                            | 127158                        | TAAAAA/TAAAAA                                                 | AAGACCGATGACCCTT<br>CCTT | TTAGTCGGTCGATAAA<br>GCCG   | 59.9                             | 546                                           | DRR                                               | Ca_25146                            | --                    | --       |
| scaffold1511_P4_191187 | scaffold1511                            | 191187                        | CTATAT/CTATATAT                                               | AACAAAGCGCTGCAAT<br>AGGT | AGCGCTGTAAAAGGTG<br>CATT   | 59.9                             | 126                                           | DRR                                               | Ca_25148                            | --                    | Trihelix |
| scaffold1511_P4_191407 | scaffold1511                            | 191407                        | ATTTTTTTT/ATTTTTTTT                                           | TGTTTGCACCTTTTACA<br>GCG | GCGGTAGTGTCTTGCC<br>TTTC   | 59.9                             | 525                                           | DRR                                               | Ca_25148                            | --                    | Trihelix |
| scaffold1521_P4_10780  | scaffold1521                            | 10780                         | CA/CATCGA                                                     | TCATGTGAACAATGCA<br>ACCA | CCACAGCTTGTCTGTC<br>GGTA   | 59.5                             | 296                                           | DRR                                               | Ca_26977                            | --                    | bHLH     |
| scaffold1521_P4_19920  | scaffold1521                            | 19920                         | CT/CGTATTTCTGTAT                                              | AGTTTCATTTTTGCCCG<br>TTG | TTCCAACCGTGTGATTT<br>TGA   | 60.0                             | 464                                           | DRR                                               | Ca_26979                            | --                    | bHLH     |
| scaffold1521_P4_21280  | scaffold1521                            | 21280                         | A/ACTTAAGGT                                                   | TTGAACCCGAAATTTTC<br>CAC | TACGAGGGACGATGTT<br>GTGA   | 59.8                             | 264                                           | DRR                                               | Ca_26979                            | --                    | bHLH     |
| scaffold153_P4_28056   | scaffold153                             | 28056                         | GAAA/GAA                                                      | AATGGCCACGAATCTG<br>AAAG | TGTTTGAAATATGACGC<br>GGA   | 60.1                             | 518                                           | DRR                                               | Ca_27484                            | --                    | --       |
| scaffold1545_P4_16569  | scaffold1545                            | 16569                         | TAAAAA/TAAAAAA                                                | CCTGTTGTGGAGGTCA<br>TGTC | CAGCGATCCCAGAGTT<br>CAAT   | 60.0                             | 789                                           | DRR                                               | Ca_23852                            | --                    | --       |
| scaffold1548_P4_24822  | scaffold1548                            | 24822                         | CAAAAAA/CAAAAAA                                               | GAGCATGCCAGTTCTT<br>AGGC | GGAGAGAATTAAGGGG<br>CAGG   | 60.0                             | 620                                           | DRR                                               | Ca_27707                            | --                    | --       |
| scaffold157_P4_11932   | scaffold157                             | 11932                         | AATATATATATATATATATA/AATA<br>TATATATATATATATATA               | TTCTTGTGCATCTTCGT<br>TGG | CAAAATTTTCAAAACAA<br>ACCCA | 59.8                             | 576                                           | DRR                                               | Ca_21061                            | R                     | Trihelix |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                              |                            |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold157_P4_307810  | scaffold157                             | 307810                        | ACAA/ACAAACAGACTCAA                                                          | CTTTTACAGCGCTCGA<br>TTCC   | TTGAAACCGGTCCTTG<br>GTTA     | 60.0                             | 538                                           | DRR                                               | Ca_21076                            | --                    | --  |
| scaffold157_P4_358753  | scaffold157                             | 358753                        | ATTTTT/ATTTT                                                                 | ATTTAGATCGGCGGTT<br>GAGA   | AACGTAGCTTTTGTGC<br>GCTA     | 59.7                             | 216                                           | DRR                                               | Ca_21079                            | --                    | SBP |
| scaffold157_P4_359689  | scaffold157                             | 359689                        | CTATCTACATA/CTATCTACATATAT<br>CTACATA                                        | AACAAATCAAACAGGC<br>CAGG   | TCTTGTTTTCTGTATG<br>TGCCCC   | 60.0                             | 620                                           | DRR                                               | Ca_21079                            | --                    | SBP |
| scaffold157_P4_360030  | scaffold157                             | 360030                        | AATATATATATA/AATATATATA                                                      | GATTTTCCCTCCACCAT<br>CAA   | TCAATCACATATATTTC<br>TCCCGT  | 59.7                             | 502                                           | DRR                                               | Ca_21079                            | --                    | SBP |
| scaffold157_P4_360093  | scaffold157                             | 360093                        | CAT/CATAT                                                                    | TTTCACGACATTCTCTA<br>TGCCT | AGTGACAAAAATGTATC<br>TCAATCG | 58.9                             | 766                                           | DRR                                               | Ca_21079                            | --                    | SBP |
| scaffold1614_P4_191446 | scaffold1614                            | 191446                        | CAAAAAAAAAAAAA/CAAAAAAAAAAAAA<br>AAAAA                                       | AGGCTTGGAGAGTGGC<br>TACA   | GCGCTGTAAATGTGC<br>AAAA      | 60.0                             | 588                                           | DRR                                               | Ca_27067                            | --                    | --  |
| scaffold1632_P4_26463  | scaffold1632                            | 26463                         | AAGTAG/AAG                                                                   | ACGTTTGTGTCGAC<br>GGTT     | ATCCAATCCACTTCTTT<br>CCG     | 60.5                             | 554                                           | DRR                                               | Ca_26993                            | --                    | --  |
| scaffold1632_P4_4760   | scaffold1632                            | 4760                          | TTATATATATATATATATATA/TTATA<br>TATATATATATATATATATATA                        | TTTTGGGTGGGATTTT<br>ACGA   | ACCAATGCATGGTGTT<br>GAAA     | 60.2                             | 465                                           | DRR                                               | Ca_26992                            | --                    | --  |
| scaffold1633_P4_15743  | scaffold1633                            | 15743                         | AAATAATAATAATAATAATAATA<br>ATAATAAT/AAATAATAATAATAATA<br>TAATAATAATAATAATAAT | AACGTTTTCGTCGAAT<br>GTCC   | TCAATTTGGATGCACC<br>TGA      | 60.0                             | 669                                           | DRR                                               | Ca_26202                            | UR                    | --  |
| scaffold1659_P4_155048 | scaffold1659                            | 155048                        | TAAAAAAAAA/TAAAAAAAAA                                                        | CGATTCTTTTGAATG<br>GTTTG   | CGCGTAAATGTGAGAT<br>TTTGAA   | 59.6                             | 620                                           | DRR                                               | Ca_24192                            | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1708_P4_68435  | scaffold1708                            | 68435                         | TCC/TCCC                                                      | GAAAAAGCGCTGTAAATGGC    | CATTGAGACGTGAGCAAAA     | 59.9                             | 510                                           | DRR                                               | Ca_27642                            | --                    | --  |
| scaffold1731_P4_49034  | scaffold1731                            | 49034                         | CATATATATATATATATATA/CATATATATATATATA                         | ATGGGAAGCAACAACGATTC    | CCGTACCGTTTCTGGGATAA    | 59.9                             | 784                                           | DRR                                               | Ca_27041                            | IR                    | --  |
| scaffold1731_P4_85329  | scaffold1731                            | 85329                         | CATATATATATATATATATA/CATATATATATATATATA                       | TCTCCGCATAAGCTTTCGAT    | GCTTCGACACTGTAGCACCTC   | 59.9                             | 478                                           | DRR                                               | Ca_27043                            | --                    | --  |
| scaffold1731_P4_86422  | scaffold1731                            | 86422                         | AATATATATATATATATATAT/AATATATATATATATATAT                     | TTTTGGGAATTCCTGCTCTG    | GTGACACCCTAAACCCCAAA    | 60.2                             | 299                                           | DRR                                               | Ca_27043                            | --                    | --  |
| scaffold1755_P4_125108 | scaffold1755                            | 125108                        | TATTACATTATTAA/TATTACATTATAATTACATTATTAA                      | TTTCCCAATCGATTTGCTTC    | GTGAGGACCAGCCCCACTTTA   | 60.0                             | 740                                           | DRR                                               | Ca_27387                            | --                    | --  |
| scaffold1771_P4_119568 | scaffold1771                            | 119568                        | A/AAAAATGATGAAAG                                              | TGTCATCAGCCAAGCAACTC    | CATCGACACATCACCAACACA   | 60.0                             | 657                                           | DRR                                               | Ca_27324                            | Q                     | --  |
| scaffold1804_P4_191033 | scaffold1804                            | 191033                        | GA/GACA                                                       | TTGGCAACACTTGGGTACATA   | TCTCCGTAAAGGATTCAACCG   | 60.0                             | 806                                           | DRR                                               | Ca_25513                            | --                    | --  |
| scaffold1844_P4_166750 | scaffold1844                            | 166750                        | TTTATTATTATTATTATTA/TTTATTATTATTATTA                          | GGCTAGACGAGTTTCGACGAC   | CTAGATGGTCGCATTCGGG     | 60.0                             | 418                                           | DRR                                               | Ca_24145                            | --                    | --  |
| scaffold1844_P4_167253 | scaffold1844                            | 167253                        | CAAAAA/CAAAA                                                  | CCCCAATTTGCGATCAATAA    | TCAAACTAAGAACTCGCCAA    | 60.6                             | 694                                           | DRR                                               | Ca_24145                            | --                    | --  |
| scaffold1867_P4_211346 | scaffold1867                            | 211346                        | TTTATTATTATTATTATTATTATTATT/TTTATTATTATTATTATTATTATTATTATT    | GCCATTGATTCATTTCCATTGA  | TGCTTTTGAAGCATTTGCAG    | 59.9                             | 503                                           | DRR                                               | Ca_25353                            | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                        |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| scaffold1928_P4_78124  | scaffold1928                            | 78124                         | ATT/ATTT                                                      | GCATCAAGCTGTCGTT<br>TGAA  | CCCCCTTTTGCATAAG<br>TGA   | 60.0                             | 663                                           | DRR                                               | Ca_26945                            | --                    | --      |
| scaffold1943_P4_180228 | scaffold1943                            | 180228                        | TAAAAAAAA/TAAAAAAAAA                                          | CCACAAGAAGACAAAG<br>GGGA  | TGGGGTATGTGAACGA<br>GACA  | 60.1                             | 599                                           | DRR                                               | Ca_21921                            | --                    | --      |
| scaffold1943_P4_281573 | scaffold1943                            | 281573                        | ATTTTT/ATTT                                                   | TGGGTTGGGATGACAT<br>TAAAA | CCAACCCAAATAAACCA<br>AACA | 60.0                             | 824                                           | DRR                                               | Ca_21930                            | --                    | M-type  |
| scaffold1943_P4_282409 | scaffold1943                            | 282409                        | CATATA/CATATATATA                                             | TTGGTTTATTTGGGTT<br>GGGA  | AGCGATGCATGTCTCA<br>AGTG  | 60.0                             | 912                                           | DRR                                               | Ca_21930                            | --                    | M-type  |
| scaffold1959_P4_47247  | scaffold1959                            | 47247                         | GC/GCC                                                        | TCCTCCTCAAGTTGGA<br>GCAT  | ATATTGCATTGCAGTG<br>GTGG  | 59.8                             | 458                                           | DRR                                               | Ca_26462                            | K                     | G2-like |
| scaffold1964_P4_11011  | scaffold1964                            | 11011                         | A/ACTC                                                        | ATGTTCTCGCCAATC<br>ATTC   | TTCCAAAAGAGGAATG<br>GTGC  | 59.9                             | 771                                           | DRR                                               | Ca_25209                            | G                     | --      |
| scaffold198_P4_267630  | scaffold198                             | 267630                        | A/AG                                                          | TCCTAGAACATGCATC<br>ACGC  | AGCCACATTCCAAGCA<br>AAAC  | 59.8                             | 473                                           | DRR                                               | Ca_20909                            | --                    | --      |
| scaffold198_P4_632725  | scaffold198                             | 632725                        | TAAAAAAAA/TAAAAAAAA                                           | TTTTGCTGTTGTGTGC<br>ACTG  | GCTGTAAACTGCACCC<br>CATT  | 59.5                             | 364                                           | DRR                                               | Ca_20924                            | --                    | --      |
| scaffold198_P4_632887  | scaffold198                             | 632887                        | A/AAAATGTACAAC                                                | TTTTGCTGTTGTGTGC<br>ACTG  | GCTGTAAACTGCACCC<br>CATT  | 59.5                             | 364                                           | DRR                                               | Ca_20924                            | --                    | --      |
| scaffold1981_P4_149526 | scaffold1981                            | 149526                        | ATTTTTTTT/ATTTTTTTTT                                          | CTCAAATTTTGTGGG<br>GGA    | TGTGAGTACGGATAAG<br>GGGG  | 59.8                             | 443                                           | DRR                                               | Ca_21257                            | C                     | --      |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')  | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|--------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                        |                                         |                               |                                                                  |                          |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| scaffold1981_P4_23471  | scaffold1981                            | 23471                         | GATATATATATATATATATATAT/GAT<br>ATATATATATATATATATATATATAT<br>TAT | CTCTCAAGGCCCAAAG<br>CATA | GATTCTCACCTCGCT<br>TTTG       | 60.3                             | 512                                           | DRR                                               | Ca_21250                            | --                    | --   |
| scaffold1981_P4_317439 | scaffold1981                            | 317439                        | TAAA/TAAAA                                                       | TCTCATTGTCTCCGA<br>CTCT  | TTGTCTCAACAATCTCC<br>CCC      | 60.0                             | 501                                           | DRR                                               | Ca_21265                            | --                    | --   |
| scaffold1981_P4_341254 | scaffold1981                            | 341254                        | TGGG/TGG                                                         | ATGCATCATTGTGG<br>GGAT   | GCACCATTAGCCAACC<br>TGAT      | 60.0                             | 644                                           | DRR                                               | Ca_21267                            | R                     | bHLH |
| scaffold1997_P4_15458  | scaffold1997                            | 15458                         | AAAAATAGACAT/AAAAATAGACATT<br>TAAAATAGACAT                       | CCTATACCGACGGGT<br>TTTT  | TTGAAGACGGAATATT<br>GGCA      | 60.1                             | 531                                           | DRR                                               | Ca_27157                            | --                    | --   |
| scaffold2005_P4_14836  | scaffold2005                            | 14836                         | CAGAA/CA                                                         | AAATCCAACAATCTCC<br>CCC  | CGGTCTCAACCTCTCC<br>CATA      | 60.0                             | 515                                           | DRR                                               | Ca_28003                            | --                    | --   |
| scaffold2010_P4_3634   | scaffold2010                            | 3634                          | AT/ATT                                                           | AATCGATTGATTCAGC<br>CCAG | TGATTCCAACGGTCAT<br>CAA       | 60.0                             | 869                                           | DRR                                               | Ca_27976                            | --                    | --   |
| scaffold2033_P4_183883 | scaffold2033                            | 183883                        | CGAAGAAGAAG/CGAAGAAGAAGAA<br>G                                   | CTTGGGGTGGCAAGTA<br>CAGT | TCGAATACATGAATTAA<br>CAAAAGGA | 60.0                             | 371                                           | DRR                                               | Ca_26143                            | --                    | bHLH |
| scaffold2040_P4_180917 | scaffold2040                            | 180917                        | TGTTCAGTTCAGTTCAGTTCAG/TAT<br>TCAGTTCAGTTCAGTTCAGTTCAG           | TTGGTTTATTTGGGT<br>GGGA  | ACCAGGAAAAGAAGAA<br>GGGC      | 60.0                             | 514                                           | DRR                                               | Ca_26621                            | O                     | --   |
| scaffold205_P4_40671   | scaffold205                             | 40671                         | AT/ATT                                                           | CTACTCTCAATTTCCG<br>CCG  | GCACAATCAGAAGCGC<br>ATTA      | 59.8                             | 761                                           | DRR                                               | Ca_25491                            | --                    | --   |
| scaffold207_P4_9636    | scaffold207                             | 9636                          | T/TAGGAAA                                                        | TGCCTTAAGTACAAA<br>GGGG  | GTGCCAGTCGATTGCC<br>TAAT      | 60.1                             | 491                                           | DRR                                               | Ca_28033                            | --                    | --   |



| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2155_P4_39661  | scaffold2155                            | 39661                         | GAAAA/GTAAAAAAA                                               | CCCCCTTTTGCATAA<br>GTGA   | CCCTGCTACTCCTGCT<br>TTTG | 59.9                             | 826                                           | DRR                                               | Ca_27850                            | --                    | --  |
| scaffold224_P4_186416  | scaffold224                             | 186416                        | A/AGGGTTG                                                     | TGAAGTGTTCGAATTG<br>CAGC  | TTGCGTTGAAAGACTC<br>GATG | 60.0                             | 462                                           | DRR                                               | Ca_26345                            | --                    | --  |
| scaffold224_P4_186566  | scaffold224                             | 186566                        | GTTTT/GTTTTT                                                  | TGAAGTGTTCGAATTG<br>CAGC  | TTGCGTTGAAAGACTC<br>GATG | 60.0                             | 462                                           | DRR                                               | Ca_26345                            | --                    | --  |
| scaffold224_P4_95002   | scaffold224                             | 95002                         | ATTT/ATTTT                                                    | CTTCACCTCCACCAG<br>ATGT   | AAAAGTTGCTCCCCG<br>TAAT  | 60.0                             | 365                                           | DRR                                               | Ca_26341                            | --                    | --  |
| scaffold227_P4_144419  | scaffold227                             | 144419                        | C/CAG                                                         | CCTCAAAC TTCCATGG<br>CCTA | CAACTGGAATTTTCGG<br>GAGA | 60.1                             | 641                                           | DRR                                               | Ca_25191                            | --                    | --  |
| scaffold2348_P4_176388 | scaffold2348                            | 176388                        | TTTTATTTATTTATTT/TTTTATTTATT<br>TATTTATTT                     | GGGAGGAAGTCTGTGC<br>TGAG  | CAACATGTTTGAGTC<br>CACC  | 60.0                             | 564                                           | DRR                                               | Ca_25471                            | --                    | --  |
| scaffold2356_P4_144020 | scaffold2356                            | 144020                        | CAAAAAAAAA/CAAAAAAAAA                                         | GGATAACAGCGATGGG<br>AAGA  | ATCCCTCATTGCAATC<br>CAC  | 60.0                             | 590                                           | DRR                                               | Ca_24345                            | A                     | --  |
| scaffold2368_P4_25942  | scaffold2368                            | 25942                         | CGTG/CGTGTG                                                   | TTGTTTGCATCCATGG<br>GTAA  | AAATCCACGTCATCCC<br>AAAA | 59.8                             | 593                                           | DRR                                               | Ca_26718                            | --                    | --  |
| scaffold2368_P4_53512  | scaffold2368                            | 53512                         | TGGG/TGGGG                                                    | AACCTGGAGATGGGA<br>AAGT   | CTAGCCATTAGCTTCG<br>ACCG | 59.8                             | 607                                           | DRR                                               | Ca_26720                            | P                     | --  |
| scaffold2368_P4_54204  | scaffold2368                            | 54204                         | GTT/GTTT                                                      | CATCGGTCAAACACCA<br>TCTG  | GCTTTGCAGAACATGC<br>GTAA | 60.0                             | 490                                           | DRR                                               | Ca_26720                            | P                     | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                              | Forward primers (5'-3')    | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------|----------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                        |                                         |                               |                                                                                            |                            |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| scaffold2371_P4_308163 | scaffold2371                            | 308163                        | CTTATTATTATTATTATTATTCTT<br>ATTATTATTATTA/CTTATTATTATTA<br>TTATTATTATTCTTATTATTATTA<br>TTA | GGCTAGACGAGTTCGA<br>CGAC   | AATAGATGGTCGCATC<br>CTGG        | 60.0                             | 345                                           | DRR                                               | Ca_23997                            | --                    | --     |
| scaffold2388_P4_19728  | scaffold2388                            | 19728                         | AATTATTATTATTATTATTATTAT<br>TATTATTATTATTAT/AATTATTATTA<br>TTATTATTATTATTATTATTAT          | ACAGCATGGCGAGAAC<br>TTTT   | CCTACCGATTGCACCA<br>AGTT        | 59.9                             | 284                                           | DRR                                               | Ca_27844                            | O                     | SRS    |
| scaffold2392_P4_354336 | scaffold2392                            | 354336                        | AAACAA/AAA                                                                                 | TGTTGCGTTTTCTATTCT<br>TTCA | TACCAAAATATCCCAGG<br>CCAA       | 59.3                             | 859                                           | DRR                                               | Ca_25138                            | KL                    | --     |
| scaffold240_P4_148270  | scaffold240                             | 148270                        | G/GTAGTAGTAGTA                                                                             | TGTGAGGCATGTCAA<br>AAGG    | CGGCTGTGTTTTCTG<br>TGTC         | 59.7                             | 822                                           | DRR                                               | Ca_25660                            | --                    | --     |
| scaffold240_P4_148297  | scaffold240                             | 148297                        | TAG/TAGAG                                                                                  | TGTGAGGCATGTCAA<br>AAGG    | CGGCTGTGTTTTCTG<br>TGTC         | 59.7                             | 822                                           | DRR                                               | Ca_25660                            | --                    | --     |
| scaffold242_P4_692807  | scaffold242                             | 692807                        | GAAA/GAAAA                                                                                 | TTGTCTTGCTTGCATC<br>CTTG   | TGTGTAAAGATTGGCG<br>GTTG        | 60.0                             | 399                                           | DRR                                               | Ca_22275                            | F                     | --     |
| scaffold242_P4_706018  | scaffold242                             | 706018                        | TCTACT/TCT                                                                                 | TGCCGGTTTTACTTGT<br>TTCTG  | GTGCACCACCTCAAAA<br>ACCT        | 60.2                             | 753                                           | DRR                                               | Ca_22276                            | T                     | M-type |
| scaffold2617_P4_234200 | scaffold2617                            | 234200                        | AATATATATATATATATATATAT<br>/AATATATATATATATATATATATA<br>TATAT                              | TTTGGGAAACTGAACC<br>AACA   | AAAATTGAAATTATCAA<br>GAAAGTTGTG | 59.0                             | 322                                           | DRR                                               | Ca_21877                            | --                    | --     |
| scaffold2617_P4_320997 | scaffold2617                            | 320997                        | TAAAA/TAAA                                                                                 | TGGGGTATTCTTTAC<br>GTCTT   | TGAAAGAGGGGAAAA<br>GAGC         | 57.6                             | 296                                           | DRR                                               | Ca_21883                            | --                    | WRKY   |
| scaffold2617_P4_321441 | scaffold2617                            | 321441                        | ATTTTTTT/ATTTTTTTTT                                                                        | TGCTCCTTTTCCCTCT<br>TTC    | TTATGTGCGCATGACC<br>AATC        | 60.7                             | 542                                           | DRR                                               | Ca_21883                            | --                    | WRKY   |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                        |                                         |                               |                                                                                           |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| scaffold2617_P4_321825 | scaffold2617                            | 321825                        | TAAAAA/TAAAAA                                                                             | TTGGTCATGCGCACAT<br>AATA | GATGGCTGTGTCGGAG<br>ACTT | 58.6                             | 529                                           | DRR                                               | Ca_21883                            | --                    | WRKY     |
| scaffold271_P4_205973  | scaffold271                             | 205973                        | GAA/GA                                                                                    | GCACCGTGAGTAAATT<br>CGGT | TATTTTGGATTTTGGCT<br>CGG | 60.0                             | 692                                           | DRR                                               | Ca_25334                            | --                    | --       |
| scaffold273_P4_190574  | scaffold273                             | 190574                        | CAAAAAAAAA/CAAAAAAAAA                                                                     | GAAGAAGGTCCCAAGG<br>GTTT | CGCTTCTTCCCTTCTC<br>TTT  | 59.9                             | 757                                           | DRR                                               | Ca_26226                            | --                    | --       |
| scaffold275_P4_687972  | scaffold275                             | 687972                        | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTAT/TTTATTATT<br>ATTATTATTATTATTATTATTATT<br>AT | TCCCTTTGTCTTCTTG<br>TGG  | TTGAAGCCGAGAAAAC<br>GACT | 60.1                             | 778                                           | DRR                                               | Ca_23469                            | R                     | --       |
| scaffold2763_P4_57690  | scaffold2763                            | 57690                         | CTATATATATATATATAT/CTATAT<br>ATATATATATATATAT                                             | ATTTAACTGGGCCAA<br>AGCC  | TGTTTCCTCAAATTGA<br>ATGC | 60.3                             | 668                                           | DRR                                               | Ca_24398                            | --                    | bHLH     |
| scaffold2763_P4_81370  | scaffold2763                            | 81370                         | T/TG                                                                                      | AACCAACTGGTCCTGA<br>CTGG | GAATGGAGAAGGTCGT<br>GCAT | 60.0                             | 536                                           | DRR                                               | Ca_24399                            | --                    | --       |
| scaffold277_P4_204924  | scaffold277                             | 204924                        | AAATTTTCTTAATTTTCT/AAATTTTC<br>T                                                          | ATTCGCCGTCACTTTC<br>AAAT | TCCACTCCCACACCTA<br>AACC | 59.6                             | 609                                           | DRR                                               | Ca_25752                            | --                    | --       |
| scaffold277_P4_205504  | scaffold277                             | 205504                        | T/TGATATATATATA                                                                           | GGTTTAGGTGTGGGAG<br>TGGA | TGATACAAGGTTCAAC<br>CGCA | 59.8                             | 444                                           | DRR                                               | Ca_25752                            | --                    | --       |
| scaffold2780_P4_1451   | scaffold2780                            | 1451                          | GTTTTTTTT/GTTTTT                                                                          | GGGGGAGAAATTTGG<br>TGTT  | TTGATCTTGCTGCATTG<br>TCC | 60.0                             | 233                                           | DRR                                               | Ca_27853                            | --                    | --       |
| scaffold2871_P4_4009   | scaffold2871                            | 4009                          | ATT/AT                                                                                    | AGCTTGGGGCCAAGTC<br>TATT | ACACCAATTTGCGATT<br>GACA | 60.1                             | 404                                           | DRR                                               | Ca_27744                            | --                    | HB-other |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                       |                                         |                               |                                                               |                           |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| scaffold290_P4_298253 | scaffold290                             | 298253                        | GAAAAA/GAAAAA                                                 | CACCGTGTTCCTTGATT<br>GGA  | GGCATCCGAGGATACG<br>ACTA       | 59.5                             | 705                                           | DRR                                               | Ca_19835                            | R                     | C2H2     |
| scaffold290_P4_299066 | scaffold290                             | 299066                        | TAAAAAAAAAAAAAAAAA/TAAAAAAAAA<br>AA                           | GTAGGACGGAAATGCG<br>AGAC  | TGTGCATTGATTTGATG<br>ACATT     | 59.7                             | 608                                           | DRR                                               | Ca_19835                            | R                     | C2H2     |
| scaffold290_P4_451319 | scaffold290                             | 451319                        | GTTTTTTTTTTT/GTTTTTTTTTTT                                     | GCAAGCTTACGCGGTA<br>TTGT  | TCAAATTGATGGAACCC<br>TTCG      | 60.3                             | 583                                           | DRR                                               | Ca_19837                            | S                     | --       |
| scaffold290_P4_662838 | scaffold290                             | 662838                        | CTTTTTTTTTTT/CTTTTTTTTTTT                                     | AGGACCTAAGCAACAC<br>CCCT  | TGTCGAATTGGGCAAT<br>AACA       | 60.0                             | 232                                           | DRR                                               | Ca_19844                            | --                    | --       |
| scaffold296_P4_261904 | scaffold296                             | 261904                        | CAAAAA/CAAAA                                                  | CCATACACATGAGAGT<br>TGCGA | TTGACTCAGCCTTAAAT<br>TTTTATTGA | 59.7                             | 534                                           | DRR                                               | Ca_20542                            | --                    | --       |
| scaffold296_P4_262823 | scaffold296                             | 262823                        | ATATTATTATTATTATTATTA/ATATT<br>ATTATTATTATTA                  | CACTTTTAAACCGGAG<br>GAATG | GCAGTGGATAAGGCCG<br>ATAA       | 58.6                             | 140                                           | DRR                                               | Ca_20542                            | --                    | --       |
| scaffold296_P4_422245 | scaffold296                             | 422245                        | CTTTTTTTTTTT/CTTTTTTTTTTT                                     | GACAAAGGCAGGCAAG<br>AAAG  | TCGGGAAACAGGAAAC<br>AAAC       | 60.0                             | 591                                           | DRR                                               | Ca_20548                            | --                    | --       |
| scaffold3015_P4_69170 | scaffold3015                            | 69170                         | AG/A                                                          | GGCCCATAAATGCTCAA<br>GTGT | TCATAGGCATGGGATT<br>TGAA       | 60.0                             | 472                                           | DRR                                               | Ca_27318                            | --                    | --       |
| scaffold3019_P4_17640 | scaffold3019                            | 17640                         | GTTTT/GTTTTT                                                  | TGCATTATGGGTAGGT<br>GCAA  | GATGTCTACCAGTTGC<br>GGGT       | 60.0                             | 570                                           | DRR                                               | Ca_28069                            | --                    | --       |
| scaffold303_P4_162542 | scaffold303                             | 162542                        | AAGCGCTGT/AAGCGCTGTGGAAAC<br>GAGCGCTGT                        | GCCATTTACAGCGCTT<br>TTTC  | TGAAATTATGGGTGGG<br>CATT       | 59.9                             | 357                                           | DRR                                               | Ca_26661                            | --                    | Trihelix |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                       |                                         |                               |                                                               |                          |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| scaffold306_P4_13557  | scaffold306                             | 13557                         | TTATTACTATTA/TTATTACTATTACT<br>ATTA                           | TCCACGGAATTCAAAT<br>CTCA | TGATTTTATGATGATGG<br>ATAATTTTGA | 59.0                             | 280                                           | DRR                                               | Ca_22704                            | A                     | --      |
| scaffold306_P4_186956 | scaffold306                             | 186956                        | CTTTTTTTTTTT/CTTTTTTTTTTT                                     | CAACGCTCCATAACCA<br>GCTT | AATCCCATGCATCCATC<br>ATC        | 60.3                             | 674                                           | DRR                                               | Ca_22713                            | --                    | --      |
| scaffold311_P4_131360 | scaffold311                             | 131360                        | A/ACAT                                                        | GAAGCTCAGATGGCAC<br>ACAA | CAATCTCCCCCTTGAG<br>TTGA        | 60.0                             | 716                                           | DRR                                               | Ca_26332                            | --                    | --      |
| scaffold3134_P4_12154 | scaffold3134                            | 12154                         | ACATC/A                                                       | TAAACGAGGTAAACCG<br>GTGC | GAAAGTCGCATGTGCA<br>ACAC        | 60.0                             | 437                                           | DRR                                               | Ca_27104                            | O                     | C2H2    |
| scaffold3134_P4_12226 | scaffold3134                            | 12226                         | TTTTTTT/TTTTTTTGTTTTT                                         | TAAACGAGGTAAACCG<br>GTGC | GAAAGTCGCATGTGCA<br>ACAC        | 60.0                             | 437                                           | DRR                                               | Ca_27104                            | O                     | C2H2    |
| scaffold3134_P4_12915 | scaffold3134                            | 12915                         | CAA/CAAA                                                      | TGACCGAATTCGCTT<br>ATTC  | CCAAACATTTTTCACCT<br>GGC        | 60.0                             | 523                                           | DRR                                               | Ca_27104                            | O                     | C2H2    |
| scaffold3134_P4_13444 | scaffold3134                            | 13444                         | TA/TATTAACAAA                                                 | CCAATCAGTTGGAGCC<br>AGTT | CCAAGAGAAAGGCAGT<br>CGAG        | 60.1                             | 891                                           | DRR                                               | Ca_27104                            | O                     | C2H2    |
| scaffold3134_P4_13740 | scaffold3134                            | 13740                         | ACTCCATC/AC                                                   | TTGATTCGTGCAATCA<br>GGA  | CCAAGAGAAAGGCAGT<br>CGAG        | 60.2                             | 289                                           | DRR                                               | Ca_27104                            | O                     | C2H2    |
| scaffold314_P4_404143 | scaffold314                             | 404143                        | AT/ATAACAGT                                                   | TTTGAACCTTGGGTG<br>GGAG  | CATTGCACTGCATGCT<br>TTTT        | 59.9                             | 651                                           | DRR                                               | Ca_21806                            | KR                    | G2-like |
| scaffold317_P4_30584  | scaffold317                             | 30584                         | CAAAAAATAAAAAAAAA/CAAAAAAT<br>AAAAAAAAATAAAAAAAAAA            | CTCGCTCGGTTACCCT<br>CATA | AGTTCGATTCAAAGAC<br>CCCA        | 60.2                             | 682                                           | DRR                                               | Ca_25635                            | D                     | --      |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3228_P4_47967 | scaffold3228                            | 47967                         | C/CAA                                                         | TGACAAAAGGGGGAGA<br>TTGA | TGCGTCTTTCTCAAGT<br>GCAT  | 60.4                             | 414                                           | DRR                                               | Ca_27761                            | --                    | --  |
| scaffold331_P4_155436 | scaffold331                             | 155436                        | CATATATATATATATATATAT/CATAT<br>ATATATATATATAT                 | TTGGAAGGAGCCCTTA<br>CCTT | TTGGTATTGAACTCGG<br>AGGC  | 60.1                             | 716                                           | DRR                                               | Ca_25647                            | FH                    | --  |
| scaffold3321_P4_25022 | scaffold3321                            | 25022                         | ATTTTTTTTT/ATTTTTTTTT                                         | TTTTCTGGTTGTAGGA<br>CGGG | CAACAACCTTCTCATGCT<br>CGC | 60.0                             | 711                                           | DRR                                               | Ca_25706                            | QR                    | B3  |
| scaffold335_P4_133682 | scaffold335                             | 133682                        | CC/CCCTAC                                                     | ATGGCTCAAATCAGAA<br>TGCC | TGATAACCTTTCTCGC<br>GTT   | 60.0                             | 578                                           | DRR                                               | Ca_26029                            | --                    | NAC |
| scaffold3397_P4_17764 | scaffold3397                            | 17764                         | AT/ATT                                                        | GATCAGATCTGGCAGC<br>AACA | GAGGATGGAAATTGCT<br>GCAT  | 60.0                             | 366                                           | DRR                                               | Ca_26271                            | --                    | --  |
| scaffold340_P4_18699  | scaffold340                             | 18699                         | CA/CAAA                                                       | GAATGCACACAGCAGA<br>AGGA | CTAACTCTAATGGGCG<br>GCAG  | 60.0                             | 639                                           | DRR                                               | Ca_24954                            | DL                    | --  |
| scaffold340_P4_274458 | scaffold340                             | 274458                        | ATTTTTTTTT/ATTTTTTTTT                                         | GCAGTGGGACGCACTT<br>ATT  | CAGCTAGCAACAATGG<br>CAAA  | 60.1                             | 702                                           | DRR                                               | Ca_24963                            | --                    | --  |
| scaffold3404_P4_2056  | scaffold3404                            | 2056                          | TAAA/TAA                                                      | GCATCAAGCTGTCGTT<br>TGAA | CCCCTTTGTCAGTTAA<br>GGCA  | 60.0                             | 319                                           | DRR                                               | Ca_27915                            | --                    | --  |
| scaffold350_P4_68142  | scaffold350                             | 68142                         | TTTCTTCGTTCTT/TTTCTTCGTT<br>CTTCGTTCTT                        | CAACATGCGGGTCTTT<br>TTCT | GGTCTCCACCCATTT<br>CTTT   | 60.1                             | 722                                           | DRR                                               | Ca_26734                            | --                    | --  |
| scaffold362_P4_15120  | scaffold362                             | 15120                         | ATATTT/AT                                                     | TCCTAGAACATGCATC<br>ACGC | TACCCTTTGCTAGCCC<br>CTTT  | 59.8                             | 521                                           | DRR                                               | Ca_24987                            | --                    | B3  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                       |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| scaffold362_P4_166434 | scaffold362                             | 166434                        | TGA/T                                                         | CCCGGTATTGTTTGTG<br>CTCT | CACATCAGCCACATTT<br>GACC | 60.0                             | 774                                           | DRR                                               | Ca_24991                            | C                     | --     |
| scaffold369_P4_10343  | scaffold369                             | 10343                         | CAAAAAAAAA/CAAAAAAAAA                                         | TGCATGCATGATTGTT<br>ATGG | TTGATCAATTTGACGG<br>CTCA | 58.9                             | 405                                           | DRR                                               | Ca_25290                            | --                    | HD-ZIP |
| scaffold374_P4_205813 | scaffold374                             | 205813                        | CAT/CATCCTGAT                                                 | AGCTGTTTCTGCTAGG<br>CTGG | TTTATTTACGCGAATGC<br>CCT | 59.8                             | 941                                           | DRR                                               | Ca_26214                            | O                     | --     |
| scaffold38_P4_239944  | scaffold38                              | 239944                        | ATTTTTTTTT/ATTTTTTTTT                                         | TTCCATGGCATTGAGA<br>AGAA | TTAGGACCAACGGTGC<br>ACTT | 59.2                             | 635                                           | DRR                                               | Ca_23619                            | R                     | --     |
| scaffold38_P4_248171  | scaffold38                              | 248171                        | CTTTTTTTTT/CTTTTTTTTT                                         | TAGCCTTGAGACCGAG<br>CATT | CAAGGACTAACTGAA<br>GCCCA | 60.0                             | 372                                           | DRR                                               | Ca_23620                            | --                    | --     |
| scaffold383_P4_77382  | scaffold383                             | 77382                         | ATTT/ATT                                                      | GTGTCTGCTTGTTCG<br>CTGA  | CAAAGGGGGAGATTG<br>GTTT  | 60.0                             | 507                                           | DRR                                               | Ca_27371                            | --                    | --     |
| scaffold3947_P4_5994  | scaffold3947                            | 5994                          | CAAAAA/CAAAAA                                                 | AAAATCCAACAATCTCC<br>CCC | TTGGTCGACAAGCAAC<br>TGAG | 60.0                             | 577                                           | DRR                                               | Ca_27632                            | --                    | --     |
| scaffold398_P4_275366 | scaffold398                             | 275366                        | ATTTTT/ATTTTT                                                 | GCACCACAGTCTTCCT<br>CCTC | TCCGTGCCCATGATAA<br>ATAA | 59.8                             | 579                                           | DRR                                               | Ca_22289                            | B                     | --     |
| scaffold398_P4_301322 | scaffold398                             | 301322                        | TTTT/TTTTATTTT                                                | TCTAGATACGGGATGG<br>GCAC | TCGCGAAGAAGGATAA<br>AATG | 59.9                             | 523                                           | DRR                                               | Ca_22290                            | A                     | --     |
| scaffold398_P4_339502 | scaffold398                             | 339502                        | T/TG                                                          | GGATGCTGGAATTTTG<br>AAGG | TTTACTCCGCCAGCT<br>TGT   | 59.5                             | 810                                           | DRR                                               | Ca_22294                            | K                     | C3H    |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                      | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                       |                                         |                               |                                                                                    |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| scaffold398_P4_339939 | scaffold398                             | 339939                        | CAAAAAAAAA/CAAAAAAAAAAA                                                            | ACAAGCTGGCGGAAGT<br>AAAA   | AATTCGACGTGATACC<br>GAGG    | 59.9                             | 203                                           | DRR                                               | Ca_22294                            | K                     | C3H         |
| scaffold398_P4_340646 | scaffold398                             | 340646                        | TA/TAAA                                                                            | ATTAGACCGTCCTGGT<br>GTGG   | AGGTCATGGGTTTGAG<br>CAAC    | 59.8                             | 496                                           | DRR                                               | Ca_22294                            | K                     | C3H         |
| scaffold398_P4_372482 | scaffold398                             | 372482                        | TTGTGTG/TTGTGTGTG                                                                  | TGGGAGTTTGTGAGGT<br>ATTTCC | GCCAAAGAAGAAGTGA<br>ACCG    | 60.2                             | 772                                           | DRR                                               | Ca_22296                            | J                     | --          |
| scaffold40_P4_1016318 | scaffold40                              | 1016318                       | CA/CAA                                                                             | CCGAGGAGCAATGTGG<br>TTAT   | TGTGGGAACAGTGGA<br>TGAA     | 60.0                             | 478                                           | DRR                                               | Ca_18998                            | --                    | MYB_related |
| scaffold40_P4_1056072 | scaffold40                              | 1056072                       | G/GGT                                                                              | ACCAGGTGCAGGAATT<br>TACG   | GCGGAGTCGGTCGACT<br>AATA    | 60.0                             | 720                                           | DRR                                               | Ca_19000                            | O                     | MYB         |
| scaffold40_P4_466383  | scaffold40                              | 466383                        | AT/ATATCTTTATATT                                                                   | ATGCAGGTTTTGGATT<br>TTGC   | TACCTCGGCATATTTCA<br>GGC    | 59.9                             | 714                                           | DRR                                               | Ca_18971                            | T                     | --          |
| scaffold40_P4_496475  | scaffold40                              | 496475                        | ATATTATTATTATTATTATTATTA<br>TTATTATT/ATATTATTATTATTATTA<br>TTATTATTATTATTATTATTATT | AGTATCCTGGGTATGC<br>GACG   | TTTGATAACAATTTTCG<br>CTCCTC | 60.0                             | 692                                           | DRR                                               | Ca_18973                            | R                     | --          |
| scaffold40_P4_973137  | scaffold40                              | 973137                        | TTGTGTAACAAATCAT/TTGTGTAAC<br>AAATCATGTGTAACAAATCAT                                | GCCAAGAAGGGTGATT<br>TTCA   | CATATGGGTTTGGCAC<br>CTCT    | 60.1                             | 314                                           | DRR                                               | Ca_18995                            | S                     | --          |
| scaffold40_P4_998454  | scaffold40                              | 998454                        | GGCG/GGCGCG                                                                        | CCAACCTCGTCGATAA<br>AGGA   | AAGTGCGAAAGGTAAG<br>CTGC    | 60.1                             | 684                                           | DRR                                               | Ca_18996                            | S                     | --          |
| scaffold4011_P4_38659 | scaffold4011                            | 38659                         | TTAATAATAATAATAATAATAAT<br>AATAA/TTAATAATAATAATAATAA<br>ATAATAATAATAATAA           | CCTTCTGTGGAAATT<br>GTGG    | TTCAATTGCAATATGCG<br>ACC    | 59.5                             | 796                                           | DRR                                               | Ca_26887                            | T                     | bHLH        |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                       |                                         |                               |                                                                           |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| scaffold4057_P4_6605  | scaffold4057                            | 6605                          | TTT/TCTTTTATT                                                             | CCTATGTGCTCTTCGT<br>GCAA | AAAGCTTATATCCCAAG<br>CTCAAA | 60.0                             | 667                                           | DRR                                               | Ca_27488                            | --                    | --       |
| scaffold408_P4_40537  | scaffold408                             | 40537                         | T/TATTATAATA                                                              | GCTTTTCCAAGAAGC<br>GATG  | AAAAAGCGTTGTAAAG<br>GGCA    | 60.0                             | 457                                           | DRR                                               | Ca_25272                            | --                    | M-type   |
| scaffold409_P4_2612   | scaffold409                             | 2612                          | GTAAATTT/G                                                                | AAGTCACAGTGGAACC<br>CCAG | TCGATTGCAACCAAAT<br>GAA     | 60.0                             | 151                                           | DRR                                               | Ca_27582                            | --                    | --       |
| scaffold414_P4_21975  | scaffold414                             | 21975                         | GAAAAA/GAAAA                                                              | TTCTATTGCTCACCC<br>CTTG  | GAAAAACAAGACCCGC<br>GATA    | 60.1                             | 516                                           | DRR                                               | Ca_27849                            | --                    | --       |
| scaffold415_P4_9749   | scaffold415                             | 9749                          | T/TCTGA                                                                   | TTGAGCTCAAAGAGG<br>TGCT  | AGCGCTGTAAATGTG<br>CCTT     | 60.3                             | 727                                           | DRR                                               | Ca_28252                            | --                    | Trihelix |
| scaffold418_P4_152839 | scaffold418                             | 152839                        | AACACACACACACACA/AAACACA<br>CACACACACACACA                                | CTGGGCAAGGGATCTG<br>AATA | TGCATTTTACAGCGCTT<br>TTG    | 60.0                             | 596                                           | DRR                                               | Ca_24681                            | --                    | --       |
| scaffold418_P4_154154 | scaffold418                             | 154154                        | AATATATATATATATATATA/AATA<br>TATATATATATATATATA                           | ACTCCTCAAACTCGG<br>CAAA  | TTGAACTTGCAATTCGTT<br>CCA   | 59.9                             | 719                                           | DRR                                               | Ca_24681                            | --                    | --       |
| scaffold420_P4_224153 | scaffold420                             | 224153                        | ACC/ACCTCC                                                                | TCGATTGACATTACCC<br>AGCA | TAGGTGGTGGTGAATG<br>GGTT    | 60.1                             | 269                                           | DRR                                               | Ca_22201                            | R                     | MYB      |
| scaffold429_P4_179314 | scaffold429                             | 179314                        | CATATATATATATATATATATA<br>TATATATATATA/CATATATATATATA<br>TATATATATATATATA | AAGCTGCAACAATCAA<br>AGCA | TAACCAATCTTGTGCAC<br>CCA    | 59.6                             | 923                                           | DRR                                               | Ca_26240                            | --                    | --       |
| scaffold433_P4_12663  | scaffold433                             | 12663                         | TAACATAAAACATAAAAA/TAACAT<br>AAAAA                                        | TGGTCTAAAGAATGCT<br>GGGG | TGCCCCAAATGAAGTG<br>TGTA    | 60.1                             | 525                                           | DRR                                               | Ca_26817                            | --                    | --       |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                       |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| scaffold433_P4_165941 | scaffold433                             | 165941                        | A/AG                                                          | AAAATTGAAACATCCGACGC    | ACTTGTCTGCTGGACGATCT    | 59.9                             | 512                                           | DRR                                               | Ca_26821                            | --                    | --       |
| scaffold44_P4_74426   | scaffold44                              | 74426                         | TG/T                                                          | GTGTCACTGGTCCGGAGATT    | TTGGTCGTTTGAGCCTTTCT    | 60.0                             | 325                                           | DRR                                               | Ca_25410                            | --                    | --       |
| scaffold450_P4_205054 | scaffold450                             | 205054                        | AATTTATATT/AATTTATATTTATATT                                   | TTGTGTGTTTAATTTTCGTTTG  | CTAAGGCAGCCAAAATCAGC    | 60.0                             | 633                                           | DRR                                               | Ca_23795                            | --                    | --       |
| scaffold451_P4_108506 | scaffold451                             | 108506                        | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA<br>A                            | ACATAGTTCGCAAAATGCCA    | GGTTGGACATCATGTTATGGG   | 59.2                             | 631                                           | DRR                                               | Ca_22605                            | R                     | SBP      |
| scaffold4511_P4_22911 | scaffold4511                            | 22911                         | CAAAAA/CAAAA                                                  | CTCCCCCTGAGTTTTGGAAT    | GACGACAATCACCCGAGAT     | 60.3                             | 753                                           | DRR                                               | Ca_28219                            | --                    | Trihelix |
| scaffold4511_P4_22953 | scaffold4511                            | 22953                         | TAAAA/TAAAA                                                   | CTCCCCCTGAGTTTTGGAAT    | GACGACAATCACCCGAGAT     | 60.3                             | 753                                           | DRR                                               | Ca_28219                            | --                    | Trihelix |
| scaffold46_P4_39790   | scaffold46                              | 39790                         | AGGGGG/AGGGG                                                  | TGTTGAGATTGGCAAGCAAG    | TCCAAGCTTTTGTTCAGTG     | 60.0                             | 744                                           | DRR                                               | Ca_27601                            | --                    | --       |
| scaffold46_P4_40359   | scaffold46                              | 40359                         | ATTT/ATTTT                                                    | TGTGCCTGAGAAAGATGCAA    | CAGAATCAATGTGCCAATCG    | 60.5                             | 509                                           | DRR                                               | Ca_27600                            | --                    | --       |
| scaffold469_P4_176029 | scaffold469                             | 176029                        | AATATATATATATA/AATATATATATA<br>TATA                           | AGAAGTTAGGCTTGGA GCCG   | CGGTTTGGTCAATTC CATC    | 60.9                             | 142                                           | DRR                                               | Ca_25911                            | I                     | G2-like  |
| scaffold480_P4_34490  | scaffold480                             | 34490                         | CA/CAGTTCAGAA                                                 | TTGGTTTATTTGGGTTGGGA    | TGGGATACAAAGACGAGCCT    | 60.0                             | 638                                           | DRR                                               | Ca_26867                            | --                    | M-type   |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                        |                                         |                               |                                                               |                              |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| scaffold4902_P4_108605 | scaffold4902                            | 108605                        | CAAAAAAAAA/CAAAAAAAAA                                         | TACAACGCTCGTTTC<br>ACAG      | CGTGAAGTGTAGCGC<br>ACTT  | 59.9                             | 507                                           | DRR                                               | Ca_26351                            | --                    | Trihelix |
| scaffold4902_P4_39096  | scaffold4902                            | 39096                         | TAAAAA/TAAAA                                                  | AAGCCGCTGCTTACGA<br>AATA     | AGTTAGTGGCTGGGG<br>AGAT  | 60.0                             | 494                                           | DRR                                               | Ca_26348                            | TU                    | --       |
| scaffold495_P4_131292  | scaffold495                             | 131292                        | ATTTTTTTTT/ATTTTTTTTT                                         | CGAGGAAATGTAATTT<br>TAGGGG   | CCCATTTGTGGCTGCT<br>ATT  | 60.1                             | 701                                           | DRR                                               | Ca_26761                            | --                    | AP2      |
| scaffold510_P4_13129   | scaffold510                             | 13129                         | CATATATATATATATATATATA/<br>CATATATATATATATATATATA<br>TATA     | TGGGTGCTATTTGCAA<br>TCAA     | CCTTCATGAACCGCAA<br>TACA | 60.1                             | 406                                           | DRR                                               | Ca_26546                            | --                    | --       |
| scaffold531_P4_83931   | scaffold531                             | 83931                         | CCGG/CCGGCCGGTTCGG                                            | GAGAACGCAAGCTAAC<br>GGAC     | ACCTTGTGGATGGCAG<br>TTTC | 60.0                             | 180                                           | DRR                                               | Ca_22395                            | --                    | --       |
| scaffold543_P4_229568  | scaffold543                             | 229568                        | ATTTTT/ATTTT                                                  | TTTGCCCCCAACTCTA<br>CATC     | ATGGGCACATGCTATC<br>ATCA | 59.9                             | 755                                           | DRR                                               | Ca_24786                            | --                    | --       |
| scaffold543_P4_250171  | scaffold543                             | 250171                        | TAAAAAAA/TAAAAAAA                                             | GTCTTGGGTGATGGCA<br>AAGT     | GAAGTTGAGCGCAATG<br>TTGA | 60.0                             | 703                                           | DRR                                               | Ca_24788                            | --                    | --       |
| scaffold543_P4_28493   | scaffold543                             | 28493                         | ATTTTTTTTT/ATTTTTTTTT                                         | GACAGCTCTCTCCAAA<br>TGCC     | AAGGAATCCGCATGCT<br>TAAA | 60.0                             | 507                                           | DRR                                               | Ca_24779                            | IR                    | --       |
| scaffold543_P4_69595   | scaffold543                             | 69595                         | GATAATAATAATAATAATAATAA<br>TAAT/GATAATAATAATAATAATA<br>ATAAT  | TTTCATTTGTTTTCAA<br>GTTATCAA | CCTCCTAATGCGTTGG<br>TTTT | 59.1                             | 619                                           | DRR                                               | Ca_24780                            | --                    | --       |
| scaffold544_P4_146396  | scaffold544                             | 146396                        | CTTTTT/CTTT                                                   | TTCTATTGCTCACCC<br>CTTG      | GAAAAACAAGACCCGC<br>GATA | 60.1                             | 520                                           | DRR                                               | Ca_26540                            | --                    | --       |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                            | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                       |                                         |                               |                                                                                          |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| scaffold544_P4_147706 | scaffold544                             | 147706                        | CAAAAA/CAAAA                                                                             | CCCCCTTTTGCATAA<br>GTGA  | GAGGAGACATCTGCTG<br>AGGG | 59.9                             | 582                                           | DRR                                               | Ca_26540                            | --                    | --          |
| scaffold545_P4_217429 | scaffold545                             | 217429                        | TTTATTATTGTTATTATTATTATTGTT<br>ATTAT/TTTATTATTGTTATTATTATT<br>ATTGTTATTATTATTATTGTTATTAT | TGATTTTGATCGACGG<br>ATGA | TGGAAATTTGTGCCAT<br>GAAA | 60.0                             | 674                                           | DRR                                               | Ca_23926                            | S                     | --          |
| scaffold548_P4_212010 | scaffold548                             | 212010                        | G/GA                                                                                     | GGAACACTTCGGTGTG<br>GACT | CATGTCCCGAAAAGAG<br>CAAT | 60.0                             | 563                                           | DRR                                               | Ca_21489                            | --                    | --          |
| scaffold553_P4_291778 | scaffold553                             | 291778                        | GATAATAATAATAATAATAATAA<br>T/GATAATAATAATAATAATAATA<br>ATAAT                             | GAACTGCCTTGTTGGG<br>GTTA | TTGCAACCTGATCTTT<br>CCA  | 60.0                             | 609                                           | DRR                                               | Ca_19933                            | R                     | MYB         |
| scaffold553_P4_463470 | scaffold553                             | 463470                        | GAA/GAATAGAAAA                                                                           | AACACCAAAATTTCTCC<br>CCC | CGACACTCGCTTCACC<br>ACTA | 60.0                             | 364                                           | DRR                                               | Ca_19939                            | --                    | --          |
| scaffold561_P4_25431  | scaffold561                             | 25431                         | CTCTTTCT/CTCT                                                                            | TTGATTCATCAACACC<br>GGA  | AAATTGGGTTCTGCCA<br>ATCA | 59.9                             | 399                                           | DRR                                               | Ca_26215                            | --                    | MYB_related |
| scaffold575_P4_65125  | scaffold575                             | 65125                         | G/GT                                                                                     | TTGAAGTTAAGGGGTG<br>CTGC | TCCATCCAACCTTGTC<br>GATT | 60.2                             | 531                                           | DRR                                               | Ca_27003                            | --                    | --          |
| scaffold5839_P4_7420  | scaffold5839                            | 7420                          | GAAAA/GAAAAA                                                                             | AAATCCAACAATCTCC<br>CCC  | GGTTTCAACCCCAATG<br>CTTA | 60.0                             | 327                                           | DRR                                               | Ca_28048                            | --                    | --          |
| scaffold587_P4_18087  | scaffold587                             | 18087                         | T/TCA                                                                                    | GTCCTTGCCTTATGC<br>TTGT  | TGCTTGATTGCTTGAG<br>ATCC | 60.4                             | 347                                           | DRR                                               | Ca_27621                            | --                    | --          |
| scaffold5891_P4_5025  | scaffold5891                            | 5025                          | TTATATAT/TTATAT                                                                          | GCCAATCGATTATCGC<br>AAGT | CCCTGTGACAAACACA<br>ATCG | 60.1                             | 481                                           | DRR                                               | Ca_27904                            | --                    | --          |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                     | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                       |                                         |                               |                                                                                                   |                             |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| scaffold593_P4_209245 | scaffold593                             | 209245                        | AACA/AACACA                                                                                       | GGGTGAAATTTTAGGG<br>GTGAA   | GGAATAAAATATGCATC<br>CGAGC    | 60.0                             | 734                                           | DRR                                               | Ca_26412                            | --                    | C2H2 |
| scaffold593_P4_209468 | scaffold593                             | 209468                        | TC/T                                                                                              | GCAAACCTTTGCAAAA<br>AGAAA   | GGAATAAAATATGCATC<br>CGAGC    | 59.4                             | 153                                           | DRR                                               | Ca_26412                            | --                    | C2H2 |
| scaffold593_P4_209698 | scaffold593                             | 209698                        | CT/CTTT                                                                                           | GCAAACCTTTGCAAAA<br>AGAAA   | GGAATGGAAATAATTG<br>AAAAGTTTG | 59.4                             | 847                                           | DRR                                               | Ca_26412                            | --                    | C2H2 |
| scaffold593_P4_210090 | scaffold593                             | 210090                        | TT/TTATTTAAT                                                                                      | GAGCACAGTTTCAATT<br>AACAGCA | GTCTCTGCTCAACCAG<br>GAGG      | 59.5                             | 862                                           | DRR                                               | Ca_26412                            | --                    | C2H2 |
| scaffold598_P4_99722  | scaffold598                             | 99722                         | ATTTTTTT/ATTTTTT                                                                                  | CATCGCCTGAATGGCT<br>TAAT    | TGACATGTACGGTGAT<br>GCCT      | 60.1                             | 795                                           | DRR                                               | Ca_21751                            | R                     | --   |
| scaffold599_P4_351148 | scaffold599                             | 351148                        | ATAAAAAGC/ATAAAAAGCTAAAAAG<br>C                                                                   | CTGTTGGGCAAGGGAT<br>CTAA    | CACGCTTGTTTTGCAC<br>ATTT      | 60.1                             | 641                                           | DRR                                               | Ca_25346                            | --                    | --   |
| scaffold599_P4_352138 | scaffold599                             | 352138                        | TTATATATATATATATATATATATATA<br>TATATATATATA/TTTTATATATATAT<br>ATATATATATATATATATATATATA<br>TATATA | GGTGGAATATTTGCAT<br>GAACC   | TGATGACAAAAGTAAG<br>GAAGAGGA  | 59.2                             | 955                                           | DRR                                               | Ca_25346                            | --                    | --   |
| scaffold599_P4_352330 | scaffold599                             | 352330                        | TAAAA/TAAA                                                                                        | AAAAATACGGCAAGC<br>AAAA     | TCAATGGACATGAGTC<br>TTCACA    | 57.5                             | 887                                           | DRR                                               | Ca_25346                            | --                    | --   |
| scaffold599_P4_373801 | scaffold599                             | 373801                        | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA<br>AAAA                                                             | CCCCCTAAGTTCATT<br>CACA     | GGCTTGCCGTCGGTA<br>AATA       | 59.8                             | 567                                           | DRR                                               | Ca_25347                            | --                    | --   |
| scaffold6185_P4_2912  | scaffold6185                            | 2912                          | GA/G                                                                                              | GCAAAGTCGCATTATG<br>GTATGA  | AGCCCTCACATTAATTC<br>GCA      | 60.0                             | 740                                           | DRR                                               | Ca_27924                            | --                    | --   |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |          |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|----------|
|                       |                                         |                               |                                                                         |                              |                          |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| scaffold6185_P4_3433  | scaffold6185                            | 3433                          | TAAAAA/TAAAA                                                            | GCAAGCCATTTGTCCA<br>TTTT     | TCAGCTCACTCTCGCT<br>TTGA | 59.9                             | 190                                           | DRR                                                  | Ca_27924                            | --                    | --       |
| scaffold626_P4_55533  | scaffold626                             | 55533                         | CTATT/CT                                                                | TGAACTCCTTTGTCCTT<br>TGGA    | TCATTGCTCCCCCGTA<br>ATAG | 59.7                             | 320                                           | DRR                                                  | Ca_25170                            | --                    | --       |
| scaffold642_P4_395178 | scaffold642                             | 395178                        | AT/ATTATT                                                               | TTTGCGACGCTTGATC<br>ATTA     | CGCACACGGGTCAAAT<br>ATAA | 60.4                             | 397                                           | DRR                                                  | Ca_19107                            | --                    | --       |
| scaffold645_P4_238730 | scaffold645                             | 238730                        | CATATATATATATATATATATATA<br>TATATAT/CATATATATATATATATAT<br>ATATATATATAT | TTGTCGAGTGTGACCT<br>CCAG     | CCAAAAC TGGGAGAA<br>ACAA | 59.9                             | 539                                           | DRR                                                  | Ca_25158                            | I                     | Trihelix |
| scaffold647_P4_200535 | scaffold647                             | 200535                        | A/AT                                                                    | CAAGCTGTCGGTTGAA<br>GACA     | AACAATCTCCCCCTTTT<br>TGG | 60.0                             | 603                                           | DRR                                                  | Ca_27495                            | --                    | --       |
| scaffold653_P4_200790 | scaffold653                             | 200790                        | TTATA/TTA                                                               | GAGGAAGACTCAAACG<br>CGAC     | CTTGACAAAACCCCAA<br>GCAT | 60.0                             | 400                                           | DRR                                                  | Ca_24313                            | E                     | --       |
| scaffold661_P4_293075 | scaffold661                             | 293075                        | TGA/T                                                                   | TGGGCAAGGGATCTGA<br>ATAG     | AATGCCACCCATAATT<br>TCA  | 60.0                             | 651                                           | DRR                                                  | Ca_23950                            | --                    | --       |
| scaffold674_P4_155701 | scaffold674                             | 155701                        | TTTTTTTT/TTTTTTTTTTTT                                                   | ACGTAGAGAGAGGCTC<br>GGAA     | CAAAAATTCGCGGGTA<br>CATT | 59.2                             | 725                                           | DRR                                                  | Ca_20156                            | R                     | --       |
| scaffold674_P4_156790 | scaffold674                             | 156790                        | CTA/CTATAATCAATTA                                                       | CCAACAAATTAGTTATT<br>GCTCTCG | TTGGTGATGGCTAAGA<br>GCCT | 59.3                             | 680                                           | DRR                                                  | Ca_20156                            | R                     | --       |
| scaffold674_P4_157426 | scaffold674                             | 157426                        | GAAAAAAAAA/GAAAAAAAAA                                                   | AGGCTCTTAGCCATCA<br>CCAA     | AGCACTTTCAGCACC<br>CAGT  | 59.8                             | 635                                           | DRR                                                  | Ca_20156                            | R                     | --       |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold674_P4_630014 | scaffold674                             | 630014                        | CATATATATATATATAT/CATATATAT<br>ATATATATAT                     | GCGAGGATTGGTATCG<br>TCAT  | GCAAAACACATTCAAAA<br>TCCAA | 59.9                             | 263                                           | DRR                                               | Ca_20173                            | BD                    | --  |
| scaffold674_P4_630332 | scaffold674                             | 630332                        | TAAAAAAA/TAAAAAAA                                             | GCGAGGATTGGTATCG<br>TCAT  | TGCACGAAAGGTATAA<br>TTGGG  | 59.9                             | 922                                           | DRR                                               | Ca_20173                            | BD                    | --  |
| scaffold682_P4_239210 | scaffold682                             | 239210                        | ACC/AC                                                        | TCCAAAGCATCACGTA<br>TCCA  | TGCGTGACAGGAACAA<br>GAAG   | 60.1                             | 667                                           | DRR                                               | Ca_23188                            | R                     | ERF |
| scaffold682_P4_239323 | scaffold682                             | 239323                        | AGATGATG/AGATG                                                | CAACTCCCCCTGCAAA<br>CTTA  | TGCGTGACAGGAACAA<br>GAAG   | 60.1                             | 417                                           | DRR                                               | Ca_23188                            | R                     | ERF |
| scaffold720_P4_179447 | scaffold720                             | 179447                        | AACACACA/AACACA                                               | CAGCCACAAAGTGCTT<br>GAAA  | ATTGCTAGTGGTGG<br>TGCC     | 60.0                             | 637                                           | DRR                                               | Ca_24736                            | --                    | --  |
| scaffold724_P4_100088 | scaffold724                             | 100088                        | ATTTTTTTT/ATTTTTTTTTT                                         | ACAGGAGGGTGATCGA<br>GAGA  | TGCATACTTGTGTGGC<br>ATTTT  | 59.8                             | 727                                           | DRR                                               | Ca_25051                            | Q                     | NAC |
| scaffold724_P4_100193 | scaffold724                             | 100193                        | TAAAAAAA/TAAAAAAA                                             | CTGTAAGCGGAGAAAA<br>TTGG  | TTGCATACTTGTGTGG<br>CATTT  | 57.5                             | 319                                           | DRR                                               | Ca_25051                            | Q                     | NAC |
| scaffold724_P4_100328 | scaffold724                             | 100328                        | TAAAAAAA/TAAAAAAA                                             | CTGTAAGCGGAGAAAA<br>TTGG  | AATGGTAGTCCCTCTG<br>GCCT   | 57.5                             | 690                                           | DRR                                               | Ca_25051                            | Q                     | NAC |
| scaffold724_P4_100591 | scaffold724                             | 100591                        | AATTTAACATAT/A                                                | AAATGCCACACAAGTA<br>TGCAA | AATGGTAGTCCCTCTG<br>GCCT   | 59.1                             | 392                                           | DRR                                               | Ca_25051                            | Q                     | NAC |
| scaffold724_P4_60095  | scaffold724                             | 60095                         | TAAAAAAA/TAAAAAAA                                             | CTGCCACGTCAACCTT<br>TTAT  | ATACCATTGACTTGCC<br>GGAG   | 60.0                             | 401                                           | DRR                                               | Ca_25048                            | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                   |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold731_P4_315903 | scaffold731                             | 315903                        | GATGA/GATGAATGA                                                                   | AACTCGAAGTGCCATG<br>CTTT | CAATACGCAATGGTGG<br>TGAG | 59.9                             | 660                                           | DRR                                               | Ca_23814                            | J                     | --  |
| scaffold731_P4_361613 | scaffold731                             | 361613                        | TGG/TGGG                                                                          | TGTGCTATTGCTCAAAT<br>CCG | AGCAGTCGTTTCCAGC<br>TGTT | 59.8                             | 640                                           | DRR                                               | Ca_23818                            | --                    | --  |
| scaffold731_P4_94332  | scaffold731                             | 94332                         | ATTTTTTTTT/ATTTTTTTT                                                              | GAGCGCTGTAAAGAC<br>CTCC  | TGAAGATGGTTTGCAA<br>TGGA | 59.1                             | 188                                           | DRR                                               | Ca_23810                            | --                    | B3  |
| scaffold731_P4_94685  | scaffold731                             | 94685                         | CATATATATATATATATATATATA<br>TATATATATATA/CATATATATATATA<br>TATATATATATATATATATATA | TCCATTGCAAACCATCT<br>TCA | AAAAATGCGCTGCTTC<br>TTGT | 60.0                             | 613                                           | DRR                                               | Ca_23810                            | --                    | B3  |
| scaffold7330_P4_2275  | scaffold7330                            | 2275                          | AG/AAGTTTTTTTG                                                                    | TTGGTCGACAAGCAAC<br>TGAG | AAAATCCAACAATCTCC<br>CCC | 60.0                             | 699                                           | DRR                                               | Ca_28207                            | --                    | --  |
| scaffold741_P4_6784   | scaffold741                             | 6784                          | AATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATATA<br>TATATATATATAT         | TTGGGATGGTGATTCT<br>CACA | TTTACCACTTGAGATTG<br>GGC | 59.9                             | 215                                           | DRR                                               | Ca_28074                            | --                    | B3  |
| scaffold750_P4_360259 | scaffold750                             | 360259                        | GA/G                                                                              | TGTTTGTCTTGCTGCTT<br>TGC | AAAATCCAACAATCTCC<br>CCC | 60.2                             | 626                                           | DRR                                               | Ca_25944                            | --                    | --  |
| scaffold752_P4_227110 | scaffold752                             | 227110                        | ATAATA/ATAGTAATA                                                                  | TTGATGTTTGTCGGGC<br>AATA | AATGGCCACGAATCTG<br>AAAG | 59.9                             | 601                                           | DRR                                               | Ca_25232                            | --                    | --  |
| scaffold752_P4_495403 | scaffold752                             | 495403                        | CAAAAAAAAA/CAAAAAAAAAA                                                            | TCCGTTGTGAAGGCTT<br>TTTC | ATTGGGCCTTTGTAGT<br>GACG | 60.2                             | 175                                           | DRR                                               | Ca_25238                            | L                     | --  |
| scaffold775_P4_449733 | scaffold775                             | 449733                        | CTTATCAATTGTGTTT/CTTATCAAT<br>TGTGTTTATCAATTGTGTTT                                | CTCTCTTCTGCGCATC<br>AACT | TTGACCATGACACATG<br>CCTT | 58.3                             | 459                                           | DRR                                               | Ca_23414                            | --                    | NAC |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                       |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| scaffold775_P4_450377 | scaffold775                             | 450377                        | TG/TGG                                                        | AAGGCATGTGTCATGG<br>TCAA  | TTTACGGGAACGAGGA<br>GAGA  | 60.0                             | 738                                           | DRR                                               | Ca_23414                            | --                    | NAC  |
| scaffold789_P4_18724  | scaffold789                             | 18724                         | GAAA/GAAAA                                                    | TTGTCAGGATTGCCAT<br>TTCA  | ATACTCAGGAGGGGCT<br>GGTT  | 60.0                             | 558                                           | DRR                                               | Ca_27694                            | --                    | --   |
| scaffold7923_P4_2123  | scaffold7923                            | 2123                          | AAGCTCA/AA                                                    | TCGGGGTCTTTAGTCG<br>TCAT  | GCGAGGAAGCAAAAGC<br>TAGA  | 59.6                             | 796                                           | DRR                                               | Ca_27506                            | O                     | --   |
| scaffold7923_P4_22242 | scaffold7923                            | 22242                         | CAAAAAAAAA/CAAAAAAAAA                                         | TTTCCCGACTTGGTCC<br>TTTA  | TTTGC GTTACGAATTG<br>ATGA | 59.5                             | 177                                           | DRR                                               | Ca_27507                            | QI                    | bHLH |
| scaffold7923_P4_2279  | scaffold7923                            | 2279                          | C/CAA                                                         | TTAGCAGGGGTTAGCT<br>CTGAA | ACCACCTATTTTCGAG<br>CACC  | 59.1                             | 858                                           | DRR                                               | Ca_27506                            | O                     | --   |
| scaffold801_P4_20920  | scaffold801                             | 20920                         | ATTTTTTTTT/ATTTTTTTTT                                         | TACCCATGTGCGTCAC<br>TGTT  | GGACATGGTTGAGGAA<br>ATGG  | 60.0                             | 223                                           | DRR                                               | Ca_26173                            | --                    | --   |
| scaffold801_P4_72301  | scaffold801                             | 72301                         | CTTTTTTTTTTT/CTTTTTTTTTTT                                     | TGTTAGCGTAACAAAT<br>GGGG  | TGTGTTTTATGGATTGC<br>GGA  | 58.6                             | 557                                           | DRR                                               | Ca_26176                            | OE                    | WRKY |
| scaffold808_P4_3720   | scaffold808                             | 3720                          | CAAA/CAAAA                                                    | GCGTTTTCCAGAACTG<br>CTTC  | GTGTTGACAAAGGGGG<br>AGAA  | 60.0                             | 357                                           | DRR                                               | Ca_27975                            | --                    | --   |
| scaffold812_P4_279194 | scaffold812                             | 279194                        | A/AG                                                          | AACAATAAAATCCGCA<br>CCCA  | AATTTGTGGGCTTAGG<br>AGGC  | 60.2                             | 764                                           | DRR                                               | Ca_23374                            | Q                     | B3   |
| scaffold845_P4_102448 | scaffold845                             | 102448                        | A/AG                                                          | CTGACCGTCAAAAGCA<br>CTGA  | ACGCATAATACCTGAA<br>CGGC  | 60.0                             | 480                                           | DRR                                               | Ca_22415                            | R                     | --   |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                       |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| scaffold845_P4_133709 | scaffold845                             | 133709                        | TCC/TC                                                        | TCACGTGGACCTAATC<br>CTCC    | TTGTTTCGCCCTTCAAA<br>TTC  | 59.9                             | 776                                           | DRR                                               | Ca_22417                            | U                     | --   |
| scaffold845_P4_134750 | scaffold845                             | 134750                        | CAA/CAAAA                                                     | CCGTTTGGGCCCTTAG<br>TTAT    | TCGTGTCCATTGCTATT<br>TTCA | 60.2                             | 546                                           | DRR                                               | Ca_22417                            | U                     | --   |
| scaffold845_P4_27150  | scaffold845                             | 27150                         | TAAA/TAA                                                      | ATCGACCGCGTAAATG<br>AAAC    | TGATCCTTTTGGCCTT<br>GAG   | 60.0                             | 689                                           | DRR                                               | Ca_22410                            | --                    | bHLH |
| scaffold845_P4_44165  | scaffold845                             | 44165                         | T/TG                                                          | CGATCGCATGTTATTG<br>CTTG    | GACCCAAAAGAGGCC<br>TAAC   | 60.2                             | 615                                           | DRR                                               | Ca_22411                            | P                     | --   |
| scaffold845_P4_52018  | scaffold845                             | 52018                         | GAA/GAAA                                                      | GCAAGTGTGCAACAAC<br>CTTC    | TTCTCCACCGAGTCATT<br>TCC  | 59.3                             | 296                                           | DRR                                               | Ca_22412                            | --                    | --   |
| scaffold845_P4_69320  | scaffold845                             | 69320                         | TAAAAA/TAAAAA                                                 | TGAGTGTGAGTCCGAA<br>TGGA    | GAACCCCAACCTGAAA<br>ACAA  | 60.2                             | 493                                           | DRR                                               | Ca_22414                            | R                     | --   |
| scaffold873_P4_199356 | scaffold873                             | 199356                        | CTTATTATTATTATTATTATT/CT<br>TATTATTATTATTATTATT               | CCCTTACTTGGACCAA<br>AGTTACC | CTGCGAACTGGACAAA<br>TGAA  | 60.1                             | 585                                           | DRR                                               | Ca_23485                            | --                    | --   |
| scaffold877_P4_10844  | scaffold877                             | 10844                         | TAAAAA/TAAAAA                                                 | GCAGCAGTTGCAGCAG<br>TTTA    | TGATTTAGCGTCGGTG<br>TCAG  | 60.3                             | 601                                           | DRR                                               | Ca_28083                            | F                     | --   |
| scaffold877_P4_11190  | scaffold877                             | 11190                         | CCTTTT/C                                                      | CTGACACCGACGCTAA<br>ATCA    | AGTGATAAGACCGT<br>TTGC    | 59.9                             | 210                                           | DRR                                               | Ca_28083                            | F                     | --   |
| scaffold886_P4_133033 | scaffold886                             | 133033                        | T/TATTATTATTA                                                 | TTGGGATTAAGCTGTT<br>TGGG    | CCGACAAAACATGATG<br>GTCA  | 59.9                             | 341                                           | DRR                                               | Ca_26670                            | R                     | --   |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                       |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| scaffold886_P4_151276 | scaffold886                             | 151276                        | AG/AGCTG                                                      | AGGGATGCTTGTAGTG<br>GTTGA  | TTTGACGTGCATCCAAT<br>GTT | 59.6                             | 162                                           | DRR                                               | Ca_26671                            | --                    | --     |
| scaffold886_P4_151448 | scaffold886                             | 151448                        | TA/T                                                          | GACAACATTGGATGCA<br>CGTC   | TCGTGGTATGCTTGAC<br>CTGT | 60.0                             | 259                                           | DRR                                               | Ca_26671                            | --                    | --     |
| scaffold892_P4_33546  | scaffold892                             | 33546                         | TTTCTT/TTTCTTCTT                                              | TCCCAATTTGGTTTGT<br>GTGT   | TGGAATCTTCACCCTG<br>ACAA | 60.1                             | 713                                           | DRR                                               | Ca_27455                            | R                     | --     |
| scaffold892_P4_33776  | scaffold892                             | 33776                         | TC/T                                                          | TCAAAAGACACCAAAT<br>GGAAAA | TGGAATCTTCACCCTG<br>ACAA | 59.5                             | 251                                           | DRR                                               | Ca_27455                            | R                     | --     |
| scaffold892_P4_34457  | scaffold892                             | 34457                         | T/TTTTATTATG                                                  | CATGCCTAACGCACGA<br>ATTA   | CCGACATGGTCTTCTT<br>CCTT | 59.7                             | 426                                           | DRR                                               | Ca_27455                            | R                     | --     |
| scaffold892_P4_42751  | scaffold892                             | 42751                         | TGGGG/TGGGGG                                                  | GACGATGAAAAATATG<br>CGGG   | TGTTGATTGGCGAACA<br>CAAT | 60.3                             | 387                                           | DRR                                               | Ca_27456                            | --                    | --     |
| scaffold916_P4_3252   | scaffold916                             | 3252                          | AATATA/AATA                                                   | AAAGCGCTGTAAAATG<br>GGTG   | TATAGGGTCAAAACGC<br>CCAC | 60.1                             | 726                                           | DRR                                               | Ca_21034                            | G                     | E2F/DP |
| scaffold916_P4_3317   | scaffold916                             | 3317                          | TTTAATT/TTT                                                   | ACATCTCATGCCATTGT<br>GGA   | GAGACAGTCAGAAGGC<br>CACC | 59.9                             | 520                                           | DRR                                               | Ca_21034                            | G                     | E2F/DP |
| scaffold916_P4_3519   | scaffold916                             | 3519                          | AATATATATATATATATAT/AAATAT<br>ATATATATATATAT                  | ACATCTCATGCCATTGT<br>GGA   | GAGACAGTCAGAAGGC<br>CACC | 59.9                             | 520                                           | DRR                                               | Ca_21034                            | G                     | E2F/DP |
| scaffold919_P4_190377 | scaffold919                             | 190377                        | CAAAA/CAAAA                                                   | GAATCCTGGGCTGAAA<br>TCAA   | CACAGGTGTTTGTCGG<br>TGAG | 60.0                             | 877                                           | DRR                                               | Ca_22832                            | --                    | --     |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold93_P4_562448 | scaffold93                              | 562448                        | TA/TAA                                                        | TATAGCCACGGCAAAA<br>ATCC    | CCGAAACACAAACCCA<br>GACT   | 59.9                             | 514                                           | DRR                                               | Ca_23082                            | --                    | --  |
| scaffold953_P4_51991 | scaffold953                             | 51991                         | TAAAAAAAA/TAAAAAAAAA                                          | AATACGCCCCATAAGG<br>AACC    | TTGCCTTCCTTTTCAGC<br>ACT   | 60.0                             | 372                                           | DRR                                               | Ca_26909                            | --                    | --  |
| scaffold953_P4_73770 | scaffold953                             | 73770                         | ATT/AT                                                        | TCGGGGTATTTAATTG<br>GCAG    | ACCACATGCAAATTGTT<br>CCA   | 59.8                             | 353                                           | DRR                                               | Ca_26910                            | --                    | --  |
| C11060010_P4_683     | C11060010                               | 683                           | ATTATT/ATTATTATT                                              | TCCGATATGCACCAAT<br>GAAA    | AGGCGTCGGTTTTTCT<br>TTCT   | 59.9                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |
| C11119398_P4_1062    | C11119398                               | 1062                          | TTAT/TTATAT                                                   | AGAAATGGAACACTCG<br>CCAC    | CCCTCAGCATGCATGA<br>TTTT   | 60.1                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |
| C11119398_P4_1161    | C11119398                               | 1161                          | TTATATATATA/TTATATATA                                         | CATGCATGCTGAGGGA<br>TATG    | TGTTTGTTTCGTCAATC<br>ACTTT | 60.1                             | 268                                           | INTERGENIC                                        | --                                  | --                    | --  |
| C11119398_P4_643     | C11119398                               | 643                           | CAAAAA/CAAAAAA                                                | AGCTCCAAATTTGATG<br>GCAC    | GTGGCGAGTGTTCCAT<br>TTCT   | 60.1                             | 281                                           | INTERGENIC                                        | --                                  | --                    | --  |
| C11122410_P4_1998    | C11122410                               | 1998                          | ATTTTTTT/ATTTTTTTT                                            | AGCACACAACGAAACC<br>ATGA    | GCAACGGGAATGTGTT<br>TTTC   | 60.2                             | 797                                           | INTERGENIC                                        | --                                  | --                    | --  |
| C11154862_P4_1914    | C11154862                               | 1914                          | ATTTT/ATTTTT                                                  | GTCCAATCCCCAAACA<br>ACAC    | TGAAATTATGAAAGG<br>AAGCTCA | 60.1                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |
| C11154862_P4_4400    | C11154862                               | 4400                          | CTTTTTT/CTTTTTTT                                              | TGTCGATATATTTACCG<br>AAACCC | GCATTAGAGCTGAGGC<br>CAAC   | 59.2                             | 296                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                          | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                        |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_10350471  | Ca1                                     | 10350471                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATATAT                                                    | TCTGAGTCCGCTACCC<br>AGTT   | ATGTCACATTGTGTGT<br>GGGG    | 59.9                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_10428835  | Ca1                                     | 10428835                      | GTTTTT/GTTTTTT                                                                                         | TCAAACAAAGCCTAAAA<br>CATCA | TCATGCCTTCTTTCACT<br>TATTCA | 57.5                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_10471260  | Ca1                                     | 10471260                      | TTATATATATATATATATATA/TTATA<br>TATATATATATATATATA                                                      | TTCTCCATTGCACTCA<br>CAC    | TCAAATTTGGAGGCTG<br>GAAC    | 59.8                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_10510182  | Ca1                                     | 10510182                      | CATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATT/C<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATT | TTGCTGAAGTCAGTC<br>AAACA   | TTGTTCCGACTTTGCA<br>ATTA    | 59.6                             | 328                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_10514048  | Ca1                                     | 10514048                      | AATATATATATATATATATAT/AT<br>ATATATATATATATATATAT                                                       | AGGACAACGCAATTAC<br>AATGA  | CCATGCAAGAAAGACA<br>GCAA    | 58.2                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_10664922  | Ca1                                     | 10664922                      | TCCCC/TCCC                                                                                             | CGAACAAAAATATCGC<br>CACA   | GTCCTTAATAGGTTG<br>GTTTGG   | 59.6                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_10801339  | Ca1                                     | 10801339                      | TTATATATATATATATATATAT/AT<br>TTATATATATATATATATATATATA<br>TATATAT                                      | ATATGGTAGTTTGCGC<br>CGTT   | TCTGCCCAACCAAACCTT<br>TTT   | 59.5                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_10803149  | Ca1                                     | 10803149                      | AATATATATATATATATAT/AAAT<br>ATATATATATATATATATAT                                                       | GGCCCCACATAATCT<br>CTCT    | ACCTGAGTTCAAGCCC<br>GAGT    | 60.3                             | 457                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_10846457  | Ca1                                     | 10846457                      | CAAAAA/CAAAAAA                                                                                         | TTCCACCTAAACGAT<br>CGAC    | CAATGAACCTGAGTTT<br>GTCCC   | 59.9                             | 865                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_11145101  | Ca1                                     | 11145101                      | TTATATATATATATATATATAT/AT<br>TTATATATATATATATATATAT                                                    | TTTGAGTCCAAATTGAA<br>GGCT  | CGGATCAAAATTCGCA<br>CAAT    | 58.8                             | 837                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                       |                           |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_11151072  | Ca1                                     | 11151072                      | CACTCTNNNNNNNNNACTCT/CAC<br>TCT                                       | CAAAGACAAGACGACC<br>ACCA  | CCTTTGCAATCCAGCA<br>TTTT      | 59.7                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_11162119  | Ca1                                     | 11162119                      | GATATATATATATATATATATA/GA<br>TATATATATATATATATATA                     | GGCGTTGGAATCATGT<br>TTTT  | TGTAGCGGAAGCATCA<br>ACAG      | 59.8                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_11162292  | Ca1                                     | 11162292                      | CAAA/CA                                                               | GGCGTTGGAATCATGT<br>TTTT  | TGTAGCGGAAGCATCA<br>ACAG      | 59.8                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_11382617  | Ca1                                     | 11382617                      | AAATAACAATAACAATAACAATAACA<br>ATAACAA/AAATAACAATAACAATAA<br>CAATAACAA | TTGCCTCCATCATTCAA<br>ACA  | ACCTTGTGTTTTTGCG<br>TGG       | 60.0                             | 378                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_11425487  | Ca1                                     | 11425487                      | TTATATATATATATA/TTATATATATA<br>TATATA                                 | TTGTCTCACGTGAATC<br>TGGG  | GGAGTTTGAGAGAAG<br>GAGTGA     | 59.7                             | 745                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1145463   | Ca1                                     | 1145463                       | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATATAT<br>ATATATATA | TTCACAAACAACACCA<br>CACAA | GTGTCTCCTCCTACCA<br>CCCA      | 58.5                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_11521081  | Ca1                                     | 11521081                      | GTTATTATT/GTTATTATTATT                                                | GGTCATGCTGATAGGT<br>GGATG | ACCACAACCTTGGAAT<br>GGAA      | 60.4                             | 908                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_11563390  | Ca1                                     | 11563390                      | ATT/AT                                                                | AATGAACATGCGGACC<br>AAAT  | TTATACTGTCTCCGC<br>CACC       | 60.2                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_11735185  | Ca1                                     | 11735185                      | GTATTATTATTATT/GTATTATTA<br>TTATTATTATTATTATT                         | TGACAGTCAGAGTGCG<br>ATCC  | TCTCTGGCAACCGTTC<br>TTCT      | 60.0                             | 441                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_11788825  | Ca1                                     | 11788825                      | AATATATATATATA/AATATATATA<br>TATATATA                                 | TGGGAATAGTGCAGAC<br>CAGG  | CCAAGTTGTTTGAGAG<br>AATTTGTTT | 59.9                             | 696                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_11930560  | Ca1                                     | 11930560                      | AG/A                                                          | CGACTTGCCAAAGAAC<br>CAGT   | TAGTAGGAGGTCGCTG<br>GACG    | 60.3                             | 812                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_11948916  | Ca1                                     | 11948916                      | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATATA       | AGGCAAAACATGGCAAA<br>ATTG  | TCTTTGCCTATGCCTAT<br>GAGC   | 59.9                             | 746                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12110141  | Ca1                                     | 12110141                      | ATTTTTTTTTTTTT/ATTTTTTTTTT                                    | TGAATTGGGCCAAGAC<br>ATTT   | TGGCAGACCACAGATA<br>ACCA    | 60.3                             | 943                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12112319  | Ca1                                     | 12112319                      | C/CTTGG                                                       | GCGAAATTATTTGACG<br>GAGTTT | CATTTCAGAAGTGAAG<br>AGCAACA | 59.5                             | 874                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12142151  | Ca1                                     | 12142151                      | ATTTTTTT/ATTTTTT                                              | TGCTCCTCATGTTGTA<br>GCAC   | AAGGGATGGACATCAA<br>ATCG    | 57.4                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12225439  | Ca1                                     | 12225439                      | CTAGTTT/CTAGTTTCTAGTTT                                        | GCATAGGTGGCAGACG<br>AAGT   | GCTTTCGGTTTCCTGTT<br>TCA    | 60.3                             | 721                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12352185  | Ca1                                     | 12352185                      | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATATAT<br>A | GATGATGGCGATTGCA<br>TAGA   | GAATAACGATGCGAG<br>GAGC     | 59.6                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12420239  | Ca1                                     | 12420239                      | CAAAAAAAAA/CAAAAAAAAAA                                        | AAATGCAATCTTGTTT<br>CCA    | TTTTGGTAATGTGCCCA<br>TGATA  | 58.1                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12544202  | Ca1                                     | 12544202                      | TTATATATATATATAT/TTATATATAT<br>ATAT                           | TCGGTGCTCCCTTCA<br>TTTC    | TCATTCAAGGATGCAA<br>CTGG    | 60.1                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12580190  | Ca1                                     | 12580190                      | TAAAAAAAAA/TAAAAAAAAA                                         | TAATCACTCACCATCG<br>CCA    | TTATGTTTGGTGTGG<br>CACT     | 60.1                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_12603890  | Ca1                                     | 12603890                      | GTTTTTTTTTTTT/GTTTTTTTTTT<br>T                                | TTGGTAGCATTGTTTT<br>GGCA | GCATCGGCTCTTTTG<br>CTAC      | 60.1                             | 834                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12644727  | Ca1                                     | 12644727                      | TGTA/TGTACGTA                                                 | TTGATTTTCAATTGGGA<br>GCC | TGCCAGGATGTAACCC<br>TTTC     | 59.9                             | 807                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12644922  | Ca1                                     | 12644922                      | AC/A                                                          | ACCCAACCGCAAAAC<br>AATA  | TGCCAGGATGTAACCC<br>TTTC     | 60.2                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12690899  | Ca1                                     | 12690899                      | TAAATAAATAAATAAATAA/TTAAAT<br>AAATAAATAAATAAATAA              | TGCTTCATACCAACGTT<br>CCA | CAGAGTTTTAAACGTAT<br>GACGGTG | 60.1                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12699932  | Ca1                                     | 12699932                      | ACCCC/ACCC                                                    | ACCGAATGTCGAATC<br>AAGG  | TTGGGAAC TTGGGAGA<br>CTTG    | 60.1                             | 768                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12766880  | Ca1                                     | 12766880                      | ATTTTT/ATTTT                                                  | TTTTCTGCAGCATTGC<br>ATTC | AGTTGGGTGCTTG TAG<br>CGAT    | 60.0                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12772337  | Ca1                                     | 12772337                      | TAAAA/TAAAA                                                   | GGAAGATGAGTGGGG<br>ATCAA | TTAATTTGGTCTTCCCG<br>GTG     | 59.9                             | 183                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12773945  | Ca1                                     | 12773945                      | GCATGCAT/GCATGCATCATGCAT                                      | GAAGCAGCCTCAACCT<br>CAAC | GAAAGGTGGAGATTGG<br>TTGG     | 60.0                             | 150                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12776177  | Ca1                                     | 12776177                      | T/TC                                                          | ATCTCCCGTCAGATA<br>TCCC  | GACAATAACCAACCCAG<br>TGCC    | 60.1                             | 225                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12783589  | Ca1                                     | 12783589                      | TAGAAACAGAAACAGAA/TAGAAACA<br>GAA                             | GCCACACAAAAGGAA<br>GGAA  | ACAATGTGGCCTCCTT<br>GAAC     | 60.1                             | 287                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_12791859  | Ca1                                     | 12791859                      | GAT/GATCTGCAT                                                 | TGTAAGATGCACGCC<br>ATAA     | TGCAAGATGATCAACG<br>TGAG  | 60.0                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12947634  | Ca1                                     | 12947634                      | ATAAATTTAAA/ATAAATTTAAAATT<br>AAATTTAAA                       | AACTTTGTGGTCGTTTT<br>GGC    | TGCTTATTGTGGCTGC<br>TTTG  | 60.0                             | 647                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12950561  | Ca1                                     | 12950561                      | T/TC                                                          | CAAGCATGCAGCAAAA<br>AGAA    | GCGGTGCCAGTGAAAT<br>AAAT  | 60.1                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12956191  | Ca1                                     | 12956191                      | ATCTC/A                                                       | TGCTAACCCAACACAA<br>TTTCT   | GTCAGATGTTTGGGCG<br>ATTT  | 57.3                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12956423  | Ca1                                     | 12956423                      | CAAAAAA/CAAAAA                                                | TTGTCGGATACCTGCT<br>CAGT    | TTGCAAAATTCGGACAAA<br>CAA | 58.3                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_12988931  | Ca1                                     | 12988931                      | A/ACCGACTTTCGGC                                               | ATCGGCATCCTTCCTT<br>CTTT    | GACGCTAAGCCCCTTT<br>CTCT  | 60.0                             | 354                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_13007507  | Ca1                                     | 13007507                      | TTAT/TTATATAT                                                 | CACGGGTCCAGATGGT<br>TAGT    | CCAAGCATCTTGGTGC<br>ATAA  | 59.8                             | 322                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_13012418  | Ca1                                     | 13012418                      | TCC/TC                                                        | TTGATGAGGATCTTTCT<br>ATGGGA | TGCGATAATATTCATCC<br>CGTG | 59.9                             | 306                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_13399858  | Ca1                                     | 13399858                      | TAAAAGAAATTTGAAAAGAAATTT/<br>AAAAGAAATT                       | TCAACTCCGAGGCCTC<br>TTTA    | GCTCTCAACACTGAAA<br>GCCC  | 59.9                             | 368                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_13487363  | Ca1                                     | 13487363                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA<br>A                            | GATGATTGCAGCAAGT<br>TGGA    | TCGTGTTGGCTAATTCA<br>ACG  | 59.8                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_13578342  | Ca1                                     | 13578342                      | GAAAAAAAAA/GAAAAAAAAA                                         | CCGGCTTGTAGGACGA<br>GTAG     | TCTGTTTTCGAGGGCA<br>CTTT    | 59.9                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1366043   | Ca1                                     | 1366043                       | CTATATATATATATATATATATAT<br>A/CTATATATATATATATATATATATA       | TTTGGGACGAGACGGA<br>TAAC     | CGAATTTTGTCAATCGA<br>ACCA   | 59.9                             | 819                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_13672025  | Ca1                                     | 13672025                      | TA/T                                                          | CCAAATTGAACCTATCA<br>TAAACCA | AAAAGACCAAATCGGG<br>AAAAA   | 59.2                             | 748                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_13680810  | Ca1                                     | 13680810                      | ATTTTT/ATTTT                                                  | TGGTTGAAGTGTGAAC<br>AGGC     | CCAATTTCCCTACCCA<br>AAT     | 59.7                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_13690393  | Ca1                                     | 13690393                      | GAAAAAAAAA/GAAAAAAAAA                                         | GCCTTTGGAAGCATAT<br>CATCA    | GCCGTAGGACTGTTCA<br>TGGT    | 60.1                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_13718939  | Ca1                                     | 13718939                      | AGATGAT/AGAT                                                  | GCCAAAATCTATTGTG<br>GGGT     | TGACTGGGATTCCATT<br>CTG     | 58.8                             | 127                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_13731515  | Ca1                                     | 13731515                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                     | TTTCACTTCCAAACAC<br>CCC      | CTGTCCAGACGGGTTT<br>GTAT    | 59.8                             | 847                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_13748109  | Ca1                                     | 13748109                      | TA/TAGCCATTGTA                                                | ATTCGGGATAAGTGGA<br>ACCC     | TGCAAATGAGATAACC<br>AGCG    | 60.0                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_13753170  | Ca1                                     | 13753170                      | ATCTCTCTCTCTCT/ATCTCTCTC<br>TCTCT                             | CGTGATATATTATTG<br>GCGT      | TTCTTATTAACACCC<br>AATTCAGC | 59.8                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_13800579  | Ca1                                     | 13800579                      | GTTTTTTT/GTTTTTTT                                             | AGGGATAACCTGGTGC<br>TGTG     | TCTTTGAACGATACCG<br>CCTC    | 60.0                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                   | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                 |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_1395879   | Ca1                                     | 1395879                       | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTAT/ATATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTAT | CATTTCTCGTCGAAGA<br>CTTTTG | TGACGGCAATTCGTA<br>TCTTC    | 59.0                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1397435   | Ca1                                     | 1397435                       | CA/C                                                                                                                            | TGGAAACAGCAACGTG<br>GTAG   | CAAAGGGTTGGATTT<br>CCAC     | 59.8                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1408705   | Ca1                                     | 1408705                       | GATATATATATATATATATAT/GATAT<br>ATATATATATATATATAT                                                                               | GGTTTGCTAAGAGGA<br>TGGA    | TGAGTTGGGTTAGAAA<br>TCAACAA | 58.1                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_14309917  | Ca1                                     | 14309917                      | G/GAA                                                                                                                           | AACCATTGGAAGGCAA<br>AATG   | TCTTCCACCTCTTTCGC<br>ATC    | 59.8                             | 106                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_14356029  | Ca1                                     | 14356029                      | CA/CATATATA                                                                                                                     | CACCCACACACACACA<br>CACA   | CATGAACAACCAATATT<br>CCCA   | 61.1                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_14426009  | Ca1                                     | 14426009                      | CATATATATATATATATATATATA<br>TAT/CATATATATATATATATATAT<br>ATATATATAT                                                             | CAGCCAAGACCCAATT<br>TCAT   | ACTCTCCAAAAAGGC<br>GATT     | 59.9                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_14541002  | Ca1                                     | 14541002                      | GATATATATATAT/GATATATATATAT<br>AT                                                                                               | CTAGTTCGTAAGCCGT<br>GCGT   | AGGCATGGTGTGGAG<br>TCAT     | 60.5                             | 259                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_14606001  | Ca1                                     | 14606001                      | TAAAAAAAAA/TAAAAAAAAA                                                                                                           | AATTTGACCAATCCCAA<br>CCA   | CAACACACTATTCCCTT<br>CCTCC  | 60.0                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_14649425  | Ca1                                     | 14649425                      | CAATAATAATAATAATAATAATA<br>ATAATAATAA/CAATAATAATAATA<br>AATAATAATAATAATAATAA                                                    | ATGCATGACACATTCT<br>CCGA   | TTCTTCAACCCATAAC<br>CCA     | 60.1                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_14832487  | Ca1                                     | 14832487                      | TCTTACTTACT/TCTTACT                                                                                                             | TTTTCCAGAAGGAATG<br>GCAG   | TTTTATTATCCGCGGC<br>AAG     | 60.2                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_14891282  | Ca1                                     | 14891282                      | AATATATATATATATATATATATAT<br>AT/AATATATATATATATATATAT         | TCACAAGATAGTTTTC<br>CTTTT    | CAAAATCATCGGAACG<br>ATTACA | 57.2                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_14893455  | Ca1                                     | 14893455                      | GTTTTTTTT/GTTTTTTT                                            | AGGGACAAGGTTGGGT<br>TTTT     | TTAAACTTTGCACGGA<br>GGG    | 59.7                             | 291                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_14995819  | Ca1                                     | 14995819                      | TTGTTATGTTAT/TTGTTATGTTATG<br>TTAT                            | CAGCGCTTTTCCCAA<br>TAAG      | CCAAAAGGGTGGAGA<br>TTGA    | 59.8                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_14995847  | Ca1                                     | 14995847                      | ACATGCATGCA/ACATGCA                                           | CAGCGCTTTTCCCAA<br>TAAG      | CCAAAAGGGTGGAGA<br>TTGA    | 59.8                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_14996344  | Ca1                                     | 14996344                      | CGTGT/CGTGTGT                                                 | TCAATCTCCACCCTTT<br>TGG      | GACATTTAACAGCGCC<br>CATT   | 59.9                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_15037301  | Ca1                                     | 15037301                      | CATATATATATATA/CATATATATA<br>TATATATA                         | GTCACACGAGCATGGA<br>AAGT     | TAACCTGGCCAGTCAC<br>CATT   | 58.7                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_15186134  | Ca1                                     | 15186134                      | AATATATATATATATATAT/AATAT<br>ATATATATATATATAT                 | AGTGGCCCACGAGTAA<br>GATG     | CCACAGCACTCTTCTG<br>TCCA   | 60.1                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_15188200  | Ca1                                     | 15188200                      | TTATATATATATATAT/TTATATAT<br>ATATATAT                         | TCAGCCAAACCACAAT<br>TTGA     | TCCTAGTGCGAGGTCG<br>TTTT   | 60.1                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_15188491  | Ca1                                     | 15188491                      | TTAATAATAATAA/TTAATAATAA<br>TAA                               | AAAACGACCTCGCACT<br>AGGA     | CGCTCATGACCTTACT<br>CGAA   | 59.9                             | 408                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_15551966  | Ca1                                     | 15551966                      | AGGGG/AGGG                                                    | TCAATTTTTAAAGTGA<br>GATCAAGC | ACTTGATTGACATGCG<br>CAAA   | 60.0                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3') | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|-------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                             |                         |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_15821162  | Ca1                                     | 15821162                      | ATT/AT                                                                      | GGGGGAATTGGTGAAAGTT     | ATTAAACCAGCCACACAGGC     | 60.0                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_15849587  | Ca1                                     | 15849587                      | AATATATATATATATATATATATATATATATATATATA/AATATATATATATATATATATATATATATATATATA | CCCCATTTTGTCTCTCCA      | ATTCTTGAGGAGCGGTAT       | 59.9                             | 872                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_15922408  | Ca1                                     | 15922408                      | ATTTTTTTTTTTTTTTT/ATTTTTTTTTT                                               | GGGAAAAGGAAGGTCTGAAAC   | TTGGGTGAATTGCTATTGTTG    | 59.9                             | 783                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16077599  | Ca1                                     | 16077599                      | CAAAAAA/CAAAAAA                                                             | GCAACATCGAACCTCAAT      | TTGTCGTTTGAGCATTTAAAAAGT | 59.9                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16092158  | Ca1                                     | 16092158                      | CTATATATATATATATAT/CTATATATATATATATAT                                       | AGCTACGGTGACTCGGTTTG    | CAACATGTCCATGCAGCATAAC   | 60.3                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16118156  | Ca1                                     | 16118156                      | AT/A                                                                        | ATGCCATTTTGAAGACTGCC    | TGGGGGCAGTTACCTCTATT     | 60.1                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16119755  | Ca1                                     | 16119755                      | T/TG                                                                        | CTGCTCCAACCATCGGTACT    | TTCTAAAAGCGTCCCAAGA      | 60.1                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16134448  | Ca1                                     | 16134448                      | TTAT/TT                                                                     | AATTGGGCCACATTTTCTG     | CGATTGATTTTTCGGTTCGT     | 59.8                             | 761                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16156646  | Ca1                                     | 16156646                      | AATATATATATATATATATATATATA/AATATATATATATATATATATATATA                       | GCCAATAGCACCTTTGCTTC    | AAGTGCCATCAAATTTGGCTA    | 59.9                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16160389  | Ca1                                     | 16160389                      | TT/TTCT                                                                     | CATGTGGATTGTCTTGGCG     | GCACAAGATCCTCAAAACTGG    | 60.1                             | 238                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_16161515  | Ca1                                     | 16161515                      | GC/G                                                          | GGGGCTTTACGTATAC<br>AACCG  | GGAATGAAAAGCCATG<br>AGGA      | 60.6                             | 253                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16176422  | Ca1                                     | 16176422                      | AAAAATATAATATAAA/AAAAATATAAA                                  | CCGTTTGATGGACATG<br>ATAAGA | ACCCTTGTGTAAAATCA<br>TAAACATT | 59.8                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16189552  | Ca1                                     | 16189552                      | C/CATTTCGA                                                    | GGGAGAAAAGTCCTCGT<br>AGGG  | TGTACGGATTGAGGTG<br>AGGA      | 60.1                             | 284                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16198179  | Ca1                                     | 16198179                      | TAAAAA/TAAAAA                                                 | AAATTTTGTGTGGTTGCC<br>TCC  | TAGCGATATCGATCAA<br>GCCC      | 58.9                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16206365  | Ca1                                     | 16206365                      | AA/AATTA                                                      | CTCGCAAGTTGTAGGT<br>TCAATC | GGGGCTTACGAGTACA<br>GACTCA    | 58.9                             | 128                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16206852  | Ca1                                     | 16206852                      | ATATTAT/ATAT                                                  | GAGTCTGTACTCGTAA<br>GCCCT  | ATTTTGACAATGGCCA<br>CACA      | 58.9                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16207830  | Ca1                                     | 16207830                      | ATTTTT/ATTTTTT                                                | CAACGCCCAACAACATA<br>ATCA  | GAGAGGGTCTTGAGTG<br>TCGC      | 59.6                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16208160  | Ca1                                     | 16208160                      | T/TA                                                          | TTGCGACGACCACAAA<br>ATAA   | GCAGCATTTCCAAGTG<br>TGGT      | 60.1                             | 245                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16210891  | Ca1                                     | 16210891                      | TA/T                                                          | CCAAGGTGGGAAAACA<br>CTTG   | GCCTCTTCCAGCTGTT<br>TGTT      | 60.4                             | 280                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16216789  | Ca1                                     | 16216789                      | TTTATTATTATTATTATTATA/TTTA<br>TTATTATTATTATA                  | ACTCTGTCTTGGGCT<br>CCAC    | AGCATGATGTGGGCAA<br>TTTT      | 60.1                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                     |                             |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_16259144  | Ca1                                     | 16259144                      | GATATATATATATATATATA/GATA<br>TATATATATATATATA                       | AAGTGTTTTGGGGAGA<br>TGAGAA  | CGTGAACTCCTAAAG<br>CCTG       | 60.0                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16308001  | Ca1                                     | 16308001                      | ATTTTT/ATTTTTTT                                                     | TTCGGGCTTAATGAGT<br>TTGG    | GAAGCACCTTCTGGCA<br>GTTC      | 60.1                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16442399  | Ca1                                     | 16442399                      | TATT/TATTAATT                                                       | AGTGTGTAACCTGTCG<br>GTCC    | AAAAAGTGGTGTTGGA<br>TGCC      | 60.0                             | 259                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16584419  | Ca1                                     | 16584419                      | AG/A                                                                | GGTGCAACCAATTGAG<br>TCCT    | AGGAATGGATCCGGAG<br>ATTT      | 60.0                             | 481                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16629521  | Ca1                                     | 16629521                      | TTTAATTAATTAATTAATT/TTTAATT<br>AATTAATTAATTAATTAATT                 | AACGTTTGAGGATTCC<br>GTTG    | GAACTCCAGCTCCAA<br>AACG       | 60.0                             | 370                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16751256  | Ca1                                     | 16751256                      | ATTTTTTTTTTTTT/ATTTTTTTTTTT<br>TT                                   | GTCAACATCAGGGACG<br>GACT    | CTAGGCCTGACCTTGA<br>CCTG      | 60.0                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16757631  | Ca1                                     | 16757631                      | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>ATATATATA | GATTCAAGACGAGACG<br>CAAA    | AAAAATGTTTTCAATA<br>AGCAAAATC | 59.0                             | 562                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16777733  | Ca1                                     | 16777733                      | ATTTTTTTTT/ATTTTTTTT                                                | GAGTGACAATTTGTG<br>CGGA     | TGGAGGAACTTAGCC<br>CTCA       | 59.7                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16835364  | Ca1                                     | 16835364                      | TG/TGG                                                              | CGACAACGCATGATCA<br>AATC    | ATTTGGCGAAGCTTTTC<br>AAC      | 60.1                             | 652                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_16836777  | Ca1                                     | 16836777                      | GTATAT/GTAT                                                         | TTAAATGAATACTCCA<br>TTCGTCA | ACATAGGCGCACATGA<br>TTGA      | 57.8                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                       | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                     |                           |                             |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_16982792  | Ca1                                     | 16982792                      | CAAAAAA/CAAAAAAAAAAAAA                                                              | GCATCAACAATACGCC<br>ACAC  | CCCCATGGAAACCTTA<br>ACTT    | 60.0                             | 316                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_1706990   | Ca1                                     | 1706990                       | TATAATAATA/TATAATAATAATA                                                            | AATGGTATGGTTGCTG<br>CATT  | TGCGATGGTGTATTGA<br>GAGC    | 58.0                             | 570                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_17107416  | Ca1                                     | 17107416                      | AATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATATA<br>TATATATATATATATAT       | GCTTTTCTCACCTCTC<br>CCCT  | TCCAAACCATGCTGTA<br>GAGG    | 59.8                             | 495                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_17158043  | Ca1                                     | 17158043                      | A/AAGCAATT                                                                          | TGATGTTGATCCAGTT<br>CGGA  | CCTCCAATCACCATG<br>AAGG     | 60.0                             | 643                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_17185713  | Ca1                                     | 17185713                      | TTTGATATTGATTAT/TTTGATATT<br>GATTATTGATTTGATTAT                                     | GCGTTAAAGTTGAAA<br>CCCA   | TGACGTGACATCGAGA<br>GTCTG   | 60.0                             | 594                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_17187364  | Ca1                                     | 17187364                      | AA/AATTTATA                                                                         | CAACAACCTCTCATTCT<br>CGCA | TGTTGCTACAAAATGA<br>ATTGACA | 59.1                             | 966                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_17215249  | Ca1                                     | 17215249                      | ATT/AT                                                                              | GGTTGGGTTGAGGAG<br>GAAAT  | TGTGAACGAACACCTT<br>CGAC    | 60.2                             | 447                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_17234877  | Ca1                                     | 17234877                      | AT/A                                                                                | CCCTATAGGCCCACTA<br>AGCC  | ACCCCAAAAGAGAAAG<br>CACA    | 59.9                             | 695                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_17242129  | Ca1                                     | 17242129                      | GATATATATATATATATATATATA<br>TATATATATATA/GATATATATATATA<br>TATATATATATATATATA       | TACGAACCCTCACAA<br>CACA   | AAAAATTTGGGCGTT<br>ACAC     | 60.0                             | 856                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_17275483  | Ca1                                     | 17275483                      | AATATATATATATATATATATATAT<br>ATATATATATATATATAT/AATATATA<br>TATATATATATATATATATATAT | TGTGTGTAGGACGGAT<br>CCAA  | CAATACTCTCTGCAG<br>TGGTTT   | 60.0                             | 503                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                       |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_17436816  | Ca1                                     | 17436816                      | A/AC                                                                  | GACGAAAAGATCACCC<br>TCACA | CATGTGCCACAGGATC<br>ATTC  | 60.1                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_17507058  | Ca1                                     | 17507058                      | CAAAAAAAAA/CAAAAAAAAA                                                 | AAATTGGACAGCAAAA<br>TCGG  | GGCAACAAGCACCAGT<br>GTTA  | 59.9                             | 231                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_17566974  | Ca1                                     | 17566974                      | ATTTTT/ATTTTT                                                         | TAATAGCGACCAACCA<br>AGGG  | TGATGCGGTATACGAT<br>TTCAT | 60.0                             | 754                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_17624683  | Ca1                                     | 17624683                      | AATATATATATATATATATATATAT<br>ATATATAT/AATATATATATATATATA<br>TATATATAT | ATACACCTCACTTCGG<br>CCAC  | TCACTGCTCTGCATCC<br>ATTC  | 60.0                             | 239                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_17633701  | Ca1                                     | 17633701                      | CAAA/CAA                                                              | TGCGCCGAAAGTTCTT<br>TACT  | ATTTTGTGGAAAAATG<br>CGG   | 60.0                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_17634013  | Ca1                                     | 17634013                      | TTATATATATATATATAT/TTATATAT<br>ATATATATATAT                           | TGATTGGATGTGGGTG<br>TGAG  | TTCAAAGGCAACAAC<br>CCTC   | 60.4                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1777586   | Ca1                                     | 1777586                       | AGATGATGATGATGATGATGA/AGA<br>TGATGATGATGATGATGATGA                    | CGTCACAAAGCATCAC<br>AGGT  | CTACGGTGCAAACAGA<br>ACCA  | 59.8                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1777834   | Ca1                                     | 1777834                       | CTCT/CTCTATCT                                                         | CGTCACAAAGCATCAC<br>AGGT  | ATTGCACAACGGCTAC<br>AACA  | 59.8                             | 906                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1778696   | Ca1                                     | 1778696                       | TATAATA/TATA                                                          | AGGGTATTTGTGGCTG<br>CAAG  | TCGATGCCAAATGGAG<br>TGTA  | 60.1                             | 237                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1780243   | Ca1                                     | 1780243                       | ATTATTTATT/ATTATTTATTTATT                                             | GAGTGAAAGGACGATA<br>GCACG | TAAAAGGTGCGATTTC<br>GGTT  | 59.9                             | 942                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                 |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_17811471  | Ca1                                     | 17811471                      | CTATATATATATATATATAT/CTAT<br>ATATATATATATATATATAT               | AGGAAAATGGATTGGC<br>AGAA     | TGCTGCTTCCTTAAG<br>CCG     | 59.5                             | 186                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_17812819  | Ca1                                     | 17812819                      | AT/ATT                                                          | CACCGCACGGAATTCT<br>AATC     | GCAATGCCATTTC AATT<br>TCT  | 60.5                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_17816780  | Ca1                                     | 17816780                      | TCC/TC                                                          | TGGCCATCAAGTGCT<br>TCTC      | TTCCAGTCCTCTGAT<br>GCC     | 58.8                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_17920630  | Ca1                                     | 17920630                      | CATATATATATATATATATATA/<br>CATATATATATATATATATATA               | CCAAAAATCAAAGGG<br>TGGA      | TTTCTTCTTCTGCTCC<br>CCA    | 59.8                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_18054297  | Ca1                                     | 18054297                      | GAAAAAAAA/GAAAAAAAA                                             | GTTTTCTGCGTAAT<br>GCGT       | TTTCATCATATCGTTC<br>ACCTTT | 60.1                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_18088     | Ca1                                     | 18088                         | TA/TAA                                                          | CCGCTTGTTTTCTTTG<br>CAG      | TTGATTGCTTGTGCTC<br>CAG    | 60.9                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_18181716  | Ca1                                     | 18181716                      | AATATATATATATATATATATAT<br>A/AATATATATATATATATATAT<br>ATATATATA | CGAATACTCATGGTTTT<br>TGATCTG | ACCCACGTCAGCACGT<br>TACC   | 59.9                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1822026   | Ca1                                     | 1822026                       | TC/T                                                            | ATGTTTGGGGCTATCG<br>ACTG     | GAGGAATTTGCTCTC<br>GTGC    | 60.0                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1822426   | Ca1                                     | 1822426                       | TG/T                                                            | TGTGCACGAGAGCAAA<br>ATTG     | TCTTCATGGGCTGAAA<br>AAGC   | 60.0                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1822473   | Ca1                                     | 1822473                       | AG/A                                                            | TGTGCACGAGAGCAAA<br>ATTG     | TCTTCATGGGCTGAAA<br>AAGC   | 60.0                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_18298376  | Ca1                                     | 18298376                      | CAAA/CAA                                                      | GGTAATGCCTCGTACA<br>AAACAA    | CATTCTTATGCCTCCT<br>ACACC | 59.1                             | 751                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_18299880  | Ca1                                     | 18299880                      | TTCCTATCCTATCC/TTCCTATCC                                      | TGGATCACTCACCTCT<br>CTTCC     | TGGAAGTGGTGGTTTT<br>GTTG  | 59.2                             | 185                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_18300620  | Ca1                                     | 18300620                      | GTTTTTTTT/GTTTTTTT                                            | TTTCCATGAGTTATATT<br>TGTCACGA | TGGCCTTCAATTTCTT<br>GCT   | 59.8                             | 134                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_18300800  | Ca1                                     | 18300800                      | ATTT/ATT                                                      | AGCAAGAAAATTGAAG<br>GCCA      | GGAAGCTTTAAAGGGA<br>GCAAA | 59.8                             | 161                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_18317638  | Ca1                                     | 18317638                      | T/TG                                                          | TCATTTTCAACCCTTAG<br>CAACA    | TGTAAGGTATACGCG<br>GGAG   | 59.6                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_18319296  | Ca1                                     | 18319296                      | T/TTAATAGATCACTC                                              | CCCTTGAGTTTCATAG<br>TCACCA    | CGATCGACAGGAAGAG<br>GAAG  | 59.1                             | 159                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_18325896  | Ca1                                     | 18325896                      | TC/T                                                          | ATTGAAAACATGGCTTT<br>GGC      | TTTTGGAGGAACTACG<br>GCAC  | 59.9                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_18327589  | Ca1                                     | 18327589                      | ATTTTTTT/ATTTTTTTT                                            | TTCAAAAATGACACAA<br>CGG       | TCCTAAGGGCTTTCTTT<br>TGG  | 58.0                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_18328227  | Ca1                                     | 18328227                      | GTCTATCT/GTCT                                                 | TTAAAACCAAAAATGG<br>GGC       | GAGGCAAAGCTTCCAA<br>ATCA  | 59.7                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_18328327  | Ca1                                     | 18328327                      | TATTATTCAT/TAT                                                | TTAAAACCAAAAATGG<br>GGC       | GAGGCAAAGCTTCCAA<br>ATCA  | 59.7                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_1835247   | Ca1                                     | 1835247                       | ATGAC/A                                                       | TCATAAGCCAGAACCC<br>AAGC  | GGTGGTGGAGATTCCA<br>AGAA   | 60.2                             | 448                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_18364053  | Ca1                                     | 18364053                      | GAAA/GAAAA                                                    | CCCGTAGCAAGACTTG<br>AAGC  | TTGGAGAACTTTTCC<br>GCTG    | 60.0                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1836414   | Ca1                                     | 1836414                       | ATTTTTTTTTTTTT/ATTTTTTTTT                                     | AAACCCTAAGGCCCAA<br>GAAA  | CGTGAAACGGTATGCA<br>AATG   | 59.9                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1836769   | Ca1                                     | 1836769                       | ATTT/ATTTT                                                    | CATTTCATACCGTTTC<br>ACG   | TTTGAGTTACGAATTG<br>ACGAAA | 60.0                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_18407793  | Ca1                                     | 18407793                      | A/ACCGGGAGG                                                   | GGCAAGGTGAGAGAAC<br>AAGC  | ATTTCTGGTTTTGGCA<br>GTGG   | 60.0                             | 162                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1841034   | Ca1                                     | 1841034                       | TTTCTTCT/TTTCT                                                | TCAAGGTGTTGATTCT<br>GTAGG | TTTTGCAACCCGGTCT<br>ATTC   | 60.0                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1841424   | Ca1                                     | 1841424                       | A/AT                                                          | GAATAGACCGGGTTGC<br>AAAA  | CCTCTTCCGGACAAC<br>ACAT    | 59.9                             | 302                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_18441371  | Ca1                                     | 18441371                      | CACAAGAGAC/CAC                                                | CCCTCTGTATGCCAGT<br>CGAT  | TGGCATTGATGATGGC<br>TTTA   | 60.1                             | 771                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1845260   | Ca1                                     | 1845260                       | GATCAT/GAT                                                    | ACATTGTTCAATTGCAG<br>CCA  | GGTGTGTCTTCGCCGT<br>TTAT   | 60.1                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1846453   | Ca1                                     | 1846453                       | AATATATATA/AATATATA                                           | TGTGGCTAAAAAGTGC<br>AGGA  | TATGGGGAAAGTCCCA<br>TTGA   | 59.5                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_1852604   | Ca1                                     | 1852604                       | TA/TAA                                                        | ACACGCGTTCATTTT<br>CTTC   | CAAACCATGGGAGAGA<br>GAGC   | 60.1                             | 843                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_18552012  | Ca1                                     | 18552012                      | ATTTTTTTT/ATTTTTTTTT                                          | TCTGATGCAGTGTTTG<br>GCTC  | GCTTCTTTGTCTGCCT<br>TGG    | 60.0                             | 331                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_18688865  | Ca1                                     | 18688865                      | TTGT/TT                                                       | TAGCAGCTGGAGGAAC<br>ATGA  | GCACCCAGTGTAAAGAC<br>CCAT  | 59.5                             | 301                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_1876420   | Ca1                                     | 1876420                       | AT/ATACGTAGTTCGGTTGAGT                                        | CGGGTCTTCAAATGG<br>AATG   | CAAAGGAAACGTGCTT<br>CCAG   | 60.3                             | 861                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_1882571   | Ca1                                     | 1882571                       | TC/T                                                          | ATATCGTTTTTACACC<br>CGC   | GGTGCAAATGCAAGAG<br>TCAA   | 59.8                             | 282                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_18868658  | Ca1                                     | 18868658                      | CGG/CGGGAATGG                                                 | AATCGATTGATTCAGC<br>CCAG  | CGTTTTTCAAAGCGAG<br>GGTA   | 60.0                             | 707                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_18868716  | Ca1                                     | 18868716                      | AT/ATT                                                        | AATCGATTGATTCAGC<br>CCAG  | CGTTTTTCAAAGCGAG<br>GGTA   | 60.0                             | 707                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_18873     | Ca1                                     | 18873                         | AAAAAAAAAAAAAAAAA/GAAAAA<br>AAAAA                             | CAGAACCGAGGAATTA<br>AGCG  | GTTTCATGTTGTGTGCG<br>GAAT  | 59.8                             | 133                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_19093958  | Ca1                                     | 19093958                      | GTTATTATTATTATTATTATTAT/<br>GTTATTATTATTATTATTATTATT<br>AT    | ATGCTAGGTCGTTTCGT<br>CAGG | AGTATGGCATGGCCTG<br>AAAG   | 60.3                             | 510                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_1914068   | Ca1                                     | 1914068                       | AC/A                                                          | GCCACATCATTATTTGA<br>GCG  | TGGTTGAGTGGTGTTA<br>ATTGTG | 59.1                             | 666                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_19150973  | Ca1                                     | 19150973                      | CTT/CT                                                        | AACTAGCCCGTCTTTG<br>GGTT      | GAAAACAAAAGCTTTAC<br>GGTCA    | 60.0                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1915229   | Ca1                                     | 1915229                       | CTCAT/CTCATCTGTTTCAT                                          | TGGATACACAAAAACC<br>GAACA     | CACCTTTTCCATCCATC<br>GAC      | 58.9                             | 709                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_19168     | Ca1                                     | 19168                         | GCTCTCT/GCTCT                                                 | CAGAACCGAGGAATTA<br>AGCG      | AGGCTTGAAGCGTGGT<br>AATG      | 59.8                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1930262   | Ca1                                     | 1930262                       | ATTTTTTTT/ATTTTTTTTTT                                         | GGCAACATTTTACAAA<br>GTTAAGG   | AGTTTGATTAATGTCGG<br>GCG      | 58.3                             | 318                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_19308411  | Ca1                                     | 19308411                      | TATTAAGATTAAAGATT/TATTAAGATTAAAGATTAAAGATTAAAGATT             | GCGAGCATGAGAAGTT<br>GTTG      | TCCTCCTTACCATTATA<br>TGATTCCA | 59.6                             | 337                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_19422873  | Ca1                                     | 19422873                      | CTTATTTATTT/CTTATTT                                           | GCCCATAACCTAGCCC<br>ATT       | TCGTGTCCCAAACTC<br>AATG       | 60.2                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_19423044  | Ca1                                     | 19423044                      | TAAAAAAA/TAAAAAAA                                             | TCCTTGAGTTGTAGG<br>ATACAAGTGG | TCGATTATGCGTAGGG<br>AAGG      | 60.0                             | 728                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_19431535  | Ca1                                     | 19431535                      | TCA/T                                                         | TCTGATGCAGTGTG<br>GCTC        | GTGATAAAGGCGTCAA<br>CGGT      | 60.0                             | 688                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1944303   | Ca1                                     | 1944303                       | CCAGCATCG/C                                                   | CCCTCCTTCTCTCATT<br>CCT       | AAGACAATGTGGCTCT<br>TGGC      | 59.6                             | 113                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_19460421  | Ca1                                     | 19460421                      | T/TTCA                                                        | CGTTGCAATTGATGAG<br>GATG      | TTGCTCCTTCTTCTTG<br>TCC       | 60.1                             | 748                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_19498678  | Ca1                                     | 19498678                      | TTTTGATCCTTTGAT/TTTTGAT                                       | GCCCGAGTTAACAACA<br>AACG | ATCGATTTCCTCAGCA<br>CTGG       | 60.5                             | 374                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_19536862  | Ca1                                     | 19536862                      | TCCCC/TCCCCC                                                  | TAGCACCTTCCTCCCA<br>GAAA | CTACCAACAGAAAGGC<br>CCAA       | 59.8                             | 352                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_19631803  | Ca1                                     | 19631803                      | CATATATATATATATATATAT/CAT<br>ATATATATATATATATATATATATA<br>T   | ATATTCGCAACGCGTA<br>TGTT | AAATGTGGCAAATTGG<br>GACT       | 58.2                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_19661120  | Ca1                                     | 19661120                      | TATATAAAT/TAT                                                 | GGCCATCACAAATGGG<br>TAAG | AAGGGCCATAAGTAGG<br>CCAG       | 60.2                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_19694253  | Ca1                                     | 19694253                      | TATATAGATATA/TATATA                                           | ATGTTTTGAATTGGCC<br>TCG  | CGAAAGACGAAAATGG<br>AGGA       | 59.9                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1970052   | Ca1                                     | 1970052                       | TTTAATTATATTAATTATA/TTTAATT<br>ATA                            | CGGATTTGGGCAGTGA<br>TATT | TTCGAATTTCCCGTAC<br>CTG        | 59.8                             | 266                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_19710704  | Ca1                                     | 19710704                      | ATTTTTTTT/ATTTTTTT                                            | GACTTTGCAAGGCCTG<br>AGTC | AGGCTTGACAGACCGA<br>CCTA       | 60.0                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1971572   | Ca1                                     | 1971572                       | AA/AAGAAATGCA                                                 | ATGTGCATCACCTCTG<br>ACGA | GCTGCCATGGAGGTAG<br>TCAT       | 60.3                             | 807                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1972044   | Ca1                                     | 1972044                       | ACTTCTTCT/ACTTCTTCTCT                                         | GCCCTCAGCCTCACTT<br>TATG | AGGGAGGCTACGAACG<br>ATTT       | 59.8                             | 356                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1981443   | Ca1                                     | 1981443                       | G/GA                                                          | GGGTGACATGTGGACC<br>ATCT | TCAAGAATCAAAATGAT<br>ACTGTCAAA | 60.7                             | 919                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_19855108  | Ca1                                     | 19855108                      | TTTTATTTATTTATTTATTTATTT/TTT<br>TATTTATTTATTTATTTATTTATTT     | TTGTTGTGCAATTTAA<br>GCGA    | CAAAAGCTTGCAATTTT<br>GATTTT   | 59.4                             | 786                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1989852   | Ca1                                     | 1989852                       | AAA/AAATAA                                                    | TTGGGCTTATTGGGTC<br>ACTC    | TATCCAATCCCAACCCA<br>AAA      | 59.9                             | 115                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_19941125  | Ca1                                     | 19941125                      | CAAAAAAAAA/CAAAAAAAAAAA<br>AA                                 | CGGGAAACAGGGGTTT<br>AACT    | AAGGAGAGCATGATAT<br>ATTTTGTA  | 60.2                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1998915   | Ca1                                     | 1998915                       | T/TTATAAAATGA                                                 | TGCTTGTTTCACCACTT<br>TGC    | CGACCGATATTCGTCC<br>ACTC      | 59.9                             | 481                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_1999397   | Ca1                                     | 1999397                       | AGTGT/AGT                                                     | GACGAATATCGGTGCA<br>ATACAA  | GTCCAAACATCGGAAA<br>AGGA      | 59.0                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2000025   | Ca1                                     | 2000025                       | TAAAAAAAA/TAAAAA                                              | TCCTTTTCCGATGTTTG<br>GAC    | TTAAGGACGTCGTTGG<br>AAGG      | 59.9                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2057177   | Ca1                                     | 2057177                       | CACCATAA/C                                                    | AATGTGGAAGGACGTT<br>GTCA    | ACGATTCAAAGAAAGT<br>GGCG      | 59.0                             | 448                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2085412   | Ca1                                     | 2085412                       | AAGTTTTAT/AAGTTTTATAGAGTTT<br>TAT                             | TTTTTGGGCTCACACA<br>ATTT    | CAATTGTCCAAAACCTCT<br>TATCCAA | 58.1                             | 723                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2085895   | Ca1                                     | 2085895                       | GAAAAATAAAAA/GAAAAATAAAAA<br>AAAAA                            | TGTTTTTGGATAAGAGT<br>TTTGGA | TCCTCAATCGCGTTCTT<br>TCT      | 57.9                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2088597   | Ca1                                     | 2088597                       | TTTTT/TTTTTTTAAAACTTTT                                        | ACAGCAACCAAGAGTT<br>GTGC    | GCATCCGGCCAAAATA<br>AATA      | 58.9                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_2088953   | Ca1                                     | 2088953                       | ATATTTATTTATTT/ATATTTATTTAT<br>TTATTTATTT                     | GGTAAATTGATGCCAC<br>CTGC     | TTTGCTGCCACCATG<br>ATTA      | 60.3                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2099948   | Ca1                                     | 2099948                       | ATTTTT/ATTTT                                                  | TTGGTATATGTATGAAT<br>GTTGGCA | TGGTGTTAATTAATCTC<br>GTCACTT | 59.2                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2113146   | Ca1                                     | 2113146                       | TAAAAAAAAA/TAAAAAAAAA                                         | TGTGGACACGTTAAGT<br>TGTGG    | TGATCTCGCCCTATTAT<br>TCAAAA  | 59.5                             | 409                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2115049   | Ca1                                     | 2115049                       | TAAAAAAAAA/TAAAAAAAAA                                         | TGGACTAAAATTGCTTT<br>TTGGAA  | TTAGAAAGAGCCACAC<br>GCAA     | 60.0                             | 897                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2116565   | Ca1                                     | 2116565                       | TT/TTGT                                                       | TTGCGTTCATTTACGTT<br>TGA     | TCAATTCACCTTCATGCC<br>CAA    | 57.8                             | 636                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2120541   | Ca1                                     | 2120541                       | AATTAT/AAT                                                    | TGTATGGAAAGAGGTA<br>AAATGGAA | AACGACAAATGTTGCC<br>ATGA     | 59.0                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2129116   | Ca1                                     | 2129116                       | GAAAA/GAAAAA                                                  | CAAGCAGAGAGAAAA<br>CGGG      | ATAGTGGACCCACAA<br>TCCA      | 60.0                             | 379                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2131188   | Ca1                                     | 2131188                       | AT/A                                                          | TGCTATTCATCCACAA<br>GCA      | CTTGATTGCATGCATT<br>CCT      | 60.2                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2131678   | Ca1                                     | 2131678                       | TAT/TATTGAT                                                   | AGGAATGCATCGAATC<br>CAAG     | CCACAAGTGCCATTCA<br>GCTA     | 60.0                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2131832   | Ca1                                     | 2131832                       | CTTT/CTTTT                                                    | AGGAATGCATCGAATC<br>CAAG     | CCACAAGTGCCATTCA<br>GCTA     | 60.0                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_2132012   | Ca1                                     | 2132012                       | CTG/CTGTG                                                     | AGGAATGCATCGAATC<br>CAAG | AATGACCAACCCACAA<br>GTGC   | 60.0                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2135161   | Ca1                                     | 2135161                       | AGTGTG/AGTGTGTG                                               | AGAATTTACTCCACGT<br>CCCG | TGAACCTCGTGCATGT<br>AATTCT | 59.1                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_21653919  | Ca1                                     | 21653919                      | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATATA<br>T   | GCTTGCAAAACAGATG<br>CAGA | ACGAAACGAAAGCGAG<br>AAAA   | 60.1                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_21657413  | Ca1                                     | 21657413                      | TTA/T                                                         | TGGAGTACGAGCTTGG<br>GTCT | TGTCTACTGCAGAAGC<br>CGAA   | 59.9                             | 786                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_21845802  | Ca1                                     | 21845802                      | GATATATATATATATATATATA/GATA<br>TATATATATATATATATATA           | GGGTATGAAAGGTTGG<br>GGTT | TCGAGTAATTTGATGG<br>CAGAAA | 59.9                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_22029011  | Ca1                                     | 22029011                      | TTATATATATATATATATATATATA<br>TA/TTATATATATATATATATATA         | CGAATCTTCACCCTCTT<br>TGG | GCCGGATCCAAATCA<br>AAAT    | 59.7                             | 839                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_22067149  | Ca1                                     | 22067149                      | GGCT/GGCTAGCT                                                 | TTCTTTGACGTTCACTC<br>GCG | TAACAAGGGCTTCAAC<br>CACC   | 60.0                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_22100599  | Ca1                                     | 22100599                      | ATATATATATAT/AATTATATATATAT                                   | ATGTGTGAGAAAACCT<br>CGGC | TGTCCAGCTTCATTCAA<br>CCA   | 60.1                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_22131328  | Ca1                                     | 22131328                      | AATATATAT/AATATATATAT                                         | GTGTGGACATGCCTAA<br>AACG | GTTGCAATTGAGGTGC<br>TGAA   | 59.1                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_22131513  | Ca1                                     | 22131513                      | GAAAAA/GAAAA                                                  | GTGTGGACATGCCTAA<br>AACG | GTTGCAATTGAGGTGC<br>TGAA   | 59.1                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_2244855   | Ca1                                     | 2244855                       | AA/AATTA                                                      | TGCATGAGCAATAATG<br>CCTAAA | GGCAATGCCAAAATAT<br>GAGTT | 60.6                             | 158                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2244906   | Ca1                                     | 2244906                       | A/AG                                                          | TGCATGAGCAATAATG<br>CCTAAA | GGCAATGCCAAAATAT<br>GAGTT | 60.6                             | 158                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2245864   | Ca1                                     | 2245864                       | TAAA/TAA                                                      | TGGGACACATAATTTT<br>ACAGG  | TTTTCCCGTGTGTTTT<br>TATG  | 59.7                             | 764                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2247683   | Ca1                                     | 2247683                       | CTATA/CTA                                                     | GATGAAGAGATGGATG<br>GGGA   | TTGACGTTTTCAATGT<br>GCAG  | 59.8                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2254683   | Ca1                                     | 2254683                       | CAAAA/CAAA                                                    | TGCCTTGTTTTAGGC<br>CTTG    | CCAACAATCCTCTCAC<br>CCT   | 60.2                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2256401   | Ca1                                     | 2256401                       | ATT/AT                                                        | CCGCCCCGTAATTAAG<br>ATTT   | TATGTGCCGCCGTAAA<br>TACA  | 60.2                             | 816                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2257787   | Ca1                                     | 2257787                       | AC/A                                                          | TCAAGCGAATCTCTTT<br>TGTGA  | AAATTATGTCGCCAC<br>ACC    | 60.0                             | 356                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2257997   | Ca1                                     | 2257997                       | GATATA/GATATATATA                                             | GGTTGTGGGCGACATA<br>ATTT   | ATTCTTCCACTTGGGC<br>AAAA  | 59.7                             | 230                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2258161   | Ca1                                     | 2258161                       | CATT/CATTGATT                                                 | GGTTGTGGGCGACATA<br>ATTT   | CTCCCTCCTCCTCAA<br>ACTT   | 59.7                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_22621219  | Ca1                                     | 22621219                      | TAAAAAAAAA/TAAAAAAAAA                                         | CATTTTCTCTGCACA<br>ACG     | GCCGTCTTTAGAAAC<br>ATCGT  | 59.3                             | 409                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                         | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                       |                             |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_2264238   | Ca1                                     | 2264238                       | T/TAG                                                                                                 | CAAATGAGTCACCACA<br>TCCG    | TGTGTTTTCTCGTCGAA<br>CCA     | 60.0                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_22737650  | Ca1                                     | 22737650                      | TAAAAA/TAAAA                                                                                          | TTTGCGCCAAAACCAT<br>TTAT    | AAGGGGATGCTCATTT<br>TGTG     | 60.3                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_22885854  | Ca1                                     | 22885854                      | TTA/TTATA                                                                                             | TGATTTGGGGTTTTGG<br>GTAA    | GGGTGAGTTCTTTGAG<br>GGTG     | 60.0                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_22886112  | Ca1                                     | 22886112                      | GAA/GAAA                                                                                              | TGATTTGGGGTTTTGG<br>GTAA    | GGGTGAGTTCTTTGAG<br>GGTG     | 60.0                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_22896758  | Ca1                                     | 22896758                      | CTTTTTTTTTTTTT/CTTTTTTTTT<br>T                                                                        | GCACCGTTTACAACGC<br>TTTT    | GATGAAACCGAGGACC<br>AGAA     | 60.2                             | 400                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23139745  | Ca1                                     | 23139745                      | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATAT<br>A                                            | TTCGGAAAAATTCATCT<br>GCC    | GCAGCGTGACAATGAA<br>CAAC     | 60.0                             | 368                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2315915   | Ca1                                     | 2315915                       | AACGTTACG/AACG                                                                                        | ACCGTCGGAGACAAAA<br>ACAC    | AGCAAACAAGCAAAGC<br>CAAC     | 60.0                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2316762   | Ca1                                     | 2316762                       | CTTTTTTTTTTTTTTTTT/CTTTTTTT<br>TTTT                                                                   | TTGTGGTTGGTGGTGA<br>TGTC    | TGCTGCAAAGTACGAA<br>AGGA     | 60.3                             | 315                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2317093   | Ca1                                     | 2317093                       | TG/T                                                                                                  | TTGTGGTTGGTGGTGA<br>TGTC    | CCTGGGTACATCATAA<br>CATTTTTC | 60.3                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2317888   | Ca1                                     | 2317888                       | TTATATATATATATATATATATATA<br>TATATATATATATATA/TTATATATAT<br>ATATATATATATATATATATATATA<br>TATATATATATA | TTGAGTTAAAAGACCA<br>CTACCCA | GTTTTCATGACGGGGA<br>TGAC     | 57.9                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                   | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                 |                              |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_23192284  | Ca1                                     | 23192284                      | TTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAA/TTAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAA | TTCGAAACTTTTGGCC<br>ACTT     | TTGGATTTTGGCCACAT<br>TTT | 59.7                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23195497  | Ca1                                     | 23195497                      | GTTT/GTTTTT                                                                                                                     | TCAAAATTTTCAAGCAA<br>AACCC   | ATGGTAGTTTCGCCAC<br>TGCT | 60.3                             | 825                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2320237   | Ca1                                     | 2320237                       | GAAGAAAGAAA/GAAGAAA                                                                                                             | TCGTATTTATCCAACAT<br>AATGGGA | ATGAACGGTGTAGCCC<br>TTTG | 59.5                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23222434  | Ca1                                     | 23222434                      | AGTTATGTTATGTTATGTTATGTTAT<br>/AGTTATGTTATGTTATGTTAT                                                                            | CACTCGACAGTTGGGA<br>GGTT     | TCGAGCAACAAAGCAT<br>CAAG | 60.2                             | 423                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23244199  | Ca1                                     | 23244199                      | AAGAGAGAGA/AAGAGAGA                                                                                                             | AAAGCACCCAAATTGT<br>CCAC     | ATGAACCTCTGCGTTT<br>GAGG | 59.8                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23250478  | Ca1                                     | 23250478                      | CAAGAAG/CAAG                                                                                                                    | TTGGTTTCATGACCTG<br>CATC     | CGGCCGTTTCTAACAT<br>CATT | 59.5                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23304825  | Ca1                                     | 23304825                      | CATATATATATATATAT/CATATAT<br>ATATATATATATAT                                                                                     | CCATTACGTGCAACCA<br>GAAA     | TGACCTGCGTCCATAA<br>ATCA | 59.6                             | 928                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23319597  | Ca1                                     | 23319597                      | CAAAAAAAAA/CAAAAAAAAA<br>AAA                                                                                                    | AAAGGCCATGTGATTT<br>TTGC     | GGCAGAGCTTTGGTGT<br>CAAT | 59.9                             | 973                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2332780   | Ca1                                     | 2332780                       | CTT/CT                                                                                                                          | CAAAATGGCACATGC<br>AAAG      | TTCACCAATTCCTGTT<br>TCA  | 60.1                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2332823   | Ca1                                     | 2332823                       | TA/TAA                                                                                                                          | CAAAATGGCACATGC<br>AAAG      | TTCACCAATTCCTGTT<br>TCA  | 60.1                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                               |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_23467419  | Ca1                                     | 23467419                      | CTATATATATATATATATATATATAT/<br>CTATATATATATATATATATATATAT               | CGGGACTTACAACCCA<br>GAAA      | TGGTGTTAGAGTCATG<br>CTTTTGA | 60.0                             | 248                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23492453  | Ca1                                     | 23492453                      | AATATATATATATATATATATATATAT<br>/AATATATATATATATATATATATATA<br>TATATATAT | TGTGTAGCGCCCTTA<br>ACTT       | ACGGTAGCTTTAACGA<br>GCGA    | 59.8                             | 935                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2351691   | Ca1                                     | 2351691                       | ATTTT/ATTT                                                              | CGACGAAGCAAAATCA<br>AAGC      | GAAAAAGGTTGGATGA<br>ATTTGTT | 60.9                             | 171                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23565928  | Ca1                                     | 23565928                      | AA/AACATCATATTA                                                         | GCGGTTAAGCCAATTT<br>TGAG      | TGGTGTAACGAGCATC<br>AACAA   | 59.7                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23569757  | Ca1                                     | 23569757                      | AT/ATTATT                                                               | CGTTTGCTTTGAGAGA<br>TTTGTG    | CAAAATTGGCGCACTT<br>TGAA    | 59.9                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23571644  | Ca1                                     | 23571644                      | AA/AAGTCTTCCGATCTTTTGA                                                  | TGTGTTGGCTTAAAC<br>ATTTGAT    | GGGCAATGTTGGTGGT<br>ACTC    | 58.6                             | 810                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23613804  | Ca1                                     | 23613804                      | CTCTTTCTTTCTTTCTTTCTTTCTTT<br>CTTT/CTCTTTCTTTCTTTCTTTCTTT<br>CTTT       | CCTAATCTTGCATGGG<br>GAAA      | CCCGAGGAAGAATCCA<br>ATTT    | 59.9                             | 402                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23622145  | Ca1                                     | 23622145                      | CTTTTTTTTT/CTTTTTTTTT                                                   | ACGATGAAGGTGGAAG<br>ATGG      | TTGCAACTTTGATAACG<br>AAAACA | 59.9                             | 767                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_236262    | Ca1                                     | 236262                        | TAAAAA/TAAAAA                                                           | TGAAAGAACAATATCC<br>ACTAAACCA | GCAGCAATTGATGGTG<br>TGAT    | 60.2                             | 129                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23637540  | Ca1                                     | 23637540                      | TTA/TTAATA                                                              | TTCATCACCTCTCCAA<br>ACC       | AATCAGGGCAGACGAC<br>AATC    | 59.9                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_23784964  | Ca1                                     | 23784964                      | ATTTTTTTT/ATTTTTT                                                       | GTCAACCAATTGACCC<br>CAAC  | TGCCAAGAAAACACCA<br>TGAA   | 60.1                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2379049   | Ca1                                     | 2379049                       | T/TCA                                                                   | AACCCAAAAACAGAAA<br>CCCC  | TTTGCTTGCAAAGCCTT<br>TTT   | 60.1                             | 129                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23838777  | Ca1                                     | 23838777                      | ATGTGTGTGTGT/ATGTGTGT                                                   | AATGCCCAACCATAAT<br>TTCA  | TGTACGAGAAGGTCGT<br>GTGC   | 60.0                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23892469  | Ca1                                     | 23892469                      | TA/TAAA                                                                 | CGTGCATACCCATAC<br>ACAA   | GGTGCAGTTGTCGTC<br>AGAA    | 60.3                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_23966814  | Ca1                                     | 23966814                      | GA/GAA                                                                  | AACTGTGGAGGAATCC<br>ATGC  | GCTTCAAGTCTTGCTA<br>CGGG   | 59.9                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2405906   | Ca1                                     | 2405906                       | T/TCAAATAAACC                                                           | TCTAAAGGGATTGCGA<br>CGTT  | CCAAATTCAGTGTTTGC<br>GTG   | 59.7                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2407002   | Ca1                                     | 2407002                       | ATTT/ATTTT                                                              | CACTTGCACATTCATG<br>CAGTT | ACAAAAATGGGTCCTT<br>CCTT   | 59.8                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_24079570  | Ca1                                     | 24079570                      | AATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>ATATATATATATATA | CGAAGCCTTTGGTTTC<br>ATTT  | GGAAAAATAAAATTGG<br>GGAACA | 59.2                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2409275   | Ca1                                     | 2409275                       | TA/T                                                                    | GCATATGCCCAAGTTT<br>TGGT  | CTAGGCTCTGAACCGG<br>TAAAA  | 59.8                             | 188                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_24104335  | Ca1                                     | 24104335                      | CGG/CG                                                                  | TCAAACAAGCGTAATC<br>AACCC | CCCTGGAGCTTTTAGA<br>GCCT   | 60.0                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                      | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                    |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_24109260  | Ca1                                     | 24109260                      | CTTTTTTTTTTT/CTTTTTTTTTTTTT                                                        | TTGGGGGAACCGGAT<br>AAAT   | CCCTGCTTAAGGCACA<br>TGAT | 60.4                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2411747   | Ca1                                     | 2411747                       | T/TA                                                                               | TGTGTCTTGTGGGGA<br>AACA   | TGACGCTTTTGAAGCA<br>GTTG | 60.0                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2412470   | Ca1                                     | 2412470                       | AATATAT/AATATATAT                                                                  | AGGACAATAGGACGAG<br>GCAA  | AGTCACAGAGCATGCA<br>CCAC | 59.7                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2412541   | Ca1                                     | 2412541                       | TTTATTA/TTTA                                                                       | AGGACAATAGGACGAG<br>GCAA  | AGTCACAGAGCATGCA<br>CCAC | 59.7                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2415241   | Ca1                                     | 2415241                       | CA/CAGA                                                                            | TATATAGGTGGTGCCC<br>GGTG  | CCCCTCTCACAACAA<br>GGCA  | 60.6                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2416072   | Ca1                                     | 2416072                       | AAA/AAACAA                                                                         | TATTTGCCATGCATCAA<br>GGA  | CCAACTTCATGGTGTC<br>ATCC | 60.0                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2416287   | Ca1                                     | 2416287                       | T/TA                                                                               | TTGCACATTGGTACCC<br>AAAA  | TAGCCTTTTTGTTGGTT<br>GGC | 59.8                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2416502   | Ca1                                     | 2416502                       | GA/G                                                                               | CAAAATCAGTCGCATG<br>TTGG  | TAGCCTTTTTGTTGGTT<br>GGC | 60.1                             | 248                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2416894   | Ca1                                     | 2416894                       | T/TC                                                                               | GCCAACCAACAAAAAG<br>GCTA  | ACAGTCCAAAACCCGA<br>AGTG | 60.1                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_24220141  | Ca1                                     | 24220141                      | TTAATTAATAATTAATAATTAATAATT<br>AATAAT/TTAATTAATAATTAATAATT<br>AATAATTAATAATTAATAAT | TGATTGAGTCGCGAAAA<br>GACG | GCAGTCGATTGGGAGA<br>AGAG | 60.0                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_24290082  | Ca1                                     | 24290082                      | A/AGAGAGAGAGAGAGG                                             | AAATGCTTCAGCCAGA<br>CACC      | CGAACCTAAAGACGC<br>AAAG     | 60.3                             | 378                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_24301670  | Ca1                                     | 24301670                      | AATATATATATATATATATA/AA<br>TATATATATATATATATATATA             | TCAAGCATGTCAAATTC<br>CCA      | GGGGTGCTACAGTGTC<br>GAAT    | 60.0                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2431426   | Ca1                                     | 2431426                       | TGTTT/TGTTTAAGTTT                                             | TCACAAAGTTGCTTTCC<br>GTG      | TGAAAATGCCCGATT<br>AAAG     | 59.9                             | 339                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2431602   | Ca1                                     | 2431602                       | GTCTATT/GT                                                    | CTTTAATCGGGGCATT<br>TTCA      | CAATCATTGTGAGATG<br>GATGAAG | 59.9                             | 269                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2434803   | Ca1                                     | 2434803                       | ATTTTTTTTT/ATTTTTTT                                           | AAGAGTGAGATGGGCA<br>CCAC      | AGGGATTTCATTTGGA<br>GAAAA   | 60.1                             | 421                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2436388   | Ca1                                     | 2436388                       | CAAAA/CAAAAA                                                  | ACAATGATTTTCTCCAC<br>GCC      | ATCGTCAATGTTGCAC<br>ATCC    | 59.9                             | 144                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2440150   | Ca1                                     | 2440150                       | ACCCC/ACCC                                                    | ATCTGCTGCTCGTAGG<br>CATT      | GAAGGGCGAAAACATG<br>AAAA    | 60.0                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2448249   | Ca1                                     | 2448249                       | TAT/TATATAAT                                                  | GGCTCCACAATATTATA<br>GTCCTTCA | AAGGATCCACGTCAGT<br>CCAG    | 59.8                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2448896   | Ca1                                     | 2448896                       | TATT/TATTAATT                                                 | CTGGACTGACGTGGAT<br>CCTT      | TGTTGTTATGGTGGGT<br>CCCT    | 60.1                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2454328   | Ca1                                     | 2454328                       | ACTCTCTCTCT/ACTCTCTCTCT                                       | TTTTGAGATAACCCAG<br>GCCA      | GCATGGGACGCTTTTG<br>TAAT    | 60.4                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_2454529   | Ca1                                     | 2454529                       | CAGA/CA                                                       | GATAGCTCATGGATGG<br>GTCC       | GCATGGGACGCTTTTG<br>TAAT  | 59.3                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_24623839  | Ca1                                     | 24623839                      | ATTTTTTTT/ATTTTTTTTT                                          | AAATTTGTTGCGAAGG<br>CAGT       | TTTTGTGATTGGGCAC<br>TTGA  | 59.8                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_24624813  | Ca1                                     | 24624813                      | T/TTAGAAA                                                     | CATCATCATTTTCAATG<br>GGCT      | ATGGTTTTATTTCGGCCA<br>CAA | 59.8                             | 801                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_24632359  | Ca1                                     | 24632359                      | GATATATATATATA/GATATATATA<br>TATATATA                         | GACGCCTGACGTTAT<br>TGTT        | CTTGCCAGAAAATCG<br>AAAA   | 60.0                             | 703                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2463656   | Ca1                                     | 2463656                       | ATTTAAATTTGTGTTTAAATTTT/AT<br>TTAAATTTT                       | GGAAACAAATTTTGC<br>CACT        | TTCACTTGATCGCACC<br>CAT   | 60.1                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_24648509  | Ca1                                     | 24648509                      | TTATATATATATATATATATATA/T<br>TATATATATATATATATATATA           | CACTTGAATTTGTTTCT<br>CTCGC     | TGCTTTTCTGGATTGG<br>TCC   | 59.0                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2475450   | Ca1                                     | 2475450                       | ATTTT/ATTT                                                    | CCCCTATGCTCCATCT<br>CAAA       | CAAAGATTGCTCACATT<br>TGTC | 60.0                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_24771219  | Ca1                                     | 24771219                      | TCT/TCTCTTTCCTCTTCCT                                          | TTGCAAGCACGATTG<br>AAAC        | TGGGTCCAAAGTGGAT<br>GAAT  | 59.9                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_24801961  | Ca1                                     | 24801961                      | CTTTTTTTTT/CTTTTTTTTT                                         | TTTCAATGATGTTGGG<br>TTGC       | CAGCATATCCCCAACA<br>AAAGA | 59.4                             | 998                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_24935055  | Ca1                                     | 24935055                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATATAT                 | TGTGTGTTTTCTACAAT<br>GTGCTAGTT | TTGGGTTTGACCCATG<br>AAAT  | 59.3                             | 730                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                              |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_25064793  | Ca1                                     | 25064793                      | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATAT<br>ATATATATATA                        | GTGAGGGTGCTTGCT<br>CACA    | AATGGGCGCTGTAA<br>TGTC   | 59.9                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_25133935  | Ca1                                     | 25133935                      | ATTTTTTTTTTTTTTT/ATTTTTTTT<br>TTTTT                                                          | TGTTGGTAGCACAATC<br>ACGAG  | CTTAGGCTTGCATC<br>ACCC   | 59.8                             | 155                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_25134278  | Ca1                                     | 25134278                      | AAATAATAATAATAATAATAATA<br>ATAA/AAATAATAATAATAATAAT<br>AATAATAATAA                           | GATCGCAAGACCTAAG<br>TGCC   | AGATGTGCCAGCAGTG<br>TTGT | 59.8                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2518243   | Ca1                                     | 2518243                       | CATATATATATATATATA/CATATA<br>TATATATATATATA                                                  | AACGGGATAAATGTTT<br>GTGCTT | GCGCTTTTACGGGACA<br>ACTA | 59.8                             | 794                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_252332    | Ca1                                     | 252332                        | AATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATA<br>TAT                                | ACACATGAAGCCCAAC<br>ATCA   | TGGTTGACTTTGTAA<br>TCGGA | 60.0                             | 132                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_25296432  | Ca1                                     | 25296432                      | CTTT/CTTTT                                                                                   | GTTGGTGGCTGGACTC<br>AGAT   | TTCCCTAGTTGTTGG<br>GTGC  | 60.1                             | 817                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_25303242  | Ca1                                     | 25303242                      | CATATATATATATATATATATATA<br>TATAT/CATATATATATATATATAT<br>ATATATATATAT                        | TAGGCAACCTTGGGTG<br>TTGT   | TCAGCATGTCAATTCC<br>CAA  | 60.4                             | 813                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_25358096  | Ca1                                     | 25358096                      | AACCA/AA                                                                                     | TCTGGAGCCCATAGGA<br>GTTG   | CCAACGGGATGGTGT<br>ATAG  | 60.2                             | 716                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_25382154  | Ca1                                     | 25382154                      | GAA/GAAA                                                                                     | GAATCACTAGGCTTGC<br>CAGG   | GGGGTGAGAGAACGTT<br>TGAA | 59.8                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_25437512  | Ca1                                     | 25437512                      | AATATATATATATATATATATATAT<br>ATATATATATATA/ATATATATATA<br>TATATATATATATATATATATATAT<br>ATATA | GACTTTGATGCAAGTC<br>ACCG   | CTCCCATCAGTTTAATC<br>GGC | 59.3                             | 875                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                     |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_25853462  | Ca1                                     | 25853462                      | TAAAAAAAAA/TAAAAAA                                                  | TCGCACGATTCTAACA<br>ACCA   | AAGGCGAGATAATAGC<br>CGGT   | 60.3                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_25948887  | Ca1                                     | 25948887                      | TTATATATATATATATATATATA/T<br>TATATATATATATATATATATATAT<br>A         | TTTCTATAAAGCAAATC<br>CGCA  | GTCGCCGACAGTTTTA<br>AGGA   | 57.6                             | 855                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_26094587  | Ca1                                     | 26094587                      | TAAAAAAAAA/TAAAAAA                                                  | CTCGAAGCCGAGAAAA<br>TGAC   | TCCCCCTCCTATTGTC<br>CTCT   | 60.0                             | 723                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2615903   | Ca1                                     | 2615903                       | GAAAAAAAAA/GAAAAAAAAA                                               | TGTGATCAATGTGTG<br>AGTGAAA | TCCAAGATTCAATCCAA<br>CCC   | 59.1                             | 221                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_26352919  | Ca1                                     | 26352919                      | TAA/TA                                                              | TAAAGGACCAACTCGG<br>GAAA   | GCATTGGATCGCTTCA<br>AGAT   | 59.5                             | 786                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_26377123  | Ca1                                     | 26377123                      | ATTTTTTT/ATTTTTTTT                                                  | TGTTCTAGATGGGGTT<br>TGGC   | GCCACTATCCAACAAAT<br>GGC   | 59.9                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_26447765  | Ca1                                     | 26447765                      | ATATTATTATTATTATTATTATTA<br>TT/ATATTATTATTATTATTATTA<br>TTATTATTATT | AAATAGGGCCACACCA<br>AAAA   | TTAATCGGAGGTATG<br>GGGA    | 59.3                             | 320                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_26447923  | Ca1                                     | 26447923                      | CACATATCTG/C                                                        | AAATAGGGCCACACCA<br>AAAA   | GTAATGGGTATGGGTA<br>CGGG   | 59.3                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2653521   | Ca1                                     | 2653521                       | T/TC                                                                | GGTGGGTGACCCTCAC<br>TTTA   | CATTCCAGTTAGTTGAA<br>CGGGT | 59.8                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2655421   | Ca1                                     | 2655421                       | TGG/TGGG                                                            | TCCGTGGAAATGAACC<br>TAGC   | CGCGTGATGATTGCTA<br>AAAA   | 60.1                             | 228                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_2656475   | Ca1                                     | 2656475                       | A/AG                                                          | TTGCACAATTTCTGATT<br>GGC    | GATCATTGCATCCCCA<br>TTCT   | 59.7                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2656961   | Ca1                                     | 2656961                       | T/TAA                                                         | TCGTAGAATGGGGATG<br>CAAT    | TGACATCAACTGGAAT<br>CAACA  | 60.3                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2659291   | Ca1                                     | 2659291                       | GACCT/G                                                       | AGGATGGTGGAGAGCA<br>AGTC    | AAACCAAACCAACTC<br>CTCC    | 59.3                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2659614   | Ca1                                     | 2659614                       | TAAA/TAA                                                      | CAATCAGGATCGGCCA<br>ATTA    | CGTGTTTAGCGGTGAG<br>TTGA   | 60.8                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_26605020  | Ca1                                     | 26605020                      | CT/C                                                          | AAAGGCATCCTACAAT<br>TCACA   | TGGAGTTTGGTGGTGA<br>AAAA   | 57.2                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2661346   | Ca1                                     | 2661346                       | TAAAA/TAAAAA                                                  | CGCCGTTTTCTTCAAA<br>CTC     | TGGTGTTTCATTTGATT<br>CAGGA | 59.9                             | 840                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_26629862  | Ca1                                     | 26629862                      | TAAAAAA/TAAAAA                                                | TTTCATTCACCTAACCT<br>TTTGG  | GGGCCATCCTATATTC<br>CCAC   | 59.1                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2663715   | Ca1                                     | 2663715                       | TGAAAAGAAAA/TGAAAA                                            | GTTGCCATGCCTATAA<br>CGGT    | TGAAGACCATGGACAC<br>CAAC   | 59.9                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2664568   | Ca1                                     | 2664568                       | GATGATGTGAATGATGTGAA/GATG<br>ATGTGAA                          | CCAAAAATTGATGAATT<br>GACGTT | TGAATCATGAAGCGGA<br>AAAA   | 60.1                             | 324                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_26651379  | Ca1                                     | 26651379                      | TTATATATATATATATATAT/TTATAT<br>ATATATATATATATAT               | GAAGCATTGGAAGTTT<br>GGGA    | GGTCCCTGTTGGTGCA<br>GTAT   | 60.1                             | 767                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_2666278   | Ca1                                     | 2666278                       | ATTTTT/ATTTTT                                                 | TCGGAATACACGACGA<br>AACA   | CTGCGGGTAGGATTGC<br>TTTA   | 60.1                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2668175   | Ca1                                     | 2668175                       | AC/A                                                          | AATGCATCACGTGGGA<br>TTTT   | CGATTGCACCCGTAGT<br>TGTA   | 60.2                             | 206                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_26683611  | Ca1                                     | 26683611                      | TG/T                                                          | CAATTGTGTAAAACGT<br>GCGG   | TTGCATTGGTTTGACT<br>CCA    | 60.0                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_26725325  | Ca1                                     | 26725325                      | CTATATATATATATATATAT/CTAT<br>ATATATATATATATAT                 | AATTAGCAGCGGAAGG<br>AAAG   | GCATCACAGTTAAATCA<br>TCGC  | 58.6                             | 352                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2674516   | Ca1                                     | 2674516                       | CTAGATTGGAT/CTAGATTGGATTA<br>GATTGGAT                         | TGTCGGAATATGGGAA<br>GCTC   | GCCGTTGTTTTAGAT<br>CCAT    | 60.0                             | 934                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2679013   | Ca1                                     | 2679013                       | CCTCT/CCTCTCT                                                 | CATCCTTATCCCTCATT<br>CCTTG | AAAATATACCCCATCTG<br>TCCCT | 59.8                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_26876468  | Ca1                                     | 26876468                      | C/CG                                                          | TTGTGCATCCGTCTAT<br>CCAC   | TCGGTGGAATTGTAA<br>TGAGAG  | 59.5                             | 937                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_26877204  | Ca1                                     | 26877204                      | TAAAAAAAAA/TAAAAAAAAA                                         | CTCTCATTACAATTTCC<br>ACCGA | GAAGGGTCATAAAATG<br>GGGG   | 59.1                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_26894036  | Ca1                                     | 26894036                      | TGTAATTATTG/TGTAATTATTGTAA<br>TTCGTAATTATTG                   | ATGCACACACTTTTGAT<br>GCC   | TCATACAAATTCGAGGT<br>TCCAA | 59.6                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_26958642  | Ca1                                     | 26958642                      | TT/TTTGAT                                                     | TGCTCCATTTGATTGCT<br>GAC   | CCGACCAATAGACTTTT<br>GTTGA | 59.8                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')   | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|---------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                       |                           |                                 |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_26958895  | Ca1                                     | 26958895                      | CAAAAAAAAA/CAAAAAAAAA                                                 | TGAGCGTGAAAAATTG<br>TGTT  | TTAGAGCGTTCAAATTA<br>TAGTTACACA | 59.2                             | 709                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2704069   | Ca1                                     | 2704069                       | GTTT/GTT                                                              | CACGCATGATTGAAAT<br>TGTTT | AAGCTTCTTCGAGCAA<br>CGAG        | 59.0                             | 264                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_27143610  | Ca1                                     | 27143610                      | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>ATATATA     | GTTCAATCAATACTCG<br>GCGG  | GGCATCTTTGATCAAT<br>GGTCTT      | 60.5                             | 681                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_27204677  | Ca1                                     | 27204677                      | C/CT                                                                  | GCCGAAGTACCAATTA<br>CCGA  | TACGGTGCTAGGGAAC<br>CAAC        | 60.0                             | 705                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_27232314  | Ca1                                     | 27232314                      | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATA<br>TATATATATAT | CTTGGAAGTGGAGAG<br>CAAG   | AGGGAGGTTTGTGTTT<br>GACG        | 60.0                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2725497   | Ca1                                     | 2725497                       | TAA/TA                                                                | GTGTAACCTCACGGGA<br>AGGA  | GGGTCAATTTGAAACA<br>ACGG        | 60.0                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2727220   | Ca1                                     | 2727220                       | GAAAAA/GAAAAAA                                                        | CCACATATTAGCCACC<br>CCAC  | TATCGCTCAATTTGCGT<br>TTG        | 60.1                             | 906                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_27282747  | Ca1                                     | 27282747                      | G/GCAGTT                                                              | AAATCCAACAATCTCC<br>CCC   | CCCTGAGACTCACGAA<br>GAGG        | 60.0                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_27282877  | Ca1                                     | 27282877                      | AAAAA/AAAAAAAAA                                                       | AAATCCAACAATCTCC<br>CCC   | CCCTGAGACTCACGAA<br>GAGG        | 60.0                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_27300538  | Ca1                                     | 27300538                      | TTGTGGTGTGGTGTG/TTGTGGTGT<br>G                                        | CAGAAATCTCTGGGTG<br>GGAA  | CTGGTTCCTTATGA<br>CCAA          | 60.0                             | 109                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_27320145  | Ca1                                     | 27320145                      | GAAAAAAAAA/GAAAAAAAAA                                         | GAAACTTCGGTGCCAT<br>CATT | CGGTCACAGAGAGGAA<br>GAGG  | 59.9                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2745007   | Ca1                                     | 2745007                       | GTTTTTTTTT/GTTTTTTTTT                                         | GAACGAACGGTGTGAT<br>GATG | GGGCCACAATAACAC<br>AAAC   | 60.0                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2761120   | Ca1                                     | 2761120                       | GA/GAATA                                                      | TCATCATGCTCCATGG<br>TTTC | CTAGCCCATTACAAG<br>CCAA   | 59.5                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2762433   | Ca1                                     | 2762433                       | T/TC                                                          | TATTTGGACAAACGAA<br>GGGC | TGGAAGGATGGATGCT<br>TAGG  | 59.9                             | 126                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_27640153  | Ca1                                     | 27640153                      | AAAGAAGAAGAAGAA/AAAGAA<br>GAAGAAGAA                           | CCAACACGTTTTCGA<br>ATCT  | TGTGTGTGTTGGAGG<br>GAAA   | 60.0                             | 297                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_27640312  | Ca1                                     | 27640312                      | CATATATATATATAT/CATATATATAT<br>ATATAT                         | TTCCCTCCAACACACA<br>CACA | TGAGTCGCGACGAGAG<br>TAGA  | 60.0                             | 147                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2765307   | Ca1                                     | 2765307                       | C/CAATGTG                                                     | CAGCCTCTGATGTTCA<br>ATGG | CTATGTGCATATCGGC<br>CCTT  | 59.2                             | 423                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2765494   | Ca1                                     | 2765494                       | TAAAAAAAAA/TAAAAAAAAA                                         | CAGCCTCTGATGTTCA<br>ATGG | CTATGTGCATATCGGC<br>CCTT  | 59.2                             | 423                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2765671   | Ca1                                     | 2765671                       | GTTTTTTTTT/GTTTTTTTTT                                         | TAAAAAGGGCCGATAT<br>GCAC | CATGCACGATTGTGGT<br>AATTG | 59.9                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2766077   | Ca1                                     | 2766077                       | CTTATGTT/CTTATGTTATGTT                                        | AAAACAATTGATTGGG<br>CTCC | CCAATCATACGCAGGT<br>GAAA  | 58.9                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_2766176   | Ca1                                     | 2766176                       | A/AG                                                          | AAAACAATTGATTGGG<br>CTCC  | CCAATCATACGCAGGT<br>GAAA    | 58.9                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2766346   | Ca1                                     | 2766346                       | AATATA/AATATATA                                               | TTTCACCTGCGTATGA<br>TTGG  | TGACCTCTTATGCTTCT<br>CGAAAT | 59.5                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2766600   | Ca1                                     | 2766600                       | CTTTTTTTT/CTTTTTTTT                                           | TTTCACCTGCGTATGA<br>TTGG  | TTGAAAGTTGAAACGT<br>GGGA    | 59.5                             | 779                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2772818   | Ca1                                     | 2772818                       | TAAAAAA/TAAAAAA                                               | TATTGGGCAACAATTC<br>ACGA  | TCGCCTACTGTGTTGG<br>ATGA    | 59.9                             | 222                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_27744633  | Ca1                                     | 27744633                      | TCCC/TCC                                                      | CAAGACTGATGCAAAAC<br>CCAA | CTCTCGAAGATCCACT<br>TGCC    | 59.7                             | 348                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_27845331  | Ca1                                     | 27845331                      | AT/A                                                          | TTATTTTCCCAATCTC<br>CCC   | TTTTGAAGATGGTGAA<br>CATGC   | 60.0                             | 731                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_27850705  | Ca1                                     | 27850705                      | CTTTTTTTTTT/CTTTTTTTTTT                                       | CACCACCGAAACCAAA<br>CTCT  | TGACAGTCAGAGTGCG<br>ATCC    | 60.0                             | 444                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2791561   | Ca1                                     | 2791561                       | ATTT/AT                                                       | ATCGAAAGCAACCATT<br>TTGG  | TCATTCAAATGGTGACT<br>CGTG   | 59.9                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2791646   | Ca1                                     | 2791646                       | TT/TTTTAAT                                                    | ATCGAAAGCAACCATT<br>TTGG  | TTGTGGTGGTTCTTTG<br>TTGG    | 59.9                             | 869                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2796283   | Ca1                                     | 2796283                       | T/TG                                                          | GGTGGACAGAGGCATC<br>AACT  | AAAAAGCGAGTTTCAG<br>GGTG    | 60.1                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_2797230   | Ca1                                     | 2797230                       | A/AC                                                          | TGTCTTAAATCTGTGC<br>ATTCAA  | AAATAGTTGACAAACC<br>GCCG       | 57.5                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2797326   | Ca1                                     | 2797326                       | A/AC                                                          | CCCTGTAAATTCAGAC<br>ACAATCG | AAATAGTTGACAAACC<br>GCCG       | 60.8                             | 272                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2797692   | Ca1                                     | 2797692                       | TTTCT/TT                                                      | ACGGCGGTTTGTCAAC<br>TATT    | AAGAAGCCAACAACG<br>AAGC        | 59.5                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2797913   | Ca1                                     | 2797913                       | ATTTTTTTTTTT/ATTTTTTTTTT                                      | ACGGCGGTTTGTCAAC<br>TATT    | GGGTGTTTTTGTCAATT<br>GGG       | 59.5                             | 743                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28015338  | Ca1                                     | 28015338                      | T/TTAA                                                        | AATGACATTGAAGGGC<br>GAAG    | ATTGGTTTCACGTTTT<br>GTC        | 60.1                             | 404                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28024777  | Ca1                                     | 28024777                      | TAGGCCAGACCA/TAGGCCAGACCA<br>GGCCAGACCA                       | GGCTACCGAATATGGA<br>ACGA    | GTGGTGAGTAGGGATG<br>GGAA       | 59.9                             | 330                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2803383   | Ca1                                     | 2803383                       | TAA/TA                                                        | ACAACGGAATTGGTCA<br>TGGT    | AAGACCCATCATCACC<br>TTGC       | 60.1                             | 172                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2803396   | Ca1                                     | 2803396                       | GTGATGATG/GTGATG                                              | ACAACGGAATTGGTCA<br>TGGT    | TTCTAATTCCAATCCC<br>ATGT       | 60.1                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2810482   | Ca1                                     | 2810482                       | CAT/CATAT                                                     | TGCATAACCAACTGAA<br>TGCC    | GCGTCGTAAAAGACGT<br>GCTA       | 59.5                             | 813                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2826983   | Ca1                                     | 2826983                       | AGT/A                                                         | CGCCCTGCCTCAAATT<br>ATTA    | TTTAATGTTGTTGTTGA<br>AGATGAAAA | 60.1                             | 962                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                            | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                          |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_2845159   | Ca1                                     | 2845159                       | TAAAAAAAA/TAAAAAA                                                                                        | CCACCTTTCAAAGACG<br>AAACA    | GCTTGATTTCAAAATCT<br>CCTCC | 60.1                             | 686                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2845363   | Ca1                                     | 2845363                       | AT/A                                                                                                     | TTTGTCAATTAATTCAC<br>GCATTC  | GCTTGATTTCAAAATCT<br>CCTCC | 59.0                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28458887  | Ca1                                     | 28458887                      | AAATAATAATAATAATAATAATA/<br>AAATAATAATAATAATAATAATA<br>ATAATA                                            | CGTCGTTTGTGTTGAC<br>ACATC    | CGTTGTTTGTGTTGACA<br>CATCT | 59.1                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2846167   | Ca1                                     | 2846167                       | AAT/A                                                                                                    | GTTTGAACACGGGTGC<br>TTTT     | ATTTTAGACGCTTGCC<br>CTCA   | 60.0                             | 165                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2846214   | Ca1                                     | 2846214                       | TT/TTGT                                                                                                  | GTTTGAACACGGGTGC<br>TTTT     | ATTTTAGACGCTTGCC<br>CTCA   | 60.0                             | 165                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28550132  | Ca1                                     | 28550132                      | ATTTTTTTTT/ATTTTTTT                                                                                      | TGGAAGCACGCTTAAG<br>GACT     | TTTCCAATCGATTGTC<br>TTC    | 60.0                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28550408  | Ca1                                     | 28550408                      | AT/ATT                                                                                                   | GAAGCAAATCGATTGG<br>GAAA     | ACGCTCAGAGTTCAC<br>GGGT    | 60.0                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2861050   | Ca1                                     | 2861050                       | CGTAGTAG/CGTAG                                                                                           | ACATCTCAATTGATGTC<br>TCAAAAA | GATGAAGCCACTAATG<br>GGGA   | 57.8                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28638034  | Ca1                                     | 28638034                      | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATT/ATATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATT | TGGCAGGAAATGTTGT<br>GTGT     | TTCGTTTTGCCAATCAT<br>CAA   | 60.0                             | 597                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2867984   | Ca1                                     | 2867984                       | AAT/AATGAT                                                                                               | ATGAGAAAGGGAAGA<br>GGGA      | AAGGGGTGAACAGTGA<br>GGTG   | 60.0                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_28692976  | Ca1                                     | 28692976                      | TCC/TC                                                        | CGTTTTTCAAAGCGAG<br>GGTA    | GCCCTCAGATGAGAGT<br>CAGG     | 60.2                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28711868  | Ca1                                     | 28711868                      | TAGAGAGAGAGAGAGAGAG/TAG<br>AGAGAGAGAGAGAGAG                   | TGTTGGGTTGACAAA<br>ACCA     | TTAATGGGGAAGCACA<br>AAGC     | 59.8                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28713213  | Ca1                                     | 28713213                      | TTA/TTAGAAAGAGTGTA                                            | TTCAATTCTCTGATTCC<br>CCG    | TCCGCATTATAACCTCT<br>GCC     | 60.0                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28903274  | Ca1                                     | 28903274                      | TAAAAAA/TAAAAAA                                               | GGGGGTTAGGATGTG<br>GTAAAA   | TTATTGGTTGCCCTCCA<br>TTC     | 59.9                             | 862                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28905129  | Ca1                                     | 28905129                      | TCTCCT/TCT                                                    | TGTTGCATTGGCGTTT<br>CTTA    | CGTGGGTTGCCATCTA<br>GTTT     | 60.3                             | 220                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28906702  | Ca1                                     | 28906702                      | TAAAAAAA/TAAAAAA                                              | TATGGAGAGCAGCGAC<br>TCAA    | TGTTGGGTTGCACAAC<br>ATTC     | 59.7                             | 184                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28929600  | Ca1                                     | 28929600                      | GTTTTTTT/GTTTTTTT                                             | AAATTCGAACTGGGCA<br>TTTG    | TGAAGGCACCATGTCT<br>TTGA     | 59.9                             | 750                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28930406  | Ca1                                     | 28930406                      | T/TA                                                          | TCAAAGACATGGTGCC<br>TTCA    | TTGGTGCCAATTTATGT<br>ATTCA   | 60.2                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28930954  | Ca1                                     | 28930954                      | A/ATT                                                         | TGAAAAGTTTCTTTGTC<br>CCTTTG | TGGTGTTGCCTTCAAAT<br>TCA     | 59.7                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28935215  | Ca1                                     | 28935215                      | ATTTTTTTT/ATTTTTTTTT                                          | TTTTGTGGCAGTTTGT<br>TTG     | CAGTCAACATTGATGT<br>GACGTTAT | 57.3                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_28939471  | Ca1                                     | 28939471                      | AAAATAAAACAAA/AAAA                                            | CCATGTGTGAACCCTA<br>ATTGTT | GTTTGGCGTTGGTT<br>CACT    | 58.7                             | 226                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28941503  | Ca1                                     | 28941503                      | CAA/CAAAA                                                     | TGGGGTTTAGGGTGTC<br>ACAT   | CTTTGTAAAGGCAGC<br>TCCG   | 60.1                             | 207                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28941872  | Ca1                                     | 28941872                      | GAAAAAA/GAAAAA                                                | TGGGGTTTAGGGTGTC<br>ACAT   | TCAATTGGATTCTTG<br>GTGG   | 60.1                             | 847                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28943560  | Ca1                                     | 28943560                      | GG/GGTG                                                       | ACTTGGGACAAATCAC<br>ATGG   | TGATCACCAGCTTTC<br>AATG   | 58.3                             | 252                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28944045  | Ca1                                     | 28944045                      | TAAAAA/TAAAAA                                                 | TTGCCCTTAATGGACC<br>AAGG   | CAATATGAAGTCTGGT<br>GCCAA | 59.9                             | 345                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_28944496  | Ca1                                     | 28944496                      | TTATATATAT/TTATATAT                                           | TTGGCACCAGACTTCA<br>TATTG  | AAATGTACTTTGCGGC<br>ACAT  | 58.6                             | 775                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_29124803  | Ca1                                     | 29124803                      | ATTT/ATTTT                                                    | AGTGGCATTGGGCAAA<br>TTAC   | ACCAAAATATACGCGTCT<br>GCC | 59.8                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2912876   | Ca1                                     | 2912876                       | GGTAC/GGTACGTAC                                               | TGTCATCCCTAGCAAC<br>ACGA   | TGTAATGCATTTCCCT<br>TGTC  | 60.3                             | 192                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_29161382  | Ca1                                     | 29161382                      | ATT/AT                                                        | TTCCACCAAGATGGAA<br>CAAA   | TTAGAAGGAAGGGAA<br>ACTCA  | 58.9                             | 331                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2918789   | Ca1                                     | 2918789                       | GTTATTATTAT/GTTATTATTATTAT                                    | TTGCAGGCAGGCTTAG<br>ACTT   | TTCCATGTTCCCTTTGC<br>TTC  | 60.2                             | 770                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_2919131   | Ca1                                     | 2919131                       | CAAAAAAAAA/CAAAAAAAAA                                         | GTATCCCATCCCCTGC<br>AATA  | TTCCATGTTCCCTTTGC<br>TTC    | 59.6                             | 202                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2920885   | Ca1                                     | 2920885                       | TTTAAT/TTTAATTAAT                                             | ATTGCCATGGATTGA<br>CGTT   | GAATTGAGGAACCAAA<br>AATGAAA | 60.2                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2921722   | Ca1                                     | 2921722                       | CAATA/CA                                                      | CAACTGGGCCAAATGC<br>TTAT  | TGATGATCACACGAGG<br>GAGA    | 60.0                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2921905   | Ca1                                     | 2921905                       | ATTT/ATT                                                      | CAACTGGGCCAAATGC<br>TTAT  | TGATGATCACACGAGG<br>GAGA    | 60.0                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2922949   | Ca1                                     | 2922949                       | CTTTTTTTTT/CTTTTTTTTT                                         | TTGTGGATCGTATTG<br>CGAA   | AGCATATGGTCCCCTT<br>TTCA    | 60.1                             | 947                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2923053   | Ca1                                     | 2923053                       | TATGAA/TATGAATGAATGAA                                         | CGCGAAATCTTATTTTC<br>ATGG | TGATGCGATTGTAGTC<br>CCAA    | 59.6                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2923274   | Ca1                                     | 2923274                       | A/ATATTAATAATAAT                                              | CGCGAAATCTTATTTTC<br>ATGG | TGATGCGATTGTAGTC<br>CCAA    | 59.6                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2923894   | Ca1                                     | 2923894                       | TAAAAAAAA/TAAAAAAAA                                           | TTGGGACTACAATCGC<br>ATCA  | ATTGACCCGATTTGCT<br>GAAC    | 60.1                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2923992   | Ca1                                     | 2923992                       | TTA/T                                                         | TTGGGACTACAATCGC<br>ATCA  | ATTGACCCGATTTGCT<br>GAAC    | 60.1                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2924550   | Ca1                                     | 2924550                       | CTT/CTTT                                                      | GTTCAGCAAATCGGGT<br>CAAT  | TGAGTTAATGCGGCCT<br>AACC    | 59.9                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                             |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_2924687   | Ca1                                     | 2924687                       | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                               | GTTCAGCAAATCGGGT<br>CAAT | TGAGTTAATGCGGCCT<br>AACC  | 59.9                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_29343809  | Ca1                                     | 29343809                      | AATA/AATATA                                                                 | AACTTTCGGTGCAAAC<br>AACC | TGGAATAAACACATG<br>CGAG   | 60.0                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2937855   | Ca1                                     | 2937855                       | G/GT                                                                        | CGGATGGAACAAGTGG<br>AAGT | GGAACCAATCTTCTAT<br>TCGCC | 60.0                             | 933                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2939248   | Ca1                                     | 2939248                       | GTCT/GT                                                                     | TTGTCCCTCGAAGTTT<br>CCTT | GCAACCGTGTGGATAT<br>GTTG  | 58.8                             | 112                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_29402165  | Ca1                                     | 29402165                      | TG/TGTAG                                                                    | GGCCGTAAACCAGACT<br>CAAA | GGGGTAAGTTTCCTTG<br>ACCA  | 60.1                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_29511714  | Ca1                                     | 29511714                      | GTATATATATATATATATATATATAT<br>ATATA/GTATATATATATATATATATA<br>TATATATATATATA | CGGTCACCACTAACAT<br>CGTG | CGCACTTGAGGAGTTG<br>GATT  | 60.0                             | 812                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_29524255  | Ca1                                     | 29524255                      | ATTTTTTTTTT/ATTTTTTTTTTTTTT                                                 | GGCTTCTTTCCAAAAT<br>GCAG | CACCATATCCCCCAAA<br>ACA   | 59.8                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2955757   | Ca1                                     | 2955757                       | CTTTTTTTT/CTTTTTT                                                           | CCTCCACTCATTTCTC<br>CCA  | TTATCATTCTTCCCCA<br>CCA   | 60.0                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2956307   | Ca1                                     | 2956307                       | TAAA/TAA                                                                    | TGGTGGGGGAAGAATG<br>ATAA | GCAACTTCCTTTGAGAT<br>GGG  | 60.1                             | 348                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2956674   | Ca1                                     | 2956674                       | TTATATATAT/TTATAT                                                           | CCCATCTCAAAGGAAG<br>TTGC | CCACTGCTGCGCTATT<br>ATGA  | 59.7                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_2958127   | Ca1                                     | 2958127                       | CTTTTTTTTT/CTTTTTTTTT                                         | GCTCTCAAAAGCTTCC<br>CGTA     | TTGAACAATCAACTGT<br>TGCG       | 59.6                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_29583858  | Ca1                                     | 29583858                      | GAAAAAAAAA/GAAAAAAAAA                                         | GGGGTGCTCAACTTGT<br>TTGT     | TAACATGGCCAAGGTA<br>AGGG       | 60.0                             | 242                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2959912   | Ca1                                     | 2959912                       | T/TTTTTTTTA                                                   | TGTTATGATCCGTAAC<br>GATGG    | TGCCGCAATAAATAT<br>TAAAAA      | 59.7                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2960581   | Ca1                                     | 2960581                       | ATTTTTTTTT/ATTTTTTT                                           | TCTGTGATAAGGGTCT<br>ATCCCG   | AAACGTGTGGAAAT<br>ATTATAATCG   | 60.3                             | 374                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2960620   | Ca1                                     | 2960620                       | ATTTTTTTTT/ATTTTTTTTT                                         | TCTGTGATAAGGGTCT<br>ATCCCG   | AAACGTGTGTGGAAAT<br>ATTATAATCG | 60.3                             | 374                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2960960   | Ca1                                     | 2960960                       | GTTTTTTTT/GTTTTTTTTT                                          | TTGTCAAATATTGATT<br>CGTGTTTT | TGGCACATATTTGTCAC<br>TCATAA    | 60.0                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2961037   | Ca1                                     | 2961037                       | ATTTTTTTTTTTTT/ATTTTTTTTT<br>TTTT                             | TTGTCAAATATTGATT<br>CGTGTTTT | TGGCACATATTTGTCAC<br>TCATAA    | 60.0                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2961596   | Ca1                                     | 2961596                       | ATTTTTTT/ATTTTTT                                              | CATGTGATTTTATGTGT<br>CAGCG   | TGGAACACATAATTTTC<br>ACCGA     | 59.1                             | 156                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2961815   | Ca1                                     | 2961815                       | A/AAT                                                         | TCGGTGAAAATTATGT<br>GTTCCA   | TTATCTTACCCCTTGCA<br>CCG       | 60.2                             | 629                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2962103   | Ca1                                     | 2962103                       | GTTTTTTTT/GTTTTTTT                                            | TCGGTGAAAATTATGT<br>GTTCCA   | TTATCTTACCCCTTGCA<br>CCG       | 60.2                             | 629                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_2963212   | Ca1                                     | 2963212                       | TA/TACAA                                                      | CATCGACCATCAATCA<br>CAATG | GGGTGAAGTGGGATGA<br>TTTG  | 59.8                             | 288                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2966165   | Ca1                                     | 2966165                       | A/AC                                                          | CCACGTCTGTAAATTC<br>GCTTT | TGACGTTGTTTTGTCTG<br>TCG  | 59.3                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2966305   | Ca1                                     | 2966305                       | T/TTC                                                         | CCACGTCTGTAAATTC<br>GCTTT | GCTCGCCACTCTCTTT<br>CTCT  | 59.3                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_29667241  | Ca1                                     | 29667241                      | AACACACACACACACACA/AACACA<br>CACACACACACACA                   | CCGAGCCAAAATCCAA<br>AATA  | TTGGGTGCACATTTTAC<br>AGC  | 59.9                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2969456   | Ca1                                     | 2969456                       | CATATATATAT/CATATATAT                                         | GCTACCAATTGGGTG<br>GAGA   | AGAAATGCACGAAAC<br>AGGC   | 59.9                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2970042   | Ca1                                     | 2970042                       | TTATAT/TTAT                                                   | GCCTGTTTTCGTGCAT<br>TTCT  | GTGAGGGGATGGTGCT<br>CTAA  | 60.3                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2970188   | Ca1                                     | 2970188                       | TAAAAAAA/TAAAAAAA                                             | GCCTGTTTTCGTGCAT<br>TTCT  | GTGAGGGGATGGTGCT<br>CTAA  | 60.3                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_29738380  | Ca1                                     | 29738380                      | GTATATATATATATATATAT/GTAT<br>ATATATATATATATATAT               | TATTTTGGATTTTGGCT<br>CGG  | AAACCGGTAAAATCTC<br>CGCT  | 59.9                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_29791416  | Ca1                                     | 29791416                      | GAAAA/GAAAAA                                                  | TCCGATAAAATCTCG<br>TTCG   | AAAAACACGTTCCCT<br>CCTT   | 60.0                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_29801275  | Ca1                                     | 29801275                      | TAAAAA/TAAAAA                                                 | GTTTTCCATCTTGGT<br>GCGT   | TCACCCAAATTTATGGC<br>ATGT | 60.0                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_29806954  | Ca1                                     | 29806954                      | ATT/ATTT                                                      | GCATGCTGCAAGGGAT<br>AGTT | CGCGCTGTAAAAATC<br>AAGG  | 60.2                             | 423                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_29817198  | Ca1                                     | 29817198                      | GTTTTTT/GTTTTTTTTT                                            | TGTTAGGAGGATCTCA<br>CGGG | TTGTACAGGTGTCTGC<br>CGAG | 60.1                             | 522                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_29818737  | Ca1                                     | 29818737                      | ACTA/ACTAAATTACCGAGGTGCTA                                     | CTCGGAATTCCAAACC<br>AAAA | ATCGATGGCTCAATTG<br>GTTC | 59.9                             | 359                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_29825526  | Ca1                                     | 29825526                      | ATTTTT/ATTT                                                   | CAAGACTTAAGGCTCC<br>CCCT | CCCATTGCTAACCAG<br>GAA   | 59.7                             | 500                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_29825613  | Ca1                                     | 29825613                      | GCTTT/G                                                       | CAAGACTTAAGGCTCC<br>CCCT | CCCATTGCTAACCAG<br>GAA   | 59.7                             | 500                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_29842423  | Ca1                                     | 29842423                      | AC/A                                                          | TCATCAAAGGCATGCA<br>AATC | GACCAAAACACAACGC<br>AATG | 59.6                             | 359                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_29843804  | Ca1                                     | 29843804                      | G/GA                                                          | ATGGATCAAGAGAAGG<br>GGCT | CCTATGCGAAGTGGTG<br>GTTT | 60.0                             | 535                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_29844165  | Ca1                                     | 29844165                      | TTTATT/TTT                                                    | ATGGATCAAGAGAAGG<br>GGCT | CCTATGCGAAGTGGTG<br>GTTT | 60.0                             | 535                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_29853119  | Ca1                                     | 29853119                      | TAA/TA                                                        | TCCACGAGATTTTCCTT<br>TGG | TGTCATCATTCTCTGCT<br>GGC | 60.0                             | 357                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_29853730  | Ca1                                     | 29853730                      | GTGGAAGTCT/GTGGAAGTCTGGAA<br>GTCT                             | TTGCATTCTAGGTTC<br>AGCC  | TATCGCTCGACCTCTG<br>CTTT | 60.2                             | 602                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_29856647  | Ca1                                     | 29856647                      | CTTT/CTTTT                                                    | GCATTCCCTGCTCAAG<br>ACTC | AGACAAGGGAGAGTCC<br>CACA      | 60.0                             | 812                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_2994165   | Ca1                                     | 2994165                       | TAAAAAAAAA/TAAAAAAAAA                                         | CCGTGACACTCACACA<br>AACC | CGCCATTGTTCTCTCCT<br>CTC      | 60.0                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_29994387  | Ca1                                     | 29994387                      | GTTTT/GTTTTT                                                  | TCCAGCTTCCTCGAAA<br>CCTA | AACAAGACCTGCGAAA<br>ATCG      | 59.9                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30125583  | Ca1                                     | 30125583                      | CCAAATTCAAATTCAA/CCAAATTC<br>AAA                              | GCTTGGGGACAAGCAA<br>TAGA | CTGCTTGGGCATAAGT<br>CTCC      | 60.2                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3014145   | Ca1                                     | 3014145                       | ATTTTTTTT/ATTTTTTTTT                                          | TGCGGCTATTACATTG<br>GTGA | GTGGGAACTTTTTCATG<br>CCAG     | 60.1                             | 700                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30152959  | Ca1                                     | 30152959                      | ACATATACCATATACCATAT/ACATA<br>TACCATAT                        | CGAATCATGCGCAAGA<br>ACTA | CGATCAGGTGGACAAT<br>GACA      | 60.0                             | 330                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3016722   | Ca1                                     | 3016722                       | ATAAAATTA/ATAAAATTACTAAATTT<br>A                              | TGGAAATGGAGGTAAG<br>TCGC | TTTGATTATGAAGCATT<br>GTCAACAT | 60.1                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3016741   | Ca1                                     | 3016741                       | AATATATATATATATATA/AATATATA<br>TATATATATATA                   | TGGAAATGGAGGTAAG<br>TCGC | TTTGATTATGAAGCATT<br>GTCAACAT | 60.1                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3017014   | Ca1                                     | 3017014                       | TAAAAAAAAA/TAAAAAAAAAAAAA                                     | GGAAATGGAGGTAAGT<br>CGCA | GGCCACATTGTGCTTC<br>ATATT     | 60.1                             | 729                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3018574   | Ca1                                     | 3018574                       | CAATTAATTAATT/CAATTAATT                                       | AGCCAACAGCCCAACA<br>TAAA | AAGGTTTCATGTCCAAT<br>CGC      | 60.5                             | 242                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_30194339  | Ca1                                     | 30194339                      | GATAAATAAATAAATAAATAA<br>TAA/GATAAATAAATAAATAA                | TGCCTTCATCTTCACT<br>GCAC   | TAGCCATTGATTCCAC<br>CCAT   | 60.0                             | 838                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3020023   | Ca1                                     | 3020023                       | ATAATATTAATAT/ATAATATTAATAT<br>TAATAT                         | CAAGCAACATGCTGAA<br>GGAA   | TTTAAGCACATCTGGTC<br>AATCA | 60.0                             | 237                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3020354   | Ca1                                     | 3020354                       | AGG/AGGG                                                      | CAAGCAACATGCTGAA<br>GGAA   | ATGTCCTTAGTGTCAC<br>GGGG   | 60.0                             | 808                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30207170  | Ca1                                     | 30207170                      | CTATATATATATA/CTATATATATATA<br>TA                             | TGATTTACACGCAGAA<br>AGCG   | CGGAAAAACACTAAGG<br>TGCAA  | 60.0                             | 266                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3020722   | Ca1                                     | 3020722                       | GGCTT/G                                                       | CCCCGTGACACTAAGG<br>ACAT   | GAAGGTCGCATCTCCA<br>TGAT   | 59.8                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3020788   | Ca1                                     | 3020788                       | TTTTA/TTTTAATTTA                                              | CCCCGTGACACTAAGG<br>ACAT   | GAAGGTCGCATCTCCA<br>TGAT   | 59.8                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30208977  | Ca1                                     | 30208977                      | GAAA/GACGAAAAAATATAAAA                                        | ATGGTGTCTTTAACGG<br>TGGG   | AGTTGAGAGGCACCCT<br>GCTA   | 59.7                             | 263                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30243449  | Ca1                                     | 30243449                      | AGG/AG                                                        | CCAAACCAATAAAACA<br>TTCCAA | GAACCTCTGCCTTCAG<br>CAAC   | 60.0                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3025881   | Ca1                                     | 3025881                       | ATTTTTTTT/ATTTTTTT                                            | CCCCACCCACCTTTTA<br>TTCT   | GCAACCATGAAACAT<br>TTTG    | 60.0                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30287511  | Ca1                                     | 30287511                      | GTTTT/GTTT                                                    | CCATCAACATCGTCA<br>TGGA    | ACTCAGATTGGTCTGT<br>GGGG   | 60.3                             | 305                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_30352443  | Ca1                                     | 30352443                      | CACA/CACAACA                                                  | TCATCTTGGGAGGTCT<br>CGAT | TTGTGGTCTAGGCGTC<br>AAAA  | 59.6                             | 673                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30398618  | Ca1                                     | 30398618                      | GTTTTTTTTT/GTTTTTTTTTTT                                       | TTAGGCCAGTACAGT<br>TCGG  | GGGGTGCTCAACTTGT<br>TTGT  | 60.1                             | 901                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3039987   | Ca1                                     | 3039987                       | C/CAT                                                         | TTCTCCGCTAATTCTC<br>AACC | ATCCCCATCTGATTTG<br>TCA   | 58.5                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3042228   | Ca1                                     | 3042228                       | ATTT/ATTTT                                                    | GAGCCAAGATCGATGG<br>GAT  | TTGTATGAACACAACC<br>C AAA | 60.0                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3043888   | Ca1                                     | 3043888                       | GAATAAATAAATAAATAA/GAA<br>TAAATAAATAAATAA                     | GGACCGAAATGTTGCC<br>TAAA | GACTTGGTCAATTGC<br>CGAT   | 59.9                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30452929  | Ca1                                     | 30452929                      | TT/TTAT                                                       | GAAGAGTTACGCGGAC<br>AAGC | AGGAAGAGTGGAGTTG<br>CGAA  | 60.0                             | 768                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30475415  | Ca1                                     | 30475415                      | A/AC                                                          | ACGGCAAGACCCTAAA<br>ACCT | AACTTCTACTCGGGC<br>CCAT   | 60.0                             | 906                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30475519  | Ca1                                     | 30475519                      | ATTT/ATTTT                                                    | AGGATGCATGGGATGA<br>AAAG | AACTTCTACTCGGGC<br>CCAT   | 59.9                             | 766                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3051235   | Ca1                                     | 3051235                       | CTTCTGA/CTTCTGAGTTCTGA                                        | TTGTGCACACAAGTCC<br>AACA | TTGATCCAAATTCGTG<br>GGTT  | 59.8                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3051311   | Ca1                                     | 3051311                       | CAAAAA/CAAAA                                                  | TTGTGCACACAAGTCC<br>AACA | TTGATCCAAATTCGTG<br>GGTT  | 59.8                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_30643052  | Ca1                                     | 30643052                      | TAAAAAAAAA/TAAAAAAAAA                                         | ACCCATGTTGGGTTCA<br>CAGT  | TAGGGGCATCTACGA<br>TGGG      | 60.1                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30682856  | Ca1                                     | 30682856                      | CATATATATATATATATATAT/CAT<br>ATATATATATATAT                   | GTTGGTCCCTAGCAC<br>CGTA   | TCCGCCTAGGAGATAG<br>CAGA     | 60.0                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30745547  | Ca1                                     | 30745547                      | C/CT                                                          | TTTTTGGGTTTCCTTTT<br>CCC  | TGCAATATGTATCGTG<br>GATGG    | 60.1                             | 817                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30755262  | Ca1                                     | 30755262                      | CAAAAAAAAA/CAAAAAAAAA                                         | AAGAGAGGTCACTTTG<br>GCGA  | TGACTGAGACAGCTCG<br>ATGG     | 60.0                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30768111  | Ca1                                     | 30768111                      | GAAAAA/GAAAAA                                                 | TCCGGTATAAAGGTT<br>TCCG   | CCGTTGAAAACAACAC<br>ATGAA    | 58.9                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30769862  | Ca1                                     | 30769862                      | TAAAAA/TAAAAA                                                 | ATGGGTCTTGAAACA<br>CTCG   | ACCAACTCCTCCAAGC<br>CACT     | 60.0                             | 354                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30770184  | Ca1                                     | 30770184                      | TAAA/TAAAA                                                    | AGTGGCTTGAGGAGT<br>TGGT   | CGTTCGGCTTTCTTCTT<br>CTG     | 61.1                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30789723  | Ca1                                     | 30789723                      | AC/A                                                          | TGCTTTTCAAGGGAGG<br>AATG  | CTCCAGTTTTGGTCCC<br>TCAA     | 60.2                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30790839  | Ca1                                     | 30790839                      | TGTAAC/T                                                      | TTTTTGATGGTTCAACG<br>AGAA | GGTTGAATAATTGAAAA<br>GAGGTGG | 58.3                             | 250                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30808046  | Ca1                                     | 30808046                      | GAA/GAAATAA                                                   | ACAACCCGAGTGATCT<br>CCAC  | TAGGGTGCTTGACACG<br>TGAG     | 60.0                             | 701                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_30844081  | Ca1                                     | 30844081                      | AATATATATATATATATA/AATATATA<br>TATATATATATA                   | TGAAAAGGGATGGAAT<br>GGTT   | AAGCATTATGAAGATGA<br>CGCC    | 59.2                             | 387                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3089236   | Ca1                                     | 3089236                       | ATTT/ATT                                                      | GCAAAACGTCTTATCG<br>GGAA   | TGCAAACTATTTGACAT<br>TGACG   | 60.1                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3093464   | Ca1                                     | 3093464                       | CATATATATATAT/CATATATATATAT<br>ATAT                           | ATATATAGGCAGGGGC<br>GGAC   | AATTGAACCCAAGTGC<br>AGGT     | 60.2                             | 481                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30938741  | Ca1                                     | 30938741                      | CTTTTT/CTTTT                                                  | TCTTCCACCCAGTTTT<br>ACC    | AAAGCATCTCACACAG<br>CACG     | 59.9                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3096084   | Ca1                                     | 3096084                       | T/TC                                                          | ACCACCTTATTTGTGG<br>CTGC   | CCAAATGCTCCGCTA<br>TGTT      | 60.0                             | 346                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3096580   | Ca1                                     | 3096580                       | TAAAAA/TAAAAA                                                 | AACATAGCGGAGCATT<br>TTGG   | CATGGTAGCCCAATC<br>CAAT      | 60.1                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30969929  | Ca1                                     | 30969929                      | ATCAATTTCAATTT/ATCAATTT                                       | CATGTTGGATACACAT<br>GCTTTG | TTCAGCAGATTTGCGA<br>CAAC     | 59.0                             | 969                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_30993040  | Ca1                                     | 30993040                      | AAAAATTAAATTAATTA/AAAAA<br>TTAAATTAATTAATTA                   | TCCTTCCGATCGAGTA<br>GTGG   | AAACATGAAATGGACAA<br>TACAAAA | 60.2                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31003439  | Ca1                                     | 31003439                      | GGGTCGGACCGGGCCGG/GGGTC<br>GGACCGGGCCGGTCGGACCGGGC<br>CGG     | CCCCAGGATAAAACAG<br>CTCA   | AGCAAATTGACCACCA<br>CACA     | 60.1                             | 220                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31004479  | Ca1                                     | 31004479                      | GTATATATATATATATATA/GTATA<br>TATATATATATA                     | ATAAAATGGGGTTTG<br>GAAA    | TCAACGGTGGAGGATA<br>GTGA     | 60.2                             | 396                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_31005058  | Ca1                                     | 31005058                      | AC/A                                                          | CACTATCCTCCACCGT<br>TGAAA | GCCTTAATTATCGCTCC<br>TCAA  | 60.0                             | 722                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31014910  | Ca1                                     | 31014910                      | TTTTTTATTT/TTTTTTATTTTATTT<br>ATTTTTATTT                      | GGAGCATGAAGCAACC<br>TCTC  | TGATGAATCTGTGTGT<br>CCATGA | 60.0                             | 199                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31022339  | Ca1                                     | 31022339                      | GTTTT/GTTT                                                    | GTTTCAACCGCATCCA<br>ATTT  | TCCCAATCGAATCTAC<br>GAGG   | 59.8                             | 442                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31028139  | Ca1                                     | 31028139                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA<br>AA                           | ACGCAAAATGGCTTAC<br>GTTC  | CATGACCTCCCTTTTC<br>GTA    | 60.1                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31072463  | Ca1                                     | 31072463                      | ATT/AT                                                        | CGCATGTGACCTACAT<br>GGTT  | CTCTATACCCGAGCTG<br>AGCG   | 59.4                             | 282                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31072943  | Ca1                                     | 31072943                      | TAAAAAAA/TAAAAA                                               | CGCTCAGCTCGGGTAT<br>AGAG  | CAAACCGGATGTGACA<br>GTTG   | 60.1                             | 615                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3107570   | Ca1                                     | 3107570                       | ATGTGTGTG/ATGTGTGTGTG                                         | TCCTTGCACGCTTTTAA<br>TCA  | AAACGTGATCGAACGA<br>ATCC   | 59.4                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3108095   | Ca1                                     | 3108095                       | GAAAAAAAA/GAAAAAAAAA                                          | GGATTCGTTTCGATCAC<br>GTTT | ACGGGCAAAGTCAACA<br>TAGG   | 59.9                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31093242  | Ca1                                     | 31093242                      | ATTTTTTTTT/ATTTTTTTTTT                                        | TTTTTAGGAGAGCGGC<br>GTTA  | TTGATCAAGCTCCAAT<br>TATCA  | 60.0                             | 597                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31095231  | Ca1                                     | 31095231                      | TTTATTAT/TTTAT                                                | GATACATTATGCACGC<br>CTCG  | TGACGATGTTTTTGGG<br>TTTT   | 59.2                             | 506                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_3110033   | Ca1                                     | 3110033                       | ATTTTTTTTTTT/ATTTTTTTTTT                                      | TGCTACAATGGTGTT<br>GGCA   | TCGAGCAAGTGAGAAA<br>TGGA | 60.0                             | 877                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31117965  | Ca1                                     | 31117965                      | AATATA/AATA                                                   | GGGACATCAGAATGCT<br>CACA  | TGCGACACACGAATTA<br>CACA | 59.6                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3112331   | Ca1                                     | 3112331                       | AC/A                                                          | AATCTTCCACGGAACA<br>ATCAA | GGGAGATGGAAATTGG<br>GAAT | 59.4                             | 877                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31141128  | Ca1                                     | 31141128                      | C/CA                                                          | ATTATTGAGGTTGGCC<br>CCTC  | TCCACTTTTGTGCTTT<br>AGGC | 60.2                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31162887  | Ca1                                     | 31162887                      | T/TG                                                          | CCGGGGATTGCCATAT<br>AACT  | CTAATAGGCTGCATCG<br>GAGG | 60.9                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31163466  | Ca1                                     | 31163466                      | T/TAGA                                                        | ACTTTTGGGAGAAGC<br>ACAT   | CGTTCGTCTTTTCCTCT<br>TGC | 59.9                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3118706   | Ca1                                     | 3118706                       | GTTAC/GTTACTTAC                                               | CCAAATGAATGCTTCG<br>GTCT  | AGCATTACAGGCAAA<br>CAAA  | 60.1                             | 799                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31212342  | Ca1                                     | 31212342                      | CTTTTTTTTTTT/CTTTTTTTTTT                                      | GCCAAAATGCCATTA<br>AGGA   | TGCCTCCAAATATCCTC<br>CAA | 59.9                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3126822   | Ca1                                     | 3126822                       | AATAT/AATATATTATGATAT                                         | TGTTGCTTGGTGTAGG<br>GACA  | CCTTTAGCCCGTGAGT<br>CTTG | 60.2                             | 987                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3130356   | Ca1                                     | 3130356                       | TAAAAAAA/TAAAAAAA                                             | TCGTTTATCCAACCCCT<br>TTG  | CTGGTCTGGCTTGAAA<br>ACCT | 59.8                             | 736                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_3131301   | Ca1                                     | 3131301                       | TATA/TATACTCATA                                               | GGCCAGACTCAGACCT<br>TTCA   | ACCCATTTTTCTGACAA<br>CCG  | 60.4                             | 506                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31324079  | Ca1                                     | 31324079                      | AAA/AAATAA                                                    | TATTCGGTTGTCGAGT<br>TCCC   | AGGGATAACCTGGTGC<br>TGTG  | 59.9                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3133490   | Ca1                                     | 3133490                       | AATTATATATTATA/AATTATA                                        | CCACATTTTGCCACTTT<br>TCA   | TCGCCTTTTAAACCAAC<br>CAG  | 59.6                             | 853                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31375439  | Ca1                                     | 31375439                      | GAAAAAAAAAAAAA/GAAAAAAAAAAAAA                                 | GCCGTTTAGCAACAAA<br>GAAAA  | TCATCGAGAACGCATC<br>CATA  | 59.4                             | 265                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3138107   | Ca1                                     | 3138107                       | A/ATT                                                         | ATCGGGGTGGACAAA<br>CATA    | GGGCTTTAAATTGAGT<br>GAGGC | 60.1                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31386654  | Ca1                                     | 31386654                      | TG/TGAAG                                                      | TTTCAACCGCTCAACAT<br>CAA   | TGTCGCGCTACCTTTC<br>TTCT  | 60.2                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31401462  | Ca1                                     | 31401462                      | CTATATTATATA/CTATA                                            | ATTCGTAGTAGGCCAT<br>GCCA   | TTTGC GGCTTCAAAAT<br>ATC  | 60.5                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31422768  | Ca1                                     | 31422768                      | ATTTTTTTTT/ATTTTTTTTT                                         | CTCCTTCAAAAGCACA<br>AGCC   | GTTGCTCCGACGAAAC<br>AAGT  | 60.0                             | 243                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31477691  | Ca1                                     | 31477691                      | CAAAA/CAAAAA                                                  | AAGGGAAACGGGTACC<br>AAAC   | ACCCGTAAACCCCAAA<br>TCTC  | 60.1                             | 629                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31481152  | Ca1                                     | 31481152                      | GT/G                                                          | GCAAATGCAACTCTGA<br>AAACTG | GTTATACCGCCAGCTG<br>CATT  | 59.9                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_31505143  | Ca1                                     | 31505143                      | GTATATATATATATATATA/GTATA<br>TATATATATATATA                   | TCCCATTCATATTATT<br>GCGG  | CATTGACTATGCCACT<br>AAATGC | 59.6                             | 831                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3156637   | Ca1                                     | 3156637                       | GTTTTTT/GTTTTTTT                                              | GCATGTGAGACCCAGC<br>CTAT  | CCTTCATGTCCACATAC<br>AATTC | 60.1                             | 829                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3156701   | Ca1                                     | 3156701                       | ATTTTTTT/ATTTTTT                                              | TGGCTGTGATATTGTC<br>GCAT  | CCTTCATGTCCACATAC<br>AATTC | 60.1                             | 696                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3156764   | Ca1                                     | 3156764                       | TAA/TAAA                                                      | TGGCTGTGATATTGTC<br>GCAT  | CCTTCATGTCCACATAC<br>AATTC | 60.1                             | 696                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31597098  | Ca1                                     | 31597098                      | TAAAAAAAA/TAAAAAAAAA                                          | GCCAAAGCCTTTCACC<br>TTCT  | CGAAAAGTTTGGAGAG<br>TGGAA  | 60.7                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31600847  | Ca1                                     | 31600847                      | TG/T                                                          | AAGGTAGTGAAAGAGG<br>GGCTG | AGGATCATGTTTGTGG<br>TTGC   | 59.8                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31602245  | Ca1                                     | 31602245                      | TTATATATATATATATATATA/TTA<br>TATATATATATATATA                 | TTTCGTGTGCGTCAAA<br>TCAT  | AGAGGCACACGGGTCT<br>AATG   | 60.1                             | 756                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31627142  | Ca1                                     | 31627142                      | TAAAAAAAA/TAAAAAAAA                                           | CTTCGAATCCAACCTT<br>GGTG  | CCGGAACCACATTCAG<br>ACTT   | 60.5                             | 892                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31645800  | Ca1                                     | 31645800                      | GTTTTTTTTTTT/GTTTTTTTTTTTTT<br>TT                             | ATGGAGAAATCCCCCA<br>AATC  | TGTTCAACCAATGTG<br>GGAA    | 60.0                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31716302  | Ca1                                     | 31716302                      | A/AC                                                          | TCGGTATTTGCCATGA<br>GACA  | AAACAACCTTCATGCCT<br>TGG   | 60.1                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                           |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_31768486  | Ca1                                     | 31768486                      | TT/TTTTTAT                                                                | ACACATTATATTAATG<br>CGCGA | TGCCAAACGATAGTT<br>GTTG  | 57.4                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31783488  | Ca1                                     | 31783488                      | AATATATATATATATATATAT/ATATATATATATATAT                                    | TGGATTGGGCTGGAAT<br>TAAA  | TATAACCGACGAGGGA<br>CGAG | 60.3                             | 466                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31783811  | Ca1                                     | 31783811                      | TTAATAATAATAATAATAATAAT<br>AATAATAAT/TTAATAATAATAATAAT<br>AATAATAATAATAAT | ATACTGCCTTCGATCC<br>GTTG  | CGGGAAAAAGGGTGGT<br>AAAT | 60.1                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31823620  | Ca1                                     | 31823620                      | ATTT/ATT                                                                  | ATGCATGTTTGGCATA<br>TGGA  | TTGGAAGGAGCCCTTA<br>CCTT | 59.8                             | 854                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31995444  | Ca1                                     | 31995444                      | ATCTTC/ATCTTCTTC                                                          | TGCTTTGAAGACCATG<br>TGGA  | AAAAGGATTCATGCGT<br>GTCC | 60.2                             | 354                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_31995500  | Ca1                                     | 31995500                      | CTTT/CTTTT                                                                | TGCTTTGAAGACCATG<br>TGGA  | AAAAGGATTCATGCGT<br>GTCC | 60.2                             | 354                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32037334  | Ca1                                     | 32037334                      | CTTTTT/CTTTT                                                              | TCCAGTCATGTGGCTT<br>CTCA  | CTGAGCTTGTGACCAA<br>ATCG | 60.4                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32037353  | Ca1                                     | 32037353                      | CTTCTTTTT/CTTCTTTTTCTTTTT                                                 | TCCAGTCATGTGGCTT<br>CTCA  | CTGAGCTTGTGACCAA<br>ATCG | 60.4                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3213987   | Ca1                                     | 3213987                       | TTATATATATATATATATATA/TTATATATATATATATATA                                 | TCGGCAATGTGGTACT<br>GAAA  | TTGCAAATGCGACTTTT<br>TTG | 60.1                             | 344                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32140100  | Ca1                                     | 32140100                      | TT/TTATTAT                                                                | GGCCAAAACCCTAATT<br>GACA  | TGGCAAAGGGGAAGTC<br>AGTA | 59.8                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)            | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                          |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_32147050  | Ca1                                     | 32147050                      | T/TA                                                                     | CGGCCTCCAAATCTTT<br>AACA  | TTGTCATGAAAGTCTC<br>GCCT  | 60.1                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32151710  | Ca1                                     | 32151710                      | TAAAAAAAAA/TAAAAAAAAA<br>AAA                                             | TGAAGGTGTGAGCAGA<br>TTCG  | TCGGGTGGAGAATTCC<br>TATG  | 60.0                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32153452  | Ca1                                     | 32153452                      | TTTATTTTAT/TTTATTTTATATTATTT<br>TAT                                      | GTTTTGGCGTTGGTTT<br>CACT  | TGGGTTTGACCCTATG<br>TG TG | 60.0                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32155872  | Ca1                                     | 32155872                      | TTATATATATATATATATATATATATAT<br>TATATATATATATATATATATATATATAT<br>ATATATA | TTACCCAAGATGGAGG<br>AAAAA | TGTTGTCCCTTGTGCT<br>GGTA  | 58.5                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32176200  | Ca1                                     | 32176200                      | CAAAA/CAAAA                                                              | CCCGTCACTTGGAGAC<br>AAAT  | ACTCTCACTGGAATG<br>GTGG   | 60.0                             | 636                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32203101  | Ca1                                     | 32203101                      | CAAA/CAA                                                                 | CCACGTTCTTGACCCA<br>TTTC  | CCTCTTTTGCAACCTCC<br>TTG  | 60.4                             | 352                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32203178  | Ca1                                     | 32203178                      | TATGA/TATGAATGA                                                          | GTTCCAAAGGTAATGC<br>CCAA  | CCTCTTTTGCAACCTCC<br>TTG  | 59.8                             | 137                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32244195  | Ca1                                     | 32244195                      | A/AG                                                                     | TGAATAGAGGGAAACG<br>GGTG  | CAGTGACCTTGTGGAG<br>AGCA  | 59.9                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32244737  | Ca1                                     | 32244737                      | CCACAA/CCACAAACCCATACACAA                                                | AATGGATCATTCCTTG<br>CAGC  | TTCAGAGATCGTGCGT<br>GAAC  | 60.0                             | 422                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32246863  | Ca1                                     | 32246863                      | TGG/TG                                                                   | CCTGGGATCATGTTGC<br>TTCT  | AAACCTCAACCAACGT<br>CCTG  | 60.1                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                           | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                         |                             |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_32254955  | Ca1                                     | 32254955                      | ATT/ATTT                                                                                | TAATTTTCAGCAACCC<br>GAGG    | GGGCTGGTTCCCATT<br>GTTA      | 60.1                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32265930  | Ca1                                     | 32265930                      | GATA/GA                                                                                 | TCCAGCATCTGTTGAT<br>TCCA    | AAAGTTTTGCCCTCCT<br>CAT      | 60.2                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32266454  | Ca1                                     | 32266454                      | GAAAAAAAA/GAAAAAAAAA                                                                    | TAATGATGAGGAGGG<br>CAAA     | GGGAGTCCGAGTGGA<br>CAAA      | 60.4                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32267410  | Ca1                                     | 32267410                      | T/TTTAA                                                                                 | TTCGTGTTAAATAGTG<br>TTAGCCA | AAAAATCACATTCCTTG<br>ACATAGC | 58.0                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32395659  | Ca1                                     | 32395659                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                                               | TTGCATCAGCCATATT<br>TTG     | TCTCGATTGCTCCGA<br>TATT      | 59.7                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32430396  | Ca1                                     | 32430396                      | TG/T                                                                                    | TCGTTTGAGCCTTTTCG<br>AACT   | GCAATCACAATGCAGC<br>AAAC     | 60.0                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32437062  | Ca1                                     | 32437062                      | CTATATATATATATATATATACAT<br>ATATATATATAT/CTATATATATATAT<br>ATATATATATACATATATATATATAT   | AGTGGAAGTGATGGGA<br>GGTG    | ACGGTAGCTTTAACGA<br>GCGA     | 60.0                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32454365  | Ca1                                     | 32454365                      | A/AG                                                                                    | AGGAAACACATGAAGG<br>CACC    | TCTTCGTTGTCCTCCA<br>TGC      | 60.0                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32551161  | Ca1                                     | 32551161                      | GGAGAGAGAGAGAGAGAGAGA<br>GAGAGAGAGAGAGA/GGAGAGAGA<br>GAGAGAGAGAGAGAGAGAGAGA<br>GAGAGAGA | TTGAACTGAAACTTG<br>GGCA     | TTCGGCACTAGTATTG<br>CGTG     | 59.3                             | 345                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_32758604  | Ca1                                     | 32758604                      | G/GAAAAA                                                                                | TCGTTTTCGACGCTTT<br>CTTT    | TCACGGGTCAACACGA<br>ATTA     | 60.0                             | 810                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_32804656  | Ca1                                     | 32804656                      | ATTTTTTTTTTT/ATTTTTTTTTTTT                                    | AGACCGAGCTCTAATG<br>CCAA    | GCCCTCAGATGAGAGT<br>CAGG    | 60.0                             | 875                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_32822582  | Ca1                                     | 32822582                      | TTATATATATATATAT/TTATATATAT<br>ATATATATATAT                   | TGGATGCAAATTGGAC<br>AGAA    | CGTAGCGTGGTAGTGA<br>GCAA    | 60.0                             | 745                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_32857397  | Ca1                                     | 32857397                      | ATTTTT/ATTTT                                                  | GCGAAAAATCTCGTTC<br>GTGT    | AGAATCGAGATCGTTG<br>GCAC    | 60.3                             | 519                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_32905999  | Ca1                                     | 32905999                      | AATATAT/AATAT                                                 | TTGCTTCGTCAGCACA<br>ATTC    | TCGTATGTCATAGCGG<br>TGCT    | 60.0                             | 920                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_32906329  | Ca1                                     | 32906329                      | TTATATATATATATATAT/TTATATAT<br>ATATAT                         | TCATTAAATCAAAGGCA<br>CACAAA | TCGTATGTCATAGCGG<br>TGCT    | 59.5                             | 488                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_32911601  | Ca1                                     | 32911601                      | AAATAATAATAATA/AAATAATAATA<br>ATAATAA                         | CAAATGGAGCAAGAA<br>ACAGG    | CAAGTTCAACGAGCGC<br>CTAT    | 59.7                             | 892                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_32917904  | Ca1                                     | 32917904                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA<br>AA                           | TCAACCGCATTAAAGTG<br>TGATG  | TTGATGAGGATGAAGT<br>TTTTCAA | 59.6                             | 711                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_32919001  | Ca1                                     | 32919001                      | TAAAAA/TAAAAA                                                 | AACTGCTCATGCGGTA<br>CCTT    | AAGAAGGACATTTGC<br>GATG     | 59.8                             | 714                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_32937588  | Ca1                                     | 32937588                      | AA/AATCCCCCA                                                  | TCCCTCCTTCACAAAAT<br>TGC    | TGGAGTGGGGTACCTA<br>GTGG    | 60.1                             | 498                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_32970710  | Ca1                                     | 32970710                      | A/ATCCATCT                                                    | AACCTAGCCATCGGTG<br>TTTG    | CTCTTCGCAAACCGAA<br>AAAG    | 60.0                             | 304                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_33018948  | Ca1                                     | 33018948                      | CTT/CT                                                        | TTCGCAACTCCACTCTT<br>CCT   | CACATCATCACACATG<br>CCA    | 60.0                             | 481                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33034774  | Ca1                                     | 33034774                      | AATATATATATATATA/AATATATATA<br>TA                             | ACCCCAACTTGTAAG<br>GCAA    | TCACGTTGATTGAGGG<br>ATGA   | 59.5                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33054577  | Ca1                                     | 33054577                      | ATTTTTTTT/ATTTTTTTT                                           | GAGCATTGGCTGCAGT<br>ATCA   | AGAATTTGGGTTTCATG<br>TCAA  | 60.0                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33055263  | Ca1                                     | 33055263                      | CTTTTTTTTT/CTTTTTTTTT                                         | CAACAATGTTCAAGTTC<br>AATGC | TTTTCATGCACGGATT<br>TGC    | 58.2                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33102523  | Ca1                                     | 33102523                      | TTT/TTTATT                                                    | AAGGCTAAATCACATT<br>CGTGG  | TCACCTCCGTCCATGT<br>CAAA   | 59.1                             | 835                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33134129  | Ca1                                     | 33134129                      | CTATA/CTATATATA                                               | CGTTGACTATTTCAATC<br>GTTGG | CACCTGTAGTCCAACA<br>CTCGTT | 59.5                             | 265                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33143190  | Ca1                                     | 33143190                      | AATATATATATA/AATATATATATATA                                   | GAGGAGGGAGGGATT<br>TGAG    | CGGTGAATCCTTTACG<br>GAGA   | 60.0                             | 319                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3322440   | Ca1                                     | 3322440                       | CAAAAAAAAA/CAAAAAAAAA                                         | GAGCGGTACATGGTTG<br>GTTT   | ATGAACCGGTTGAATA<br>CCCA   | 59.9                             | 834                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33237244  | Ca1                                     | 33237244                      | GATGTATGTATGTATGTATGTATG/<br>GATGTATGTATGTATGTATGT            | TGCTGCGAGAAATAAC<br>ATCG   | ACGTTGCTTTAGAGG<br>GAAA    | 60.0                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33240319  | Ca1                                     | 33240319                      | A/AT                                                          | AAACGCAATCCTTGAG<br>TTCG   | CTATCTAGCGTCGGAG<br>TCGG   | 60.2                             | 280                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_33244510  | Ca1                                     | 33244510                      | ATTTTT/ATTTTTTT                                               | AATTCAGACGCGAAAG<br>AGGA    | CAAGTCTCCCACTTC<br>CCAA   | 60.0                             | 221                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33247147  | Ca1                                     | 33247147                      | TA/T                                                          | GTGTTGGACCGGTTCT<br>TGAT    | GTCTGATGACAAAAGG<br>GGGA  | 59.8                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33247360  | Ca1                                     | 33247360                      | GTTTTATTT/GTTTTATTTTTATT<br>T                                 | TCCCCCTTTGTCATCA<br>GAC     | CATGCCAACACAGAA<br>GTTGA  | 59.9                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33269540  | Ca1                                     | 33269540                      | AGGTTTTGTGGGTTTTG/AGGTTT<br>TTGTGGGTTTTGTGGGTTTTG             | CTCCACGTCAAACCA<br>CCTT     | CTGTCTGCACTCCACT<br>CCAA  | 60.0                             | 629                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33286471  | Ca1                                     | 33286471                      | ATTT/ATTTT                                                    | ATTATCAGAGAGTCCC<br>CGGC    | CAGATTGGCACCTATG<br>AGCA  | 60.4                             | 879                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3329136   | Ca1                                     | 3329136                       | CATAAAATAAAATAAA/CATAAAATA<br>AAATAAAATAAAATAAA               | TTTGATTAATGTTTTCA<br>TACGCA | CATTAATGGGTTTCATTG<br>GGC | 57.4                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33300564  | Ca1                                     | 33300564                      | ATTTTTTTTTTT/ATTTTTTTTTT                                      | CTCAACCATCAGAGCA<br>CCAA    | TTATACGGCGGAGGAA<br>TGAG  | 59.8                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33379812  | Ca1                                     | 33379812                      | GTTTTTTTT/GTTTTTTT                                            | AGAATTGGTGGTTGAG<br>GACG    | TTGGGAAAGAAATCGA<br>AAACA | 60.0                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33379930  | Ca1                                     | 33379930                      | ATTTTTTT/ATTTTTTTT                                            | GTA CTGGCCAAAGTGA<br>TGGG   | TTGGGAAAGAAATCGA<br>AAACA | 60.4                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33401507  | Ca1                                     | 33401507                      | AAGAGAGAG/AAGAGAGAGAG                                         | AGCTCTTTGATGACCG<br>TTGG    | GGAGGATGGCAGACCT<br>ATGA  | 60.3                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_33407768  | Ca1                                     | 33407768                      | TA/TAA                                                        | TGGCCATCAATTAATC<br>CACTC  | GATCTGCAACTGGGG<br>TAAA       | 59.8                             | 230                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33408081  | Ca1                                     | 33408081                      | TATAATAATAATAATAATAAT/TA<br>TAATAATAATAATAATAATAAT            | ACTAGATGGTCGCATC<br>CTGG   | TCACAATCCACTAATGC<br>GGA      | 60.1                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33442658  | Ca1                                     | 33442658                      | TAA/TA                                                        | CGTTGTACGCATGCTC<br>AAGA   | TGTTTACCGAGGACCA<br>AAGG      | 61.0                             | 824                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33451777  | Ca1                                     | 33451777                      | TG/T                                                          | TGCCACTTCTGTTTCT<br>GCTG   | TGCAAAATTTGAAAACGTG<br>GTATTG | 60.2                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33559859  | Ca1                                     | 33559859                      | GCC/GC                                                        | CAACGCCAAGAGAAAT<br>GGAT   | GAAGTCGGGGTGTAC<br>TCCA       | 60.1                             | 913                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33560144  | Ca1                                     | 33560144                      | TAAAAA/TAAAAA                                                 | CTCAAAATCTGTTTGG<br>GGGA   | GAAGTCGGGGTGTAC<br>TCCA       | 59.9                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33566643  | Ca1                                     | 33566643                      | CCTTCTTCTTCTTCTTCTT/CCTTCT<br>TCTTCTTCTTCTTCTTCTT             | TACCTTTGGCACATGC<br>TTCA   | TTCACAAAAACGTTGTG<br>CATC     | 60.3                             | 753                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33597493  | Ca1                                     | 33597493                      | ATT/ATTT                                                      | CGGCTTTGGTCCCTTC<br>TTA    | CTGGATCATGAAAGCC<br>CTGT      | 60.2                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33620705  | Ca1                                     | 33620705                      | T/TC                                                          | TTCATGAACCAATGTTT<br>TAGCC | AACAGCGGTTAACACA<br>ACACC     | 59.0                             | 916                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_33653494  | Ca1                                     | 33653494                      | TTTATTATTATTATTATTATA/TTTA<br>TTATTATTATTATTATTATA            | TGGGCAAAATGTTAAG<br>AACACA | AGAACAAATGCATGATT<br>CTTGG    | 60.4                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_34057382  | Ca1                                     | 34057382                      | C/CA                                                          | GGGGATTAAGTGCTTG<br>GACA | AAAGAAAGGCACTAAG<br>GCCC | 59.9                             | 156                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34132085  | Ca1                                     | 34132085                      | TTTA/TTTATCAATTA                                              | ACCTCCTTTGTTATCG<br>GCAA | CGAATGACAAACATCC<br>GTTG | 59.6                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34132998  | Ca1                                     | 34132998                      | CTA/CTAATTA                                                   | GAGGGGGAGATTGTTG<br>GATT | GTTTTGGCGTTGGTTT<br>CACT | 60.1                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34143148  | Ca1                                     | 34143148                      | ATTTT/ATTT                                                    | TGAAGGGGTGCTATT<br>TGTT  | TGTCGAATTTGTTTAGG<br>GGG | 59.4                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34143398  | Ca1                                     | 34143398                      | CTTTATTTTATTTTATTTT/CTTTATT<br>TTATTTTATTTTATTTT              | CCCCCTAAACAAATTC<br>GACA | TTAGGGTGCTTTGTCA<br>CACG | 59.8                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34160007  | Ca1                                     | 34160007                      | C/CAT                                                         | TGGAGACACTTGCCCT<br>CAAT | TTTTATGTCAGGGCGA<br>AACC | 60.7                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34164170  | Ca1                                     | 34164170                      | TC/T                                                          | GCACTCATGCCACAAC<br>ACTT | TAAAAAGCGGATAAAT<br>GGGC | 59.8                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34169923  | Ca1                                     | 34169923                      | GAA/GAAA                                                      | CCATTTCTTTGTCCTC<br>GTG  | AAGCCTTGGAAGGAGA<br>AAGC | 60.5                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34193507  | Ca1                                     | 34193507                      | TAT/TATAGAT                                                   | ATTCTCAACGCCTTCA<br>TGG  | ACGAAGTTTCTTGCGA<br>TGCT | 60.1                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34199097  | Ca1                                     | 34199097                      | CAAAAAAAAA/CAAAAAAAAA                                         | GACACTCGGCACTACC<br>GTTT | GTCCATTGGTTATGG<br>GTGC  | 60.2                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_34200799  | Ca1                                     | 34200799                      | CTTTTTTTTTTT/CTTTTTTTTTTT                                     | AGGTTGGTGCCATTAT<br>GAGG | AGAGGAAGCCCTACGT<br>GGAT      | 59.8                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34203117  | Ca1                                     | 34203117                      | CAAAAA/CAAAA                                                  | CGTATGTGCCCTGCTT<br>ACAA | GAAGAAGACCCTTTTT<br>GCCC      | 59.8                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34250780  | Ca1                                     | 34250780                      | CTT/CTTCATTTTTATTTT                                           | TTGAGTCTGAAGTGAA<br>ACCC | ACATTCAGGTGGTGGT<br>GGAT      | 60.1                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34286273  | Ca1                                     | 34286273                      | ATATTTTTTATTTTTATTTTT/ATAT<br>TTTTTATTTTTT                    | TATGCATGCGGACAAG<br>AGTC | TTGGAAAAGCCACCT<br>ACAC       | 59.8                             | 448                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34311038  | Ca1                                     | 34311038                      | ATT/ATTT                                                      | GGTGTGGGAAGCAAAA<br>GTGT | GATGAGATCAACGAAG<br>GGGA      | 60.0                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34332058  | Ca1                                     | 34332058                      | CATATAT/CATATATAT                                             | AATTGGAAGCAGGGGT<br>TTTT | TGAACCCGTTATAAATA<br>TTTTTCCT | 59.8                             | 356                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_343407    | Ca1                                     | 343407                        | CATA/CA                                                       | ATCAACTTCAGGTTGG<br>GTGG | CCAAAGATGAGCCCAA<br>GAAA      | 59.8                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34345340  | Ca1                                     | 34345340                      | ATTT/ATTTT                                                    | CTACACGAATCCCGT<br>TCACT | TGAAATAATTGGTCGG<br>AGCC      | 59.1                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34362589  | Ca1                                     | 34362589                      | GATAAATA/GA                                                   | GGAGGAAACAAGCGTA<br>CGAA | TAAGGAGGCCTTTTAC<br>AGCG      | 60.2                             | 859                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34363515  | Ca1                                     | 34363515                      | GCC/GCCC                                                      | GCGTTGTAAAAGACGC<br>ACTG | TGGAATGATGAGCTT<br>TTGG       | 59.5                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                               | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                             |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_34386272  | Ca1                                     | 34386272                      | GTTT/GTTTT                                                                                  | AATCTGGAGGGCGTA<br>AGTT  | ATATCGGTCAAACGCA<br>CACA | 60.0                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34396578  | Ca1                                     | 34396578                      | CAAAAAAAAA/CAAAAAAAAA                                                                       | TTCGCATATGGTACTT<br>GGCA | GGCTCAATGCATTTTC<br>CACT | 60.1                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34413066  | Ca1                                     | 34413066                      | TTCTCTCTCTCTCTCTCTCT/TTCTCT<br>CTCTCTCTCTCTCTC                                              | GACGGCACTTGGTGGA<br>TACT | GTGGTTTTGATTGAG<br>CCAT  | 60.0                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34469736  | Ca1                                     | 34469736                      | AT/ATT                                                                                      | CACATAAAGGCATCAT<br>CCCC | ATTAAAGGGCAACCG<br>ATTG  | 60.2                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34509630  | Ca1                                     | 34509630                      | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATA<br>TATATATATATATAT                   | GTGCATTGCGACTGA<br>AGAA  | AAGAAGCCGTCTCCGT<br>CTTA | 60.0                             | 391                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34565446  | Ca1                                     | 34565446                      | GGAGAGAGAGAGAGAGAGAGAGA<br>GAGAGAGAGAGAGAGAGAGAGA/G<br>GAGAGAGAGAGAGAGAGAGAGAGA<br>GAGAGAGA | CGAGCCAAAATCCAAA<br>ACAT | AGACCACCATCGACAA<br>CCAT | 59.9                             | 341                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34593389  | Ca1                                     | 34593389                      | CTA/CTATA                                                                                   | AACTTTTGTGCGACG<br>GTGT  | CTAGGAAGGCCTAAAG<br>CGGT | 59.5                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34634594  | Ca1                                     | 34634594                      | TTCTCTCTCTCTCTCTCTCTCTCT<br>CTCT/TTCTCTCTCTCTCTCTCT                                         | CTAACAATCACCCGCA<br>ATGA | AAAAGCAGAGGGAGAG<br>GGAG | 59.5                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34667053  | Ca1                                     | 34667053                      | ATTTTTTTTT/ATTTTTTTTT                                                                       | AGACTGCTCGGTCCAA<br>AGAA | GTTACCGCAGAGGGAC<br>GTAA | 60.0                             | 264                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34694319  | Ca1                                     | 34694319                      | AGCAAGTG/AGCAAGTGATTGATC<br>GTTGCAAGTG                                                      | GTCGGCATTTTCGCAA<br>TTAT | CGCAATCTTTGAGTTC<br>GACA | 59.9                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_34694405  | Ca1                                     | 34694405                      | TAAAAAAAAA/TAAAAAAAAA                                         | TGACAATTTCTGGCAA<br>CAGC | CCAAGGTTGGATTCTGA<br>AGTG    | 59.8                             | 247                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34697560  | Ca1                                     | 34697560                      | GAAAAAAAA/GAAAAAAAA                                           | ATGTTTCATCAAAGTCG<br>CCC | TGGGTGTAAATGCTTT<br>GTGC     | 59.9                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34768259  | Ca1                                     | 34768259                      | AAATAAATA/AAATAAATAAATA                                       | ATCGCCAGTGTCAATT<br>TTCC | TGCGATTTTACGTGTAT<br>ATGTGAG | 59.9                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34810237  | Ca1                                     | 34810237                      | GTTTT/GTTTT                                                   | ATTGCCTCGCTTGAAG<br>AATG | TTTGGATGAGCAACAA<br>GCAG     | 60.4                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34814277  | Ca1                                     | 34814277                      | T/TG                                                          | GCGTGAACAAAAATCA<br>AGCA | TCGAAGACGTCTCGTT<br>GTTG     | 59.9                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34822198  | Ca1                                     | 34822198                      | ATTTTTTTTT/ATTTTTTTTT                                         | AACATTCTGGTATCGC<br>GTCC | TTCAATGAGGTGGAAG<br>GAGG     | 60.0                             | 935                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34845186  | Ca1                                     | 34845186                      | CTGTATATTGCTTAGAAGTGA/CTG<br>TA                               | TTGGGTGGAAGGTTAG<br>TCCA | TTGTTCAAACGGTTATG<br>CCA     | 60.3                             | 391                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34853862  | Ca1                                     | 34853862                      | CAAAAAAAAA/CAAAAAAAAA                                         | AGTTTGGCTAGATGGG<br>CCTT | TAATTCAAACCGCACTG<br>CAA     | 60.1                             | 256                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34886508  | Ca1                                     | 34886508                      | AAAATAATAAT/AAAATAATAATAA<br>TAAAT                            | AGTGAAGTTGAACCAA<br>CGCA | CACCACCTTCACCTCC<br>AGTT     | 59.3                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34913480  | Ca1                                     | 34913480                      | AAT/AATAT                                                     | TTGTGTTACCGAGGT<br>TGTC  | CAACAACCACTTCGT<br>GCAT      | 59.6                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_34921085  | Ca1                                     | 34921085                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                 | TCAATCGCATCTCGAA<br>ACAC  | AAGGCTTTTATAGAGG<br>CGGC  | 59.8                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34935340  | Ca1                                     | 34935340                      | GAAAAAAA/GAAAAAAA                                             | CCGTATGAATCATGTAT<br>GGGA | TGCGTCCGTACAAATC<br>TAGG  | 58.2                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34971020  | Ca1                                     | 34971020                      | CAAAAAA/CAAAAA                                                | AAATACCCCTTTTCCC<br>ACG   | TGAAAACGCTCAATGC<br>CATA  | 60.0                             | 689                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_34981671  | Ca1                                     | 34981671                      | CAACATAACATAA/CAACATAA                                        | TGGTCTTGCTTTTCCG<br>TCTC  | TGATTGACATGTGCAA<br>CAAAA | 60.4                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35044743  | Ca1                                     | 35044743                      | AG/A                                                          | GTACCGAATAGCCCGC<br>ATAA  | CCAGTCCATATCGGGT<br>CAGT  | 60.0                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35059495  | Ca1                                     | 35059495                      | TAAAAAAAAA/TAAAAAAAAAAAAA                                     | CTGACCACAAAGAAAA<br>AGCCT | ATGGGTTTCCAACCAC<br>AAAA  | 58.5                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35060041  | Ca1                                     | 35060041                      | CAAAAAA/CAAAAAA                                               | TTTTGTGGTTGGAAC<br>CCAT   | TCCCAACATTGAAAGTT<br>CCC  | 60.1                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35061932  | Ca1                                     | 35061932                      | TAAA/TAA                                                      | GGCCTTGAGAAGCATT<br>TGTT  | TTCTAAGGCCTCTCAC<br>CATGA | 59.3                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35072166  | Ca1                                     | 35072166                      | CTA/CTATATA                                                   | AGTTGGCTCACTAGCA<br>CCGT  | CACAAGTGGATGAACA<br>ACCG  | 59.9                             | 696                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35091571  | Ca1                                     | 35091571                      | CTAT/CT                                                       | CGAGCTGTTGAGGAAC<br>ACAA  | GTTGCTCTTGCACTCG<br>GTCA  | 60.0                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_35096364  | Ca1                                     | 35096364                      | AT/A                                                          | TTGATGTGGTCGGAGA<br>TTGA  | ACAATTTTCAGCAACCC<br>GAG  | 60.0                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35141865  | Ca1                                     | 35141865                      | T/TAA                                                         | GCCCACTTCGGTACAT<br>ATTTC | TTTCAGTTCAAAATCCG<br>CAA  | 58.5                             | 173                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35155669  | Ca1                                     | 35155669                      | AATTTGGTGATTGGTGATT/AATT<br>TGGTGATT                          | TCATCCCCTTCTCCCT<br>TCT   | TTAATCCGCAAAATCACC<br>CAT | 60.0                             | 838                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35156057  | Ca1                                     | 35156057                      | GAA/GAAA                                                      | TTGTGATTGAGGGGTG<br>GTTT  | GTGCAGTCTCTCACGG<br>ACAA  | 60.2                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35167911  | Ca1                                     | 35167911                      | GTT/GT                                                        | CAATGTGTGGAGATC<br>GGTG   | ATTGGGACGTGCTTTT<br>CTTG  | 60.0                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35180632  | Ca1                                     | 35180632                      | CAAAA/CAAAAA                                                  | ATGCCCCAATGAATTG<br>TGAT  | CCTTCTCGTGTGTTGCA<br>CCTT | 60.0                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35186204  | Ca1                                     | 35186204                      | ATTTTTTTTT/ATTTTTTT                                           | CCAAGAAACCCTAGCA<br>CCAA  | AGCCTCGAAAATGAAC<br>TCCA  | 60.1                             | 287                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35186475  | Ca1                                     | 35186475                      | ATTTT/ATTTTT                                                  | GGTCAGTGAGCCAAGG<br>GATA  | CCGTTTAAACCCACCT<br>GCTA  | 60.1                             | 729                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35221996  | Ca1                                     | 35221996                      | T/TGCTGAAATAAGTC                                              | CACGTGCCCAAATGTT<br>ATGA  | TGATTCTCCTGGGAT<br>CTGG   | 60.4                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35227202  | Ca1                                     | 35227202                      | TAAAAA/TAAAAA                                                 | ATCAGTGGTCCCCTGA<br>GAAG  | GTCAAGAGTGCGGTCA<br>CATC  | 60.1                             | 764                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_35227782  | Ca1                                     | 35227782                      | AGG/AGGG                                                      | AGATGTGACCGCACTC<br>TTGA    | TCAACCACAAGTACC<br>AACG    | 59.4                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35233074  | Ca1                                     | 35233074                      | AAT/A                                                         | TTGGTTCCTTTGGGGT<br>GTAA    | CACAAAACAAGCCAA<br>CCCT    | 60.2                             | 218                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35235861  | Ca1                                     | 35235861                      | CATTATTATTATT/CATTATTATTATT<br>ATT                            | GGGATGCGACCTTGTA<br>CTGT    | TCCTCCTCTTTTGGCAC<br>ATT   | 60.0                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35236185  | Ca1                                     | 35236185                      | ATTTTT/ATTTT                                                  | ATGTGCCAAAAGAGGA<br>GGAA    | GGGATGCGACCTTGTA<br>CTGT   | 59.7                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35236504  | Ca1                                     | 35236504                      | ATTTTTTT/ATTTTTTTT                                            | CAACTTCCTCCTCTTTT<br>GGC    | GGGATGCGACCTTGTA<br>CTGT   | 58.9                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35246080  | Ca1                                     | 35246080                      | AT/ATT                                                        | AAGAGGGATTGGGGA<br>AGAG     | TGGTTCAACATACGGA<br>AGAAAA | 59.5                             | 289                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35252010  | Ca1                                     | 35252010                      | GAAAA/GAAAAA                                                  | CGTTGCACTAATGGCA<br>TCAC    | CCGACACATAATGCCC<br>TTTT   | 60.1                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35260458  | Ca1                                     | 35260458                      | ATT/ATTT                                                      | ATGGCTCATACTGGGA<br>TTGC    | AAGACTGGGTTGCCT<br>GCTA    | 59.9                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35261821  | Ca1                                     | 35261821                      | ATT/AT                                                        | TGGATTGTCATGGTCT<br>GGAA    | AATGGTCTTGAATTTG<br>CCG    | 59.9                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35264601  | Ca1                                     | 35264601                      | TAAAAAAAA/TAAAAAAAAA                                          | TTCTTTGAGTTTTGAG<br>ACACAAG | TCATGAATGTCGCGGT<br>CTAA   | 57.8                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_35264715  | Ca1                                     | 35264715                      | CTTTTTTTTTTT/CTTTTTTTT                                        | CGGGAGATACGTAGGA<br>GCAA  | TCATGAATGTCGCGGT<br>CTAA     | 60.2                             | 379                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35265473  | Ca1                                     | 35265473                      | TAAAAAA/TAAAAA                                                | TTCCCTGAATCGAGTG<br>AACC  | TTTCCAATAACTCTAC<br>CGCGT    | 60.1                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35266220  | Ca1                                     | 35266220                      | ATAT/ATATTAT                                                  | CGCGGTAGAGTTATTG<br>GAAAA | TGGGGATACGTAGGAG<br>CAAG     | 59.3                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35282790  | Ca1                                     | 35282790                      | TCCCC/TCCC                                                    | AATTTGCACGGTTCAG<br>TTCC  | CATACATGCCAAAACAA<br>ATGC    | 60.0                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35283797  | Ca1                                     | 35283797                      | TGGGGG/TGGGG                                                  | GGGTGTGTTTGATAGG<br>AGGG  | CTCCCTTCCATCTCCT<br>CTT      | 59.3                             | 139                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35284017  | Ca1                                     | 35284017                      | ATTT/ATT                                                      | GAGATGGAAGGGGAG<br>GAAAG  | GCACAAAAGAAAAATAC<br>AAGTCCA | 60.0                             | 273                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35284253  | Ca1                                     | 35284253                      | TT/TTGT                                                       | GAGATGGAAGGGGAG<br>GAAAG  | TCTGATCAAATATGTGG<br>CAGAAA  | 60.0                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35284860  | Ca1                                     | 35284860                      | CAAAAA/CAA                                                    | TGAAGGGAGTGCTATT<br>TGGT  | TCACCTTTTGACTTCCT<br>CATGTT  | 57.3                             | 108                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35285068  | Ca1                                     | 35285068                      | GACACA/GACA                                                   | TGAAGGGAGTGCTATT<br>TGGT  | GCGAGCATTAAATGTTG<br>GAAAA   | 57.3                             | 688                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35285526  | Ca1                                     | 35285526                      | ATTTTT/ATTTTT                                                 | CGAGTCCTCCAAAAC<br>AATGC  | GCCAGAGTGCAATAGG<br>AAGG     | 58.8                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_35285573  | Ca1                                     | 35285573                      | TG/T                                                          | CGAGTCCTCCAAACT<br>AATGC  | GCCAGAGTGCAATAGG<br>AAGG | 58.8                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35285638  | Ca1                                     | 35285638                      | TATT/TATTAATT                                                 | GACCTTATGCTCGTGC<br>AATGT | GCCAGAGTGCAATAGG<br>AAGG | 60.2                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35288350  | Ca1                                     | 35288350                      | ATTTT/ATTTT                                                   | CAACAAGTCAGTGGCA<br>AAACA | GTGGGCATTGTTCCAA<br>GAGT | 59.8                             | 219                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35290921  | Ca1                                     | 35290921                      | ATTT/ATTTT                                                    | CACACCTAATGCCTGT<br>CACG  | TGATGGACCAACAAG<br>TCCA  | 60.2                             | 760                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35300452  | Ca1                                     | 35300452                      | AAAGTAA/AAA                                                   | TTGGAAAAGCCACCT<br>ACAC   | TATGCATGCGGACAAG<br>AGTC | 60.0                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35310736  | Ca1                                     | 35310736                      | ATTTTTTTTT/ATTTTTTTT                                          | TTGATGCAACCTGTGA<br>CTCC  | TTGGATCCATCCCCTA<br>GATG | 59.7                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35310853  | Ca1                                     | 35310853                      | ATTTTTTTTT/ATTTTTTTTT                                         | TTGATGCAACCTGTGA<br>CTCC  | AATGCCCAGTTAGGGA<br>GGAT | 59.7                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35335691  | Ca1                                     | 35335691                      | ATTTT/ATTT                                                    | TTCTAGGCATGTTCC<br>CCTG   | GAGGCTGTGCATTTTG<br>GAAT | 60.1                             | 615                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35337257  | Ca1                                     | 35337257                      | CTTTTT/CTTTTTT                                                | TACATGCACACTCC<br>ACCA    | TGGGAGCCTCAATTGC<br>TTAG | 59.6                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35349139  | Ca1                                     | 35349139                      | GAAAAAAA/GAAAAAAA                                             | TCTGTTGGCACAAAAT<br>GGAA  | CAAGGCTTCTGAACCT<br>GGG  | 60.1                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)  | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_35353052  | Ca1                                     | 35353052                      | G/GTTGA                                                        | TCAGCAGCAATAGGC<br>TTCA     | AGCCCATTCAGATTTTG<br>TGG | 59.7                             | 352                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35353239  | Ca1                                     | 35353239                      | GAA/GAAA                                                       | CCAACAACCTCCTTTC<br>GAGC    | AGCCCATTCAGATTTTG<br>TGG | 59.9                             | 147                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35362478  | Ca1                                     | 35362478                      | TTATATATATA/TTATATATATATA                                      | TTCAGCTTGCCCGTTA<br>GTCT    | AAACTCTTGACCAGAG<br>GCGA | 60.0                             | 975                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35377236  | Ca1                                     | 35377236                      | TGG/TGGAGG                                                     | TGAAAATTGTAGCAAG<br>TCGCTTA | CAAAGGAAACATGCC<br>AAAT  | 59.1                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35422117  | Ca1                                     | 35422117                      | TAAAAAAAAA/TAAAAAAAAA                                          | TGTAGTGGCATGTTTG<br>GCAT    | CACTTTTGGAGGACTTT<br>CGG | 60.0                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35430389  | Ca1                                     | 35430389                      | GATAT/GATATAT                                                  | TCTTGCTTCGCACAAT<br>CTTT    | CGCCGAACCAAGAACA<br>TTAT | 60.0                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35442355  | Ca1                                     | 35442355                      | GGTGTGTGTGTGTGTGTGTG/G<br>GTGTGTGTGTGTGTGTGTGTGT<br>GTGTGTG    | AGGCCGAGAAACCCTA<br>GAAG    | CATTTTGGATTCAACTC<br>GGG | 59.8                             | 309                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35500602  | Ca1                                     | 35500602                      | TGACCTTTCCTATGGTAG/TGACCTT<br>TCCTATGGTAGGACCTTTCCTATGG<br>TAG | TTTTGTTGGGTCCTGG<br>TTTC    | GGCCATATCGAGATGC<br>AGAT | 59.8                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35505624  | Ca1                                     | 35505624                      | GTTTTTTTTTTT/GTTTTTTTTTTT                                      | GGGATTTCCCCTGTTT<br>TCAT    | TGAAGCGCTCTCCCAT<br>AGTT | 60.0                             | 448                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35537314  | Ca1                                     | 35537314                      | T/TG                                                           | ACATGGAACCCATCCA<br>AAGA    | AATCGATTGATTCAGC<br>CCAG | 60.2                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_35540202  | Ca1                                     | 35540202                      | AT/ATT                                                        | TTGTTTATGCCCTTTG<br>AGC    | ACAAACAAGTTGAGCA<br>CCCC  | 60.1                             | 146                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35553587  | Ca1                                     | 35553587                      | CA/CAA                                                        | TATGGACCGGAAATGG<br>ATGT   | TTTGAATCGTCTTCACT<br>GCG  | 60.0                             | 779                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35553773  | Ca1                                     | 35553773                      | GTATCCTA/GTA                                                  | GTCGAGGAGATTGCAA<br>AAGC   | TTTGAATCGTCTTCACT<br>GCG  | 60.0                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3556309   | Ca1                                     | 3556309                       | TTATATATATACATATATATAT/TTAT<br>ATATAT                         | TGACCTCATGGATACC<br>CACA   | AAGGTCGCATCTTCAT<br>CCTG  | 59.8                             | 371                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35563563  | Ca1                                     | 35563563                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                 | ATGGGAATGCTTGACT<br>GGAG   | CGACTGTAACACCCCG<br>TTTT  | 60.1                             | 390                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35565045  | Ca1                                     | 35565045                      | TTAAT/TTAATAAT                                                | AGCGATGCATGTCTCA<br>AGTG   | GCCCTTCTTCTTTTCCT<br>GGT  | 60.0                             | 427                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35767551  | Ca1                                     | 35767551                      | GTGAT/GT                                                      | TGGGAGATGCGATATG<br>TTTT   | ACAAC TTGTGATTTTCG<br>GGG | 58.0                             | 867                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35798308  | Ca1                                     | 35798308                      | GTTGGTTTTAATT/GT                                              | CACTTCTTCCGCGCTG<br>ATAA   | TTGGAAGGAGCCCTTA<br>CCTT  | 60.2                             | 753                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35832819  | Ca1                                     | 35832819                      | CAAAAA/CAAAAA                                                 | GGGTTTTCTAACCC<br>CGAT     | TGGTCATGCAGAACT<br>CAGC   | 60.1                             | 769                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35842524  | Ca1                                     | 35842524                      | GAAAAAAAAAAAAA/GAAAAAAAAAAAAA                                 | TCATGACCTTATGACAA<br>CGCTT | CAGGGGCACTACACCA<br>AAAT  | 59.6                             | 247                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                           | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                         |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_35899211  | Ca1                                     | 35899211                      | TTTTAGACAC/TTTTAGACACATT<br>GACAC                                                       | CACCTCCCCTGAGTTC<br>GTTA  | GCAAGCTCCAAATGGA<br>TTACA | 60.1                             | 404                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35946765  | Ca1                                     | 35946765                      | AG/A                                                                                    | GCGCCATTTTGTTCTTT<br>GTT  | ATTCTTGCCCTTTGTC<br>CCT   | 60.1                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35946848  | Ca1                                     | 35946848                      | AT/ATTTT                                                                                | GTTTCGTAGCGCCGTT<br>TATC  | ATTCTTGCCCTTTGTC<br>CCT   | 59.7                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35973449  | Ca1                                     | 35973449                      | TTATATATATATATATATATATATA<br>TATATATATAT/TTATATATATATATA<br>TATATATATATATATATAT         | GCCCACCCAACAAATA<br>CATC  | TTGGCACCAGAGAAAA<br>ACAA  | 60.1                             | 733                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_35977319  | Ca1                                     | 35977319                      | TA/TAA                                                                                  | AACGCGTTGGAAGTTC<br>CCTCT | GCAAGCAGCCTTGTTG<br>ACTA  | 59.2                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_36035161  | Ca1                                     | 36035161                      | AAGAGGGAGAGGGAGAGGGAGAG<br>G/AAGAGGGAGAGGGAGAGGGAGA<br>GGGAGAGG                         | TTCGTGATCCGTGAAT<br>TTGA  | AACGAAACAATGCCGA<br>ACAT  | 60.0                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_36044248  | Ca1                                     | 36044248                      | CGG/CG                                                                                  | CGATTTCCCTGCATGT<br>TTTT  | GCCTGTGATAGGCGGT<br>ACAT  | 59.9                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_36063199  | Ca1                                     | 36063199                      | T/TTTTTCC                                                                               | CGTTCGTGGTCCCTTA<br>ACTT  | TTGCGTTACGGATTG<br>ATGA   | 59.1                             | 227                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_36100635  | Ca1                                     | 36100635                      | CAATAATAATAATAATAATAATA<br>ATAATAATAATA/CAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAA | TGCATACACGTAGTGG<br>CACA  | GTGACGGCACATTTGT<br>GTTC  | 59.8                             | 854                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_36124030  | Ca1                                     | 36124030                      | GTTTTT/GTTTT                                                                            | TTTTCAGCTTTAAGTTC<br>CGCA | TTTAGGAAGACTGGCT<br>CGGA  | 60.0                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                        | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                      |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_36154229  | Ca1                                     | 36154229                      | ACTGCTGCT/ACTGCT                                                                                     | TTGCATTGATAATTGG<br>CTGC | TGTTCTTTTCTGCAA<br>TCA    | 59.7                             | 849                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_36249439  | Ca1                                     | 36249439                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATT/TTTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATT | TCCCCCTTTGTCTTCTT<br>GTG | TCCATCTAATTGCTACC<br>GGC  | 60.1                             | 930                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3636721   | Ca1                                     | 3636721                       | TAA/T                                                                                                | TTCATGGAACATTCTG<br>CCAA | CGACAAGTTTGAGGG<br>TTGT   | 60.0                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3642296   | Ca1                                     | 3642296                       | ATTTTTTTTTT/ATTTTTTTTTT                                                                              | AACCTCCCTAGTGCCG<br>AAAT | AAGTTGATGCCGAACA<br>AAATG | 60.0                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_36467494  | Ca1                                     | 36467494                      | AGGGG/AGGGGG                                                                                         | AGAGCACGGAGAAGGA<br>ACAA | CCCAGTTGGGTGAAC<br>TATG   | 60.0                             | 571                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_36603071  | Ca1                                     | 36603071                      | CTTTTT/CTTTT                                                                                         | TGCTTTGTCCCTTAG<br>TTGG  | CATAGAGCTGTGCGTG<br>GAAA  | 60.1                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_36642222  | Ca1                                     | 36642222                      | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATAT                                                | GATTGGATTGGCAAA<br>ATGC  | AGCAGAGTCACATGTC<br>CACG  | 60.3                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_36724754  | Ca1                                     | 36724754                      | CTTTTTTTT/CTTTTTTTTTT                                                                                | TTGCACCACACTTCTTC<br>ACC | CTTATTTGACGCTTTT<br>CGC   | 59.7                             | 279                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_36726460  | Ca1                                     | 36726460                      | GAAA/GAAAA                                                                                           | ACAGGAACGACCGAGA<br>GAAA | ATAGTTTTTGGGCGGG<br>CTAC  | 59.8                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_36746332  | Ca1                                     | 36746332                      | ATTTTTTTTTTTT/ATTTTTTTTTTTT                                                                          | GCTCAAACCTCTAACT<br>CGGC | TGGTGATGAAGGGAGA<br>AATGA | 59.1                             | 411                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_36869128  | Ca1                                     | 36869128                      | CA/CAAA                                                       | TCCACAACAACCTACG<br>TCCA    | CCCAGAAATCGATTAG<br>GCAA  | 60.0                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_36876798  | Ca1                                     | 36876798                      | AGGG/AGGGG                                                    | GTTTCCAGCCATCCAA<br>CACT    | AATTGGTTTCATGACCT<br>GCAC | 60.0                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_36962435  | Ca1                                     | 36962435                      | TA/TATAA                                                      | CAAGTCTCCCAACTTC<br>CCAA    | CAAGCATGATCCAGGG<br>AAAT  | 60.1                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_370295    | Ca1                                     | 370295                        | AAAGAAGAAGAAGA/AAAGAAGAAG<br>AAGAAGA                          | TTGCATGTGAAAAACA<br>GAAAGAA | ACTCCATTGTCGATTCC<br>CTG  | 59.8                             | 195                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37078918  | Ca1                                     | 37078918                      | A/AAATTAATG                                                   | TGTGACACCCTAAACC<br>CTAAGAA | TTGATTGCTTGCGTGTT<br>CTC  | 59.9                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37079213  | Ca1                                     | 37079213                      | CTCACAT/CTTCACAT                                              | TAAATATGGTCCCAAC<br>CCGA    | TTGATTGCTTGCGTGTT<br>CTC  | 60.0                             | 257                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37092021  | Ca1                                     | 37092021                      | CTTTTTTTTT/CTTTTTTT                                           | TATCAGAGTTCTCCCC<br>ACCG    | TTGAGGTGTGGTTTGT<br>GGTG  | 60.1                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37122105  | Ca1                                     | 37122105                      | AAAAAAAA/AAAAAAAAAAAAA                                        | CGTATCTCGTATCACC<br>GACG    | AGTTGCGCTCCTCCTA<br>ATCA  | 59.2                             | 873                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37122520  | Ca1                                     | 37122520                      | AGG/AG                                                        | TGCAATCATTGGTGCT<br>TAGG    | AAAAAGCGCCGTAAAA<br>TGAG  | 59.7                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37122699  | Ca1                                     | 37122699                      | GTTT/GTT                                                      | GGAGGAGCGCAACTTA<br>ATCA    | AAAAAGCGCCGTAAAA<br>TGAG  | 60.4                             | 372                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_37122810  | Ca1                                     | 37122810                      | TACAAC/TACAACAAC                                              | GGAGGAGCGCAACTTA<br>ATCA | AAAAAGCGCCGTAAAA<br>TGAG       | 60.4                             | 372                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37125192  | Ca1                                     | 37125192                      | GATGGAGATGGTTTGCAATGGAGA<br>TG/GATGGAGATG                     | AGCGGTTTAGGGTTTA<br>GGGA | CCAAATGTGCATACGA<br>ACCA       | 60.0                             | 113                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37128515  | Ca1                                     | 37128515                      | ATTTTTTT/ATTTT                                                | CAATCCCACAGGTAC<br>GCTT  | TTGGTCTCATCAATGAT<br>TGTA AAAA | 60.0                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3717542   | Ca1                                     | 3717542                       | ATT/AT                                                        | AGTGATGGTGTGGGT<br>GGAT  | CAATAATGTCCTCTCTA<br>TGCACCTT  | 60.1                             | 597                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37176254  | Ca1                                     | 37176254                      | TATA/TATACATA                                                 | TCAAGTTTGGAGGAAC<br>CCAG | CTGGACGTAGCCCGAG<br>TTAG       | 60.1                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37207886  | Ca1                                     | 37207886                      | TA/T                                                          | GGACCGACTAAAATCC<br>CACA | TTTTGCTTTGTGTCCCA<br>TCA       | 59.8                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37243078  | Ca1                                     | 37243078                      | AAATTAT/AAATTATAGAATTAT                                       | TCATCCACATCAGCCA<br>AAAA | TTTGTGCATTTTAATAA<br>TTGGAAG   | 60.0                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37410363  | Ca1                                     | 37410363                      | GAAAAAA/GAAAAAAA                                              | TGAATGAGGAGCACGT<br>CTTG | CTGTTGTTGCCAACGG<br>TTTT       | 60.0                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37420494  | Ca1                                     | 37420494                      | ATTTTTTTTT/ATTTTTTT                                           | GGGAAAAGGAACCCA<br>AAAA  | TAGTGGAGTCCCCGTC<br>AAGT       | 60.1                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37420598  | Ca1                                     | 37420598                      | ATTTT/ATTT                                                    | GGGAAAAGGAACCCA<br>AAAA  | TGAGTGAGGGAGACAA<br>AGGG       | 60.1                             | 950                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_37421082  | Ca1                                     | 37421082                      | CCTCACTCACTCACTCACTCAC/CC<br>TCACTCACTCACTCAC                 | ACTTGACGGGGACTCC<br>ACTA    | ACATGTTCTTGTGCTC<br>GTG      | 59.6                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37422521  | Ca1                                     | 37422521                      | TAAAAAAAA/TAAAAAAAAA                                          | CATCGTACTTCGTTGC<br>CCTT    | AGGTGTGCTAGCTAGG<br>GGTG     | 60.1                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37424329  | Ca1                                     | 37424329                      | CATATATATATATATATATAT/CAT<br>ATATATATATATATAT                 | AAAAAGTATTGAACAAA<br>CACGCT | TGAAATCCAAATTAAT<br>TGCTGAA  | 57.2                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37424604  | Ca1                                     | 37424604                      | CTTTTT/CTTTT                                                  | AAAAAGTATTGAACAAA<br>CACGCT | TGAAATCCAAATTAAT<br>TGCTGAA  | 57.2                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37424983  | Ca1                                     | 37424983                      | AC/A                                                          | GCAATTTAATTTGGATT<br>TCATGG | TCACATCCATCCACGG<br>TACA     | 59.6                             | 761                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37425070  | Ca1                                     | 37425070                      | ATTTTTTTTT/ATTTTTTTT                                          | GCAATTTAATTTGGATT<br>TCATGG | TCACATCCATCCACGG<br>TACA     | 59.6                             | 761                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37425153  | Ca1                                     | 37425153                      | G/GAT                                                         | GCAATTTAATTTGGATT<br>TCATGG | TCACATCCATCCACGG<br>TACA     | 59.6                             | 761                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37425439  | Ca1                                     | 37425439                      | TG/T                                                          | TGTACCGTGGATGGAT<br>GTGA    | TGACACGTATCAATTTA<br>GGGAGAA | 60.8                             | 222                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37425620  | Ca1                                     | 37425620                      | ACG/A                                                         | TGTACCGTGGATGGAT<br>GTGA    | TATGCATCCTCACGGT<br>TTTG     | 60.8                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37433380  | Ca1                                     | 37433380                      | CAA/CAACGTAAA                                                 | AATAAATTAGTGCAGC<br>AAACCAA | GGCAAAGAGAGGAAAG<br>TGGA     | 58.0                             | 756                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)      | Forward primers (5'-3')        | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------|--------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                    |                                |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_37433540  | Ca1                                     | 37433540                      | TATAATAGATAATAGATAATA/TATAA<br>TAGATAATA                           | TGAAAAACATCTCTCTA<br>ATAGGCG   | ACCACTGCACCAAGGG<br>TAAG | 59.0                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37489932  | Ca1                                     | 37489932                      | CAAAAA/CAAAA                                                       | ATTGTCCAGTTTCCTCA<br>CCG       | CGATTGGTAAATCGATT<br>GGG | 60.0                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37489959  | Ca1                                     | 37489959                      | AT/ATT                                                             | ATTGTCCAGTTTCCTCA<br>CCG       | CGATTGGTAAATCGATT<br>GGG | 60.0                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37490066  | Ca1                                     | 37490066                      | A/AATGTAT                                                          | ATTGTCCAGTTTCCTCA<br>CCG       | TGAACTCTGAGCGTGT<br>GACC | 60.0                             | 775                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37567284  | Ca1                                     | 37567284                      | CATATATATATATATATATATATAT<br>TAT/CATATATATATATATATATAT<br>ATATATAT | AGGTGCCCTAACCA<br>GTTT         | TTTGAGCAGAGAGAAC<br>CCGT | 59.9                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3764450   | Ca1                                     | 3764450                       | GATATATATATATATATATATATA/GA<br>TATATATATATATATATATATATA            | TTTTGGAGGTGTGATT<br>AATGTATTTT | TGGTTGATGTGTCGAG<br>TGCT | 59.2                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37686545  | Ca1                                     | 37686545                      | TCCCC/TCCCC                                                        | GAACCTCCCTTCATGAC<br>CCAA      | TTTGTGGTGGTGGAG<br>AACA  | 59.9                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37694287  | Ca1                                     | 37694287                      | AAAATTTTATAAA/AAAA                                                 | TTTGATTCTTCAATCCA<br>GCAA      | TTGATATCGGGTGGTC<br>CAAT | 58.3                             | 371                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37701839  | Ca1                                     | 37701839                      | AT/A                                                               | ATGCAGTCGCAATTGT<br>GGTA       | TGCACTTGTGGGGAC<br>AAAA  | 60.1                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37710484  | Ca1                                     | 37710484                      | AATTATTATTAT/AATTATTAT                                             | GCGCTCTTTTGCTTGT<br>TGAT       | GGATACAGTGGTCGCC<br>AAAT | 60.5                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_37712787  | Ca1                                     | 37712787                      | A/ACATGTG                                                     | GGTGTGGAGGTGTAA<br>TGGG    | CATGTCCCGTATTCGC<br>TTTT     | 60.1                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37714757  | Ca1                                     | 37714757                      | ATTT/ATTTT                                                    | TCGCTCACATATAAGG<br>TTGCAT | TTCGCCCATATTTCTT<br>TTG      | 59.6                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37716222  | Ca1                                     | 37716222                      | T/TTA                                                         | ATGGACAAACTACATG<br>GGGC   | TCCAACAACAACAACA<br>CATCA    | 59.7                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37716984  | Ca1                                     | 37716984                      | CTTT/CTT                                                      | TGATGTTGTTGTTGT<br>GTTGGA  | GTTTTGGGTACACCC<br>ATTG      | 59.9                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37728195  | Ca1                                     | 37728195                      | TAAAA/TAAA                                                    | CTCAAACTCGTTCCTG<br>CCTC   | CCCGCACCCTTACTAC<br>ACAT     | 60.0                             | 687                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37747301  | Ca1                                     | 37747301                      | TAAA/TAAAA                                                    | ATGGGTTTGATGGCGA<br>TTAG   | GGAAACAACATGTGGC<br>ATAAAA   | 59.8                             | 125                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37747367  | Ca1                                     | 37747367                      | GTTTTTTTT/GTTTTTTTTTTT                                        | ATGGGTTTGATGGCGA<br>TTAG   | TGCCACGTCTTAGTTTA<br>ATTAGCA | 59.8                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37747411  | Ca1                                     | 37747411                      | C/CGTTTATGT                                                   | ATGGGTTTGATGGCGA<br>TTAG   | TGCCACGTCTTAGTTTA<br>ATTAGCA | 59.8                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37754968  | Ca1                                     | 37754968                      | CAAAAA/CAAAA                                                  | ATTGTTCAACAGGGCA<br>CTTC   | CGCGCACAAAAGTAAT<br>TGAA     | 60.0                             | 852                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37759391  | Ca1                                     | 37759391                      | GT/G                                                          | CCATCTTGATCCTTTG<br>CCTC   | TCAAACGGTCAAATTG<br>GATG     | 59.6                             | 268                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                             |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_37761657  | Ca1                                     | 37761657                      | TCC/TC                                                        | GTTGGGCAACAATTGC<br>TTTT      | TAATCCTTGTGGAGGC<br>GATT    | 60.0                             | 375                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37773157  | Ca1                                     | 37773157                      | CTT/CT                                                        | GACGAGGAGTGGTTTG<br>GTGT      | AGCCGACATTGGAAAA<br>ACTG    | 60.0                             | 687                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37775837  | Ca1                                     | 37775837                      | TAAAAAAAA/TAAAAAAAAA                                          | GCGAGGTATGGTGATT<br>TCGT      | GAGGTATGCTTTTAAAC<br>CCCTTT | 60.0                             | 283                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_377760    | Ca1                                     | 377760                        | TAAAAA/TAAAAA                                                 | TCGGCTTTTAATACAAG<br>AGTGATTC | GCAACGCTCCTTTCCTT<br>CAC    | 60.0                             | 553                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37776874  | Ca1                                     | 37776874                      | A/AC                                                          | CTCCTTTGTCGCCATAA<br>CGA      | TGGAATTTTGAGTTTGC<br>GTTC   | 60.1                             | 622                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37781056  | Ca1                                     | 37781056                      | TCA/T                                                         | CCGGTAATCTGAAGTT<br>TGCC      | ACAGAGGCAAAACAGG<br>TTGG    | 59.6                             | 796                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37782834  | Ca1                                     | 37782834                      | AATATATATATATATATATA/AATA<br>TATATATATATATATATATA             | CTTTGGATCTACGCAT<br>CGGT      | CAAGGCTTGACAGTGA<br>GCAA    | 60.1                             | 699                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37783462  | Ca1                                     | 37783462                      | TTT/TTTCTT                                                    | ATACCAGACGCACCGA<br>AGAG      | CAAACTCAAAGAGAG<br>GGCG     | 60.3                             | 106                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37800107  | Ca1                                     | 37800107                      | TA/TATTTAAA                                                   | TGGGTCCTAAACCGCA<br>ATAC      | CAAAAATGATGCAACCA<br>TCG    | 59.8                             | 371                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37800689  | Ca1                                     | 37800689                      | ATATTATTATT/ATATTATTATT                                       | ACCGATGGTTGCATCA<br>TTTT      | CAACATGCAAACATGC<br>ACAA    | 60.2                             | 731                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                           |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_37802286  | Ca1                                     | 37802286                      | CAAAAAAAAA/CAAAAAAAAAAAA<br>AAA                                           | GAAAGGAGTTCGTTCT<br>CGGA   | TTGCGTCAAATCCACA<br>CAAT  | 59.4                             | 625                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37811315  | Ca1                                     | 37811315                      | A/ATC                                                                     | GCACTCAAATGCATGA<br>AAGC   | TGGCAAAAGAATGGAT<br>GATG  | 59.4                             | 213                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37811375  | Ca1                                     | 37811375                      | TAAAAA/TAAAAAA                                                            | CATCATCCATTCTTTG<br>CCA    | CACACCGAGCCAAATT<br>TTAAG | 59.5                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37811640  | Ca1                                     | 37811640                      | GTTTTTTT/GTTTTTTT                                                         | CATCATCCATTCTTTG<br>CCA    | AGTTCCCATATGTTGCA<br>GCC  | 59.5                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37812183  | Ca1                                     | 37812183                      | GTTTTTTT/GTTTTTT                                                          | GGCTGCAACATATGGG<br>AACT   | ACCTGAGTTTAACGGG<br>GATG  | 60.0                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3783626   | Ca1                                     | 3783626                       | TATTTCATTG/TATTG                                                          | TTCACAATTACCACAAA<br>GATCG | GCGACTATCCAGGAAA<br>TCCA  | 57.7                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37836904  | Ca1                                     | 37836904                      | CAGTTAGTTAGTTAGTTAGTT<br>A/CAGTTAGTTAGTTAGTTAGT<br>TAGTTAGTTA             | ATGGATGTAGCGATTA<br>CGCC   | CCAATACTCCACCTGC<br>GATT  | 60.0                             | 442                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3784964   | Ca1                                     | 3784964                       | TTAAATAAATAAATAAATAAAT<br>AAATAAATAA/TTAAATAAATAAATA<br>AATAAATAAATAAATAA | CTCCTTCTATGGGGCA<br>TCAA   | ATAAGCCCCTTCCAAA<br>GCAT  | 60.0                             | 272                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37852569  | Ca1                                     | 37852569                      | TAAAAAA/TAAAAAA                                                           | TGTGGTATGTGCGGTT<br>CCTA   | TTTGATGGGTTCA GTT<br>CCA  | 60.0                             | 814                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_37913622  | Ca1                                     | 37913622                      | AATATATATATATA/AATATATATATA<br>TATA                                       | ACGTTGCGCCACCTATC<br>TCAT  | CCTTATGCGGTAATCC<br>CTGA  | 59.6                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                        | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                      |                             |                               |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_37917967  | Ca1                                     | 37917967                      | ATATGACAGTTA/ATA                                                                                                     | TCCACAAGTTATTCTGA<br>CGAAAC | TTCCATTGATCTACGTT<br>AATGTTTG | 59.1                             | 558                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37927331  | Ca1                                     | 37927331                      | TAAA/TAAATTGTATCAAA                                                                                                  | ATTTTGATCGCGGAAG<br>TTTG    | TCAATCAACCAGATTTT<br>GCATT    | 60.1                             | 553                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37927862  | Ca1                                     | 37927862                      | G/GTA                                                                                                                | TGCAAAATCTGGTTGA<br>TTGAG   | TCCCAGATCAAAATTG<br>GGTT      | 58.8                             | 745                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37928853  | Ca1                                     | 37928853                      | CT/CTGAAT                                                                                                            | CCGTGCAACAATGTCA<br>ATTC    | GACCACCATATTAACC<br>GTCACA    | 60.0                             | 571                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37929646  | Ca1                                     | 37929646                      | TAAAAAAAA/TAAAAAAAAA                                                                                                 | TGTGACGGTTAATATG<br>GTGGTC  | TTGACTTGTTTTCGG<br>ATTG       | 59.6                             | 817                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37929711  | Ca1                                     | 37929711                      | ATTTTTTT/ATTTTTTTT                                                                                                   | TGTGACGGTTAATATG<br>GTGGTC  | TTGACTTGTTTTCGG<br>ATTG       | 59.6                             | 817                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37929753  | Ca1                                     | 37929753                      | ATTTTTTTTT/ATTTTTTTTTT                                                                                               | TGTGACGGTTAATATG<br>GTGGTC  | TTGACTTGTTTTCGG<br>ATTG       | 59.6                             | 817                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37935823  | Ca1                                     | 37935823                      | TAAAAAAAA/TAAAAAAAA                                                                                                  | TTGTGGATAGTTTCTC<br>CCTGAA  | CTCAAACCTCCCGAT<br>CAAA       | 60.0                             | 767                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37954337  | Ca1                                     | 37954337                      | GTTTTT/GTTT                                                                                                          | TCTTTTCTCCGATCCCA<br>TTG    | CGACTCCCGAACTCAA<br>AATC      | 60.0                             | 868                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_37980254  | Ca1                                     | 37980254                      | GTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TA/GTAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATA | CCATTTTGTCCATGTTT<br>CCC    | AATTGGGGTGTCCATT<br>TTGA      | 60.0                             | 348                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                 |                            |                           |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_37993665  | Ca1                                     | 37993665                      | CAAAAAA/CAAAAA                                                                                  | GTGAGCCCTTTACCAA<br>TCCA   | CAATTCCCACAGGTAC<br>GCTT  | 59.9                             | 654                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_37993738  | Ca1                                     | 37993738                      | TG/T                                                                                            | GTGAGCCCTTTACCAA<br>TCCA   | CAATTCCCACAGGTAC<br>GCTT  | 59.9                             | 654                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_38043395  | Ca1                                     | 38043395                      | GATATATATATATATATATATATA<br>TATATATATATATATATAT/GATATAT<br>ATATATATATATATATATATATATA<br>TATATAT | TCTGAATTTGGCAACAT<br>CATT  | CTTTCGCGATT CAGTC<br>AAAA | 58.1                             | 846                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_38064927  | Ca1                                     | 38064927                      | AT/ATT                                                                                          | GTGGATTCTCCTTCA<br>TCCA    | CCCGACGTTAAAGCAG<br>AAAG  | 59.9                             | 392                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_38067157  | Ca1                                     | 38067157                      | ATT/AT                                                                                          | TTCGTAAATCATTCGCC<br>CAT   | ACAAACAGGGTCCTTT<br>CCAA  | 60.3                             | 655                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_38070666  | Ca1                                     | 38070666                      | T/TA                                                                                            | AACCATTGGGGGAGAA<br>TAGAA  | TTGTTAGAACCATTGG<br>GGGA  | 59.7                             | 362                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_38070895  | Ca1                                     | 38070895                      | ATGTGTGT/ATGTGT                                                                                 | CTCCCCCAATGGTTCT<br>AACA   | CACTGGAATCCGTTTC<br>TTTTG | 59.8                             | 587                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_38071534  | Ca1                                     | 38071534                      | TACACACAC/TACACAC                                                                               | CTCCTCCTCATTCACC<br>CAAC   | ACACACCCACTCTCCTT<br>TGC  | 59.5                             | 189                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_38090626  | Ca1                                     | 38090626                      | CTTTTTTT/CTTTTTTTT                                                                              | TATTCGTGGCCCTTA<br>ACTT    | TGATTTGATGCCGTGA<br>GTGT  | 58.6                             | 821                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_38090984  | Ca1                                     | 38090984                      | CAT/CATATATAT                                                                                   | GGAATAAGGACTAAA<br>TCGGGAA | TGATTTGATGCCGTGA<br>GTGT  | 59.7                             | 545                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_38106060  | Ca1                                     | 38106060                      | TATA/T                                                        | AGGAGAAAATTGCAAC<br>ACCC     | TGCATATACAGTAAAT<br>TCGCC     | 59.0                             | 291                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38108337  | Ca1                                     | 38108337                      | ATTTTTT/ATTTTTTT                                              | CTTTTGAGCCGTAAGG<br>CAAG     | CCAAGCCAGTCAAAAC<br>ACAA      | 60.0                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38130303  | Ca1                                     | 38130303                      | C/CG                                                          | AAAGGGGGAGAACCAT<br>CTGT     | TGCATTTGCTTGACTTG<br>GAG      | 59.8                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38131605  | Ca1                                     | 38131605                      | C/CT                                                          | CGTAACTCGTGTGGG<br>TGAA      | GAAGCAAGAGGCAACT<br>CCAC      | 59.6                             | 379                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38141538  | Ca1                                     | 38141538                      | GGAA/GGAAGAA                                                  | TCATCAAATCCGTAATG<br>CAAA    | TGTTTTATAAGCATCAT<br>GTGTCATC | 59.0                             | 166                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38143864  | Ca1                                     | 38143864                      | GAAAAAAAA/GAAAAAAAA                                           | TTTGTCTCTCACCCG<br>CTTT      | TGATAGGTCTCATAGC<br>CCCG      | 59.9                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38147657  | Ca1                                     | 38147657                      | TC/TCC                                                        | TGTTGACACATCACAT<br>CCTTAACA | TTTCATGTCTCATTTCC<br>CCA      | 60.3                             | 858                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38148096  | Ca1                                     | 38148096                      | CAAAAAAAAA/CAAAAAAAAA                                         | TGGGGAAATGAGACAT<br>GAAA     | ACGTTGCGCAGGTGTA<br>ATTT      | 58.9                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38148667  | Ca1                                     | 38148667                      | GAAA/GAAAA                                                    | GCAACGTGCGGGTTAT<br>ATTT     | GAAGGCGCTGTAA<br>TGCC         | 59.9                             | 228                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38170055  | Ca1                                     | 38170055                      | C/CT                                                          | GAAGAGGGAGCTTCA<br>TCCC      | TTGGAGCTCAAGAGG<br>AGGA       | 60.0                             | 935                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_38185784  | Ca1                                     | 38185784                      | ACC/ACCC                                                      | TCCATGCTCCATGCAT<br>TAAA    | GGAAGTGTGATTCACT<br>TGGTGA | 60.0                             | 686                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38193113  | Ca1                                     | 38193113                      | CAAAAAAAAA/CAAAAAAAAAAAAA                                     | CGAACAACTCACCGG<br>ATCT     | CCAATGGAGTCCCAAA<br>AAGA   | 60.1                             | 724                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38223459  | Ca1                                     | 38223459                      | GAA/GAAA                                                      | ATTGCTTTCCCAATCA<br>ACG     | GCCCTTTTTCATCATGC<br>TTC   | 59.9                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_3822628   | Ca1                                     | 3822628                       | AATATATATATATATATATATAT/A<br>ATATATATATATATATATATATAT         | GCACGTTTTTAAAAGG<br>AGTCAAA | TGGAGAAATTGTTCGT<br>GAGC   | 59.7                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38227247  | Ca1                                     | 38227247                      | GT/GTT                                                        | CTGAGAATGGCAGCAC<br>AAAA    | TTGATGTATTTTGCGCA<br>TTCA  | 60.0                             | 348                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38236366  | Ca1                                     | 38236366                      | A/AGAT                                                        | AGCAAAGAGTCTGCCT<br>TGGA    | TTCTTGCTTTGCTCCTG<br>GAT   | 60.1                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38242184  | Ca1                                     | 38242184                      | AGTGTG/AGTG                                                   | CCTTGAGTTCGACACT<br>CGGT    | CCATTTGGAACGAAGA<br>AAGC   | 60.3                             | 768                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38243964  | Ca1                                     | 38243964                      | ATTTTTTT/ATTTTTT                                              | GCCTCCTTTTAATGGC<br>ACAA    | GCCCAGAAGTCCTGTG<br>TAGC   | 60.1                             | 791                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38281902  | Ca1                                     | 38281902                      | TTCT/TT                                                       | GAAACACGCTCGAACT<br>CCTC    | TGGAAGAAAGAACCTT<br>TGGC   | 60.0                             | 888                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38283164  | Ca1                                     | 38283164                      | T/TCA                                                         | ATTCGTAGCAACGCAT<br>CCTT    | GTGGGCCAAAAGCTAC<br>ACAT   | 59.7                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_38288491  | Ca1                                     | 38288491                      | ATGTTGTTGT/ATGTTGT                                            | CATCAAGAAAATTGCC<br>CAGAA  | TGAGTTGGCAAAATAT<br>CCATGA | 60.1                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38291576  | Ca1                                     | 38291576                      | CA/C                                                          | TTGGGCATTGCAACTT<br>ACAC   | AGGGCTTATGGCCCTA<br>GGTA   | 59.6                             | 964                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38303577  | Ca1                                     | 38303577                      | TT/TTGT                                                       | GGTCGTGCTGCAAGGA<br>TTAT   | GTGTGGTACTCATGCG<br>ATGC   | 60.1                             | 873                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38393926  | Ca1                                     | 38393926                      | CAAAAAA/CAAAAAAA                                              | GTTGAGGCAGTAGCCT<br>TTGC   | GGTCACATTAAGGAAG<br>CCGA   | 60.0                             | 730                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38450592  | Ca1                                     | 38450592                      | ATGTGTGTGTGTGTG/ATGTGTG<br>TGTGTGTG                           | TGCTTGACAATCTCCT<br>GCAC   | TTATCTTCGATCCCACC<br>AGG   | 60.0                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38483352  | Ca1                                     | 38483352                      | TAAAAAAAAA/TAAAAAAAAA                                         | AGACCTCAATGTTGCG<br>AACC   | TCGGTGAATGATGGAG<br>TGAA   | 60.1                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38493608  | Ca1                                     | 38493608                      | ATTTTTTT/ATTTTTTT                                             | TCTGGGGAAGCGACTT<br>CTAA   | TGTGATTGTAATGTG<br>GCAAA   | 59.9                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38494341  | Ca1                                     | 38494341                      | TAAGAAGAAGAAGAAGAAGAA/<br>TAAGAAGAAGAAGAAGAAGAA               | ATCCGTCTTCAAGTTG<br>TGCC   | ACGCCCTTGAGTGAG<br>ATTA    | 60.1                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38514075  | Ca1                                     | 38514075                      | GTTTTTTT/GTTTTTTT                                             | GACGTGGTTACAAGGG<br>AGGA   | TGTGGGAATCTTCTGC<br>AAAC   | 60.0                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38568165  | Ca1                                     | 38568165                      | GTTTTTTT/GTTTTTTT                                             | GGTTCGGTTTAGATTG<br>AACTCG | GCAACGGTCATTTCAA<br>GGTT   | 60.0                             | 229                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_38577185  | Ca1                                     | 38577185                      | GTTTTT/GTTTT                                                  | CCATTTTCTGTCCCTT<br>TCA    | GCATTGGCTAAGCATG<br>GATT   | 59.9                             | 760                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38613531  | Ca1                                     | 38613531                      | GAAAAA/GAAAAA                                                 | CCTTCCTTCATGGTGA<br>TTTGA  | TCCCTGATCACACTTC<br>CTCTG  | 59.9                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38623512  | Ca1                                     | 38623512                      | ATTTTTT/ATTTT                                                 | AGCAACTGCTTCAACC<br>CACT   | CGTCACGGCTTCCATT<br>TATT   | 59.9                             | 858                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38636457  | Ca1                                     | 38636457                      | AAT/AATAT                                                     | AATATCCCAACAGCCT<br>CACG   | TTGATTGAAACATTGAT<br>TTCCG | 60.0                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38639253  | Ca1                                     | 38639253                      | ATTTATTTTT/ATT                                                | TGCCCTTCATGTACCA<br>ATCA   | ATGTGCGCATGATTGA<br>TGTT   | 59.9                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38656327  | Ca1                                     | 38656327                      | T/TG                                                          | AATGGGTTTTGGAGTG<br>CAAG   | ACAAAGAGAGAACATG<br>GCCC   | 60.0                             | 261                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38657360  | Ca1                                     | 38657360                      | TAAAAAA/TAAAAA                                                | CCATCAGTGATAACTT<br>GTCCCA | CACAGGACAAGTGCAA<br>TCTCA  | 59.9                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38671088  | Ca1                                     | 38671088                      | CTTGTGATT/CTTGTGATTATTTGT<br>TGTGATT                          | TGTTGGGTCCTTGAT<br>GGTT    | TTAGAGCGGAGCTTCT<br>TCCA   | 60.2                             | 825                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38708599  | Ca1                                     | 38708599                      | AATATATATATATATATAT/AATATAT<br>ATATAT                         | TTTGGTTGCAAATTGT<br>GTGG   | GAAGGCATGAAACATC<br>ACGA   | 60.4                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38708894  | Ca1                                     | 38708894                      | AATTATTA/AATTA                                                | TTTGGTTGCAAATTGT<br>GTGG   | CAGCTCTTGGGATCGA<br>GAAG   | 60.4                             | 781                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_38744149  | Ca1                                     | 38744149                      | CTTTTT/CTTTTT                                                 | GAACAGTCTCATTAAAT<br>GTCGCAA | TGTGCTTGTCCCACAC<br>ACTT  | 59.3                             | 283                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38746497  | Ca1                                     | 38746497                      | A/AAATC                                                       | TCAAGCCACAAAATTG<br>GAAA     | CCCGTGTAAGCATTG<br>ATGG   | 59.1                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38757124  | Ca1                                     | 38757124                      | TAAAAAAA/TAAAAAAA                                             | CACACACCTCAGCAA<br>ATGG      | TGGAATCCCTCCTTC<br>CTCT   | 60.2                             | 895                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38759589  | Ca1                                     | 38759589                      | TG/T                                                          | TGTACTCCCCAGACG<br>TAGG      | TGTGCTTGTCCCACAC<br>ACTT  | 60.0                             | 883                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38766572  | Ca1                                     | 38766572                      | CTT/CTTT                                                      | GCTTGAGGCATTGTCC<br>ATTT     | GAGCCACCGACTTGAA<br>GAAG  | 60.1                             | 443                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38771127  | Ca1                                     | 38771127                      | GTTATTATTATTAT/GTTATTATTAT<br>ATTATTAT                        | CCTTGTTGGAAGAAGC<br>TTGA     | ATATTGAGCGTCGTAA<br>CCCC  | 60.4                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38773402  | Ca1                                     | 38773402                      | AT/A                                                          | GTTTTGGCGTTGGTTT<br>CACT     | TGGGTGCTTTCTATAAT<br>GTGC | 60.0                             | 977                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38800314  | Ca1                                     | 38800314                      | TTCTCTC/TTCTCTCTCTC                                           | TGGCACAAAAGAGTTG<br>GTCA     | AAATATTTGGTTTTCGG<br>CCC  | 60.3                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38852863  | Ca1                                     | 38852863                      | A/AAT                                                         | ATGACCCGGAGGCTAT<br>AGGT     | TATGGCTCAACACAAA<br>CCCA  | 59.8                             | 187                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38852972  | Ca1                                     | 38852972                      | AATTAGGAT/AAT                                                 | TGGGTTTGTGTTGAGC<br>CATA     | TTTGAGTTCCTAAGGTC<br>CCG  | 60.0                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_38853658  | Ca1                                     | 38853658                      | AA/AATAATA                                                    | CGGGACCTTAGGAAC<br>CAAA   | GGTGTGTTTTTGGGGT<br>TTGT   | 59.2                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38872978  | Ca1                                     | 38872978                      | TAAAAAAA/TAAAAAA                                              | TGGCCACTTCTTATCA<br>CAAAA | TGAAGCAAGAAAATTGT<br>GCTGT | 58.3                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38874695  | Ca1                                     | 38874695                      | TTA/TTATA                                                     | AAAGTTTTTGCCAAGTC<br>CCA  | AGGTCGTCAACTGGA<br>TTCG    | 59.6                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38875592  | Ca1                                     | 38875592                      | TCA/T                                                         | ACCGAATCCAGTTGAA<br>CGAC  | GGTCAATCCATCCATA<br>GCCA   | 60.0                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38875978  | Ca1                                     | 38875978                      | CAAA/CAA                                                      | GCCGGCAACTCTTTTC<br>AATA  | AGACTGCGAACTGTCA<br>TCCA   | 60.2                             | 679                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38886569  | Ca1                                     | 38886569                      | TAAAAAAA/TAAAAA                                               | GCAACACTAGAACAA<br>AGACGG | ATTTATCCATCCATGTC<br>GCC   | 59.8                             | 786                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38887147  | Ca1                                     | 38887147                      | GTTTTTTT/GTTTTTTT                                             | GGCGACATGGATGGAT<br>AAAT  | TTTCCGGTGGTACGAG<br>AGAG   | 59.6                             | 438                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38890999  | Ca1                                     | 38890999                      | AAGT/A                                                        | CTGGGGGCCATAAAC<br>TAAT   | TAAATGAGTCGGATAG<br>CCCG   | 60.0                             | 329                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38895300  | Ca1                                     | 38895300                      | ATTTTTTTT/ATTTTTTTT                                           | AATGGGTGTGTTTGT<br>TGAGA  | TTTGAAATCCCAAATT<br>GCC    | 58.0                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38896192  | Ca1                                     | 38896192                      | CAAAA/CAA                                                     | ATATGCAGCGGCTCTT<br>GTTC  | CAATGCTTCTTGCTTGT<br>TTCA  | 60.4                             | 378                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_38897537  | Ca1                                     | 38897537                      | TATAATAATAATAATAA/TATAAT<br>AATAATAA                          | GCTGCTCGTAGAGCCA<br>AATAA  | GGACTACTTTTGCATT<br>CAGC  | 59.6                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38915417  | Ca1                                     | 38915417                      | CATATATTATATATTATATTAT/CA<br>TATATTATATATTAT                  | TTTTCACACAAATAACG<br>CGG   | AATGACGGTGGCAGAG<br>TTTC  | 59.6                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38922989  | Ca1                                     | 38922989                      | GCCCC/GCCC                                                    | GAACCGGCATTCTTG<br>TGTT    | ATGGAAAGGTTCGAAT<br>GTGC  | 60.0                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38941583  | Ca1                                     | 38941583                      | AAAAA/AAAAATATATAAAA                                          | TCACATTAAGTCAAAA<br>GCACA  | TCGACTTCTTGGTGA<br>GTTTG  | 59.4                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38943432  | Ca1                                     | 38943432                      | TA/TAA                                                        | GCTCTTGTGAGTTGGT<br>GTTGC  | TGGCCTCTTCGGTACT<br>GATT  | 60.9                             | 571                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38944490  | Ca1                                     | 38944490                      | T/TC                                                          | TGAAGGGGATCCATCA<br>TATAAC | GCGATATCCAGAATGG<br>GCTA  | 57.8                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_38945208  | Ca1                                     | 38945208                      | ATTTTTTTT/ATTTTTTTTTT                                         | CCCATTCTGGATATCG<br>CACT   | CCCGAAAACCTTCATTCC<br>AAA | 59.9                             | 825                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_390566    | Ca1                                     | 390566                        | TATATCATATCATA/TATATCATATCA<br>TATCATA                        | TTGGTGGATCGTTTAG<br>GAGG   | TACGGTCCCCACTCAT<br>TCTC  | 59.9                             | 782                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39105122  | Ca1                                     | 39105122                      | GTAATTAATTA/GTAATTA                                           | CATTTTCTGACGCACC<br>TTCA   | TCTATGTTGGCTTACG<br>CACG  | 59.8                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39110990  | Ca1                                     | 39110990                      | ATT/ATTT                                                      | TTTTATGGGTCTGTGT<br>AATGCG | ACACGGGGCACTTATT<br>TTGA  | 59.9                             | 273                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')     | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|-----------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                     |                             |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_39141870  | Ca1                                     | 39141870                      | AATATAATATATAATATAATAT/AA<br>TATAATATATAATAT                        | CAGCAAAACAACGCAC<br>ATTCT   | AACAAGTGGGTGACCT<br>GCAT        | 60.3                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39143008  | Ca1                                     | 39143008                      | CTTTTTTTTT/CTTTTTTTTTT                                              | TTCACAAATGTTGTTTT<br>CCTCG  | TCCATCTCCAACAACAT<br>CAAA       | 60.0                             | 422                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_392320    | Ca1                                     | 392320                        | CA/CAGAA                                                            | TGAGTTGCATCAAATG<br>GTGTT   | CCTAACGCAGAGAGGG<br>TTTG        | 59.0                             | 851                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39254298  | Ca1                                     | 39254298                      | AAATAAAT/AAATAAT                                                    | TTCAATTTTTCCGCCCT<br>ATG    | ATGGCTACACCAATGC<br>ATCC        | 59.9                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39261977  | Ca1                                     | 39261977                      | A/AT                                                                | GGTTTGCTGTCGAGCC<br>TTAG    | AAACACAAGTCCAATCA<br>AAAGG      | 60.0                             | 421                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39265068  | Ca1                                     | 39265068                      | GTTTTT/GTTTTTT                                                      | TTGGAAGCTAAGAAGC<br>CGAA    | ATAATGGCCAAGGAAC<br>ATGC        | 60.1                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39303782  | Ca1                                     | 39303782                      | ATTTT/ATTTTT                                                        | CCATCCACATTTTCAAG<br>TGATTT | TGAATCGTGAGGGTGT<br>TATGA       | 60.1                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39319575  | Ca1                                     | 39319575                      | TTTATTTATTTGCTTATTTATTT/TTT<br>ATTTATTTGCTTATTTATTTGCTTAT<br>TTATTT | TTTGCTCTTCTCCTCC<br>AGA     | CCACCAAATACAAATAA<br>ATTACTTACG | 60.1                             | 970                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39382557  | Ca1                                     | 39382557                      | AC/A                                                                | ATACGGTAGCAAGACC<br>GCAC    | ATCGCCGATTGATCATT<br>TTC        | 60.2                             | 915                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39387109  | Ca1                                     | 39387109                      | TC/TCC                                                              | GAAAGTAAAGACGCGT<br>CCCA    | CTGGGCCAAGGTTGAG<br>ACTA        | 60.2                             | 548                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_39390988  | Ca1                                     | 39390988                      | TA/TAA                                                        | GCCAGCTCACGTCTAA<br>TGAA   | GCCTAATTTTGCCACC<br>GATA | 59.0                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39392138  | Ca1                                     | 39392138                      | ATTTTTTTT/ATTTTTTTTT                                          | CGCCCTGGGTAATAT<br>GTTT    | AATCTATCAGGCACCC<br>ATGC | 60.9                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39399195  | Ca1                                     | 39399195                      | CAT/CATAT                                                     | CATTGCCCCAAGAATC<br>ATCT   | GGATCTTTTGGCAGGT<br>TGAA | 60.0                             | 278                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39400591  | Ca1                                     | 39400591                      | TATTAATT/TATT                                                 | GTCGTGTGCAGCCCC<br>TATT    | CAAATGACCAATCGG<br>AAAAA | 60.0                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39400871  | Ca1                                     | 39400871                      | CTTTTTTTTT/CTTTTTTTTTT                                        | TGGTAAGCATGAAGAA<br>GGCA   | TTTCTTCTCGATTGGT<br>CCTG | 59.4                             | 813                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39403148  | Ca1                                     | 39403148                      | CTTTTTTT/CTTTTTTT                                             | TCTCTAATCAATGGTTG<br>CAAAA | CAGTGCGAATGCTGA<br>CCTA  | 57.5                             | 806                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39406657  | Ca1                                     | 39406657                      | CA/CAAA                                                       | ACCATGAAACCTTCGA<br>CCTG   | AAAAAGGTGACGTGGC<br>AGAC | 60.0                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39428106  | Ca1                                     | 39428106                      | CTTTT/CTTT                                                    | AGAGCGGAGATAATGG<br>GTCA   | GTGCCAGTCGATTGCC<br>TAAT | 59.7                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39428398  | Ca1                                     | 39428398                      | TAAATCGATTGGGAAATCGATT/TAA<br>ATCGATT                         | CGGAACCAATTGTTGG<br>ACTT   | GTGCCAGTCGATTGCC<br>TAAT | 59.8                             | 284                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39430506  | Ca1                                     | 39430506                      | ATT/ATTTT                                                     | TGCATCTCCCTCAAGC<br>TTTT   | TGGAAAAATTTGGGGT<br>TCAA | 60.0                             | 976                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_39431107  | Ca1                                     | 39431107                      | A/AC                                                          | TTGAACCCCAAATTTT<br>CCA    | TCATTACCCCTTCCAC<br>TTG      | 60.1                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39431958  | Ca1                                     | 39431958                      | CAAA/CAA                                                      | TCAAGTGGGAAGGGGT<br>AATG   | ACCCCAATCTGCATA<br>AAAA      | 59.8                             | 902                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39432122  | Ca1                                     | 39432122                      | CTTTTTTT/CTTTTTTTTTTTT                                        | CAATTGCACAAATCATT<br>GTTGA | CAGGTGCATTATTCGG<br>TGTG     | 59.5                             | 870                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39450720  | Ca1                                     | 39450720                      | TAAAAA/TAAAAAA                                                | CCTGTGCCTTTGCTTT<br>ATTTG  | TTGCATAAATGGGAGG<br>GAAG     | 59.8                             | 705                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39460851  | Ca1                                     | 39460851                      | ACCCCC/ACCCCC                                                 | GTGCCTTAGAAACCC<br>ATCA    | CCAACATTGCATTGAAC<br>CTG     | 59.9                             | 820                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39463854  | Ca1                                     | 39463854                      | AAATTTAAT/AAAT                                                | ATATTGAGAGGTTGCG<br>TGGG   | ACCATCTCGATGCAAC<br>ACAA     | 60.0                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39463964  | Ca1                                     | 39463964                      | TAAA/TAAAA                                                    | ATATTGAGAGGTTGCG<br>TGGG   | ACCATCTCGATGCAAC<br>ACAA     | 60.0                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39472871  | Ca1                                     | 39472871                      | CAAAAAAAAA/CAAAAAAAAA                                         | CATCAAACCTAGACG<br>GGGG    | TTTTAGGCGAATATGG<br>AGCAA    | 59.5                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39504560  | Ca1                                     | 39504560                      | T/TTATTA                                                      | CAACTCGGTTACACC<br>TTCA    | CAGCTAAAAACGGGG<br>ACCA      | 59.7                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39508256  | Ca1                                     | 39508256                      | GAAAAAAAA/GAAAAAAAAA                                          | ACCTTTAGACTTGGGG<br>CACA   | CGGTTACCATTGTAAAA<br>ACAATCA | 59.6                             | 254                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_39511343  | Ca1                                     | 39511343                      | CA/CAA                                                        | CGACGAAAGTGATGTG<br>CATT  | TGGATTTACAATCATG<br>GGTT       | 59.7                             | 136                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39574370  | Ca1                                     | 39574370                      | T/TA                                                          | CACACATCTATACAACC<br>GCGA | TCAAAGCGTTGTTGAG<br>TGCT       | 59.6                             | 164                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39584232  | Ca1                                     | 39584232                      | CAAAAAAAAA/CAAAAAAAAA                                         | GCAGCTGGCAGACATA<br>ATGA  | ATTGCTTCAGCGCTG<br>CTAT        | 60.0                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39595566  | Ca1                                     | 39595566                      | ATTTTTTTTT/ATTTTTTTTTTTTTTT                                   | GAGCTCACTCAAGCAT<br>GTCG  | TTTGAGATCTTATTTT<br>GGTTTAATGA | 59.7                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39605985  | Ca1                                     | 39605985                      | CTTTT/CTTTTT                                                  | TTGGCCAAATTTTCACA<br>ACA  | TTGGTACTATGCACGG<br>CTTG       | 59.9                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39606006  | Ca1                                     | 39606006                      | CTT/CT                                                        | TTGGCCAAATTTTCACA<br>ACA  | TTGGTACTATGCACGG<br>CTTG       | 59.9                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39608275  | Ca1                                     | 39608275                      | AGGG/AGGGG                                                    | GGTCGACACATGGAGA<br>GTTG  | TTATTACAAACTGCCC<br>CCA        | 59.1                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39609113  | Ca1                                     | 39609113                      | AATAT/AAT                                                     | ATGGCCTTTCATTTTCA<br>ACG  | TTGTCTCAAGCGTTCAA<br>TTTTT     | 59.9                             | 725                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39621400  | Ca1                                     | 39621400                      | TC/T                                                          | TGATCGTTGATCCAAT<br>CAAAA | TCTTCCAGCCTCTTTAC<br>CGA       | 59.0                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39652228  | Ca1                                     | 39652228                      | ACCC/ACCCC                                                    | GGAGTGACAATGCCCT<br>CAAT  | CGGGAGATACGTAGGA<br>GCAA       | 59.9                             | 774                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_39654601  | Ca1                                     | 39654601                      | CT/CTGTT                                                      | CAGGGTTTGACAGTGA<br>ACAAAG | CCAAATTGCCTCAAACA<br>CCT  | 59.7                             | 696                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39682708  | Ca1                                     | 39682708                      | GCT/G                                                         | TCAATTGGCATTGTCAT          | AAATTCAGCACTGCAC<br>CAAA  | 59.9                             | 802                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39718500  | Ca1                                     | 39718500                      | TTCATAGTCATA/TTCATA                                           | TTTGAGAAAAATCTTGACATCCAA   | CCAAACGTCGTGATTT<br>GTTG  | 60.0                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39773308  | Ca1                                     | 39773308                      | TTTTAAATATTAAATTTAAATATTAA/TTTTAAATATTAA                      | AAATGTATTGTTGTGG<br>GGTGA  | TTGGTTGTAAGGGGAA<br>CCAG  | 59.1                             | 958                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39782012  | Ca1                                     | 39782012                      | TA/T                                                          | TTTCCTAGACCATCTG<br>CGG    | CGATCAAATATTTTCA<br>CCGAA | 60.2                             | 678                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39783200  | Ca1                                     | 39783200                      | ATT/ATTGACCTT                                                 | TGGACGGATGGTTATT<br>GTTG   | GTCGTTGTCAGGTTGT<br>GTGG  | 59.2                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39793723  | Ca1                                     | 39793723                      | CAAA/CAAAA                                                    | TGTGAGGCATGTTGA<br>AAGG    | TGCGGGTTCAATTTTA<br>GACA  | 59.7                             | 930                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39837467  | Ca1                                     | 39837467                      | GT/GTCCTTT                                                    | TTTCATGGTGTCTTGGCA         | CGAGAAATAGCTCAG<br>AGGC   | 60.1                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39847433  | Ca1                                     | 39847433                      | AAATA/AAATAATA                                                | GAGGAAATTATCCCG<br>CAAA    | TTTGGACTTCGTCGTTT<br>TGA  | 59.0                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39853129  | Ca1                                     | 39853129                      | AACAGACA/AACAGACAATTAGAAAA<br>ACACAGACA                       | ATTGCCCACTTGGCTA<br>TGAC   | CGTGGGAACCTGAACC<br>TTGT  | 60.0                             | 813                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_39871055  | Ca1                                     | 39871055                      | TAAA/TAAAA                                                    | CATTGGCCACCTTTAG<br>GAAA      | TGCATTGCTTCAGTCAT<br>GGT   | 59.9                             | 329                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39906834  | Ca1                                     | 39906834                      | CATGAGTA/CATGAGTATGAGTA                                       | TTAAAAATGCGCTCATG<br>GTGT     | CACGCTAATCTGAGCC<br>AACA   | 59.2                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39949239  | Ca1                                     | 39949239                      | GAAAAAA/GAAAAAAA                                              | TGAAGAATTTACAAATG<br>CAATCTGA | TAGTCTGACAACCCCG<br>GACT   | 60.0                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_39955215  | Ca1                                     | 39955215                      | GTA/GTATA                                                     | CAATGGATGAAGAGG<br>AAAAGG     | AACGACTTGCAATTGT<br>CCCT   | 59.9                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40010790  | Ca1                                     | 40010790                      | TCCCCC/TCCCC                                                  | CCAACAATCTCCCCAT<br>TTGT      | TGTCAACAACAGAGGA<br>TGGG   | 59.6                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40021624  | Ca1                                     | 40021624                      | AC/A                                                          | TGAAGCATGCAATTAG<br>CAAAA     | CATACCCCCATTAGCG<br>GATA   | 59.5                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40035747  | Ca1                                     | 40035747                      | T/TG                                                          | AACTGGAGCCTACCGG<br>AAAT      | GAACCCAAGGGGTAAG<br>GGTA   | 60.0                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40056652  | Ca1                                     | 40056652                      | ATTTTTT/ATTTTTT                                               | TTGGTCCCATCAAAAC<br>CACT      | TTTGCCAGATTGTTCT<br>TCC    | 60.2                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40081687  | Ca1                                     | 40081687                      | AATTTATATAT/AAT                                               | TTCCACCATTGGATG<br>ATGA       | TTGCCTGAAAAAGAGA<br>TGTCAA | 59.7                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40086233  | Ca1                                     | 40086233                      | GAAAA/GAAA                                                    | ACAACCTCTCACACGG<br>GAAA      | TTGACTCAATCCACGA<br>GCAG   | 60.5                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_40091424  | Ca1                                     | 40091424                      | GAAAAAAAAA/GAAAAAAAAA                                         | AACTTGGATTGGCAC<br>GAAC     | CAACACCTTCTCTGATT<br>TGAACA | 60.0                             | 705                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40121038  | Ca1                                     | 40121038                      | AATATATATATATATATATAT/AAT<br>ATATATATATATAT                   | ATTTCCGGTGATCAGCG<br>GTT    | TCGAACCAAGGATTTT<br>CCAC    | 60.5                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40126750  | Ca1                                     | 40126750                      | CATA/CA                                                       | AGGCGCCACAATCTAG<br>AAGA    | TTCTCCATCACAGCGTT<br>CAG    | 60.0                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40147055  | Ca1                                     | 40147055                      | CGTTTCAAATTAAGT/CGT                                           | ACGAAACAATCATTGA<br>ACGTA   | AGCGTTGCCAAAATA<br>ATGC     | 57.3                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40149739  | Ca1                                     | 40149739                      | TCAACCA/TCA                                                   | GAAAGGGAGACATTGA<br>TCGG    | TCTGCAACAACATTAG<br>AAGCA   | 59.5                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_401568    | Ca1                                     | 401568                        | ATT/AT                                                        | CAAATTAATGCAGGC<br>CCAT     | CCACGCTAAATCACATT<br>CCA    | 60.0                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40176468  | Ca1                                     | 40176468                      | GTTTT/GTTT                                                    | AAACGCAATCTATGTG<br>AAAACAA | TTTGTCATCACCACCA<br>AGA     | 58.7                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40177252  | Ca1                                     | 40177252                      | TAAAAAAAAAAAAA/TAAAAAAAAA                                     | TCTTGGGTGGTGATGA<br>CAAA    | GCATCATGAGATATGG<br>AAAGGA  | 59.9                             | 764                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40181142  | Ca1                                     | 40181142                      | AATGGTGATGCGATGATGGTGATG<br>CGATG/AATGGTGATGCGATG             | GATGTGATGACGGTGA<br>TTCG    | CAATGGAGCTGTGAT<br>GTGG     | 59.9                             | 273                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40214195  | Ca1                                     | 40214195                      | CT/C                                                          | ACAAAGGCAGGATTTT<br>GTGG    | AAGCTCTCACAAGGG<br>CAAA     | 60.0                             | 158                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_40216460  | Ca1                                     | 40216460                      | GTT/GTTCTT                                                    | GTCTCTTCTGATTGGG<br>GCAA     | TGGGTGGAAAGCAATA<br>GAGG | 60.2                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40219666  | Ca1                                     | 40219666                      | TG/T                                                          | GACAACTTCCACCTC<br>CGTG      | CCTTCCCTGCAAAGAT<br>ACCA | 60.5                             | 701                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40224219  | Ca1                                     | 40224219                      | TAAAAAAAAA/TAAAAAAAAA                                         | CATTGCATCTGATTG<br>GTGG      | TCCTTGCCTCATAGGA<br>GCGT | 59.9                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40231747  | Ca1                                     | 40231747                      | GT/GTT                                                        | CGGTGTAATAAATAAG<br>ACGGAGTG | CTCAAATCCAAACACT<br>TGG  | 59.0                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40232307  | Ca1                                     | 40232307                      | CAAAAA/CAAA                                                   | TCCAAGGTGTTTGAT<br>TTGAG     | CAGAAATTTGGTTGAG<br>GGGA | 60.0                             | 717                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40246424  | Ca1                                     | 40246424                      | TACA/TA                                                       | CAATGGAAATGTCCGA<br>AACC     | TGGTCCCAAGATTTCG<br>AAAA | 60.2                             | 186                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_4026071   | Ca1                                     | 4026071                       | CAAAAAAAAAAAAA/CAAAAAAAAA<br>AAAA                             | GCATCATGTTTGTTAT<br>GCG      | CAAGGTCTCGAGCAAT<br>AGCC | 60.0                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40264315  | Ca1                                     | 40264315                      | CAAAAAAAAA/CAAAAAA                                            | TCAAATCATTGGTGAA<br>GCCA     | CCACCAGTCCAAATCA<br>ACCT | 60.0                             | 712                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40281112  | Ca1                                     | 40281112                      | AGGG/AGG                                                      | CGCATAATTGACTCCC<br>GAAC     | TTGTTTGTCTTCGCC<br>CTT   | 60.5                             | 214                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40298582  | Ca1                                     | 40298582                      | TAAAAAAAAA/TAAAAAAAAA                                         | TTTAAAGATGCTGAAA<br>CAAACAAA | AGCCGTGTTGATTTTC<br>GCTA | 59.3                             | 251                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_40300289  | Ca1                                     | 40300289                      | GA/GAA                                                        | TGGGCTAGCAAAGGAG<br>AGAA | CACCTGAAACCCCTTT<br>GAA   | 60.1                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40313158  | Ca1                                     | 40313158                      | TCT/TCTAACT                                                   | CGAATTGAGTTTACGC<br>GGTT | GGATGCTTCTGAATGA<br>ATGGA | 60.1                             | 466                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40313177  | Ca1                                     | 40313177                      | CTCTCTTCTCTCTTCTCTCT/CTC<br>TCTCTTCTCTCT                      | CGAATTGAGTTTACGC<br>GGTT | GGATGCTTCTGAATGA<br>ATGGA | 60.1                             | 466                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_403262    | Ca1                                     | 403262                        | TA/TAA                                                        | TGCAATGACAAAATAG<br>GGCA | ACCGTTAATTGGGTG<br>GAAA   | 60.1                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40326561  | Ca1                                     | 40326561                      | GTT/GTTT                                                      | CCGGCAAATATGACGA<br>ACTT | AAACCAAGAACAAAATG<br>GCG  | 60.0                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40394902  | Ca1                                     | 40394902                      | ATT/AT                                                        | GGTAGCCTTCATTGGG<br>TGAA | GAGAACCTTGCTCTGA<br>TGCC  | 59.9                             | 235                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40398387  | Ca1                                     | 40398387                      | CT/C                                                          | TGAAAAATACTTTTGGG<br>CCG | AAACGCCATGGATTG<br>TCAT   | 59.9                             | 858                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_403989    | Ca1                                     | 403989                        | CT/CTCGTATTGACAGT                                             | TTGCACCTTATGCTTCA<br>CCA | CAATGGGAGCGCAGTT<br>TTAT  | 60.3                             | 228                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40400180  | Ca1                                     | 40400180                      | TG/T                                                          | TTGGGGGAATTGGTGT<br>AAAA | ATCACACAAATCACGA<br>GCCA  | 60.0                             | 801                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40407895  | Ca1                                     | 40407895                      | GAAAAA/GAAAAAA                                                | TGGATGTAGCCTTCAT<br>TGGG | TTCAAAAGAAGCAAAAC<br>CGA  | 60.9                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_40408466  | Ca1                                     | 40408466                      | CTTATTTATTTATTTA/CTTATTTATT<br>TATTTATTTA                     | TCACAAACAATTGCGA<br>AAACA  | CCACCTCCATGCCTCT<br>AAAA       | 60.1                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40408801  | Ca1                                     | 40408801                      | ATT/ATTGAGCCAACTT                                             | TTTGTAGAGGCATGGAG<br>GTGG  | TTTGTCAAATGTTGGGT<br>TCA       | 60.1                             | 343                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40424012  | Ca1                                     | 40424012                      | GTTTTTTTT/GTTTTTTTTTT                                         | TTTGTAGAGGCATGGAG<br>GTGG  | TCCAAGAGGTCAAACG<br>TCAA       | 60.1                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40424034  | Ca1                                     | 40424034                      | TTATATATATAT/TTATATAT                                         | TTTGTAGAGGCATGGAG<br>GTGG  | TCCAAGAGGTCAAACG<br>TCAA       | 60.1                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40424994  | Ca1                                     | 40424994                      | C/CCAAAATATTATAA                                              | TGCAAAACTTTGTTCAT<br>CGAG  | GCATCATTCTCCTTCGA<br>GACA      | 59.0                             | 748                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40425232  | Ca1                                     | 40425232                      | AAA/AAATAA                                                    | CATTTTTAAGCTTTTGT<br>TGCCA | GCATCATTCTCCTTCGA<br>GACA      | 59.3                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40425317  | Ca1                                     | 40425317                      | GTCTC/GTCTCTC                                                 | CATTTTTAAGCTTTTGT<br>TGCCA | TTTCATTAAAGGTGAATC<br>GTTCCAGA | 59.3                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40425540  | Ca1                                     | 40425540                      | ATTTTTTTTT/ATTTTTTTTT                                         | TGTCTCGAAGGAGAAT<br>GATGC  | AAACCGGTTCAAAAAT<br>GCAC       | 60.4                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40482336  | Ca1                                     | 40482336                      | GAAAAAAAAA/GAAAAAAAAA                                         | CAAAGTCTAGTTCGGC<br>CCAG   | TATGCATAAGGGTGTG<br>GCAA       | 59.9                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40516551  | Ca1                                     | 40516551                      | CATATATATATATATATATATATA<br>TATA/CATATATATATATATATATA<br>TATA | TGGTTGGCATGTTGTT<br>CCTA   | TCTAAGCAAAGCTCCA<br>CTTTTT     | 60.0                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                         | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                       |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_40535465  | Ca1                                     | 40535465                      | TTAATAATAATAATAATA/TTAAT<br>AATAATAATAATAATA                                                          | CATGCGTTCCTTGTGG<br>TAGA    | ATCACAGTTTGGCCAA<br>GTCC   | 59.7                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40535882  | Ca1                                     | 40535882                      | AATATATATATATATATATAT/AAT<br>ATATATATATATATATATATAT                                                   | GATGATGATGATGTGCG<br>TGCC   | ATCACAGTTTGGCCAA<br>GTCC   | 59.9                             | 311                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40611283  | Ca1                                     | 40611283                      | GATATATATATATATATATATATA<br>TATATATATATATATATAT/GATATAT<br>ATATATATATATATATATATATA<br>TATATATATATATAT | ATGCATGTGTGTCGAG<br>TGGT    | TGTCCGAATTGCATTCT<br>CAA   | 60.0                             | 632                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40665843  | Ca1                                     | 40665843                      | TTATATATATATATATAT/TTATAT<br>ATATATATATATATAT                                                         | CCACGTCAATTTTGAC<br>ATACATC | ACCAAGATCCGCTTAC<br>ATGG   | 59.3                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40735911  | Ca1                                     | 40735911                      | AATATATATATATATATATATATAT<br>ATATATATATATATATAT/AATATATA<br>TATATATATATATATATATATAT                   | AAATGCAAAATTTTAAG<br>CGTGA  | CCATTGGAAAGTGTGT<br>AGTGC  | 58.8                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40814692  | Ca1                                     | 40814692                      | TA/T                                                                                                  | TGGGGAATCTCTTAAT<br>GTTTCG  | CTATCACAAGCCCCTA<br>CCGT   | 60.3                             | 100                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40889769  | Ca1                                     | 40889769                      | TTATATA/TTA                                                                                           | GCATCTCTTGATGCCC<br>TTTT    | AACATACGCCATACCC<br>AAGC   | 59.3                             | 289                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40890559  | Ca1                                     | 40890559                      | ATTTTT/ATTTTTT                                                                                        | CGGATTTGCAAGTGTT<br>CGTA    | TGGGGTTTAGGATATC<br>ACATCA | 59.7                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40890662  | Ca1                                     | 40890662                      | CAAA/CA                                                                                               | CAAGAAACAAATTGCA<br>ATGGA   | TCAAGTTTGGGAGGAA<br>CCAC   | 58.7                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_40899161  | Ca1                                     | 40899161                      | GTTTTTTTTTTTT/GTTTTTTTTT                                                                              | ATTGGTTCCATTGAT<br>CCG      | TTATGTTAGGCAGGG<br>TTTGA   | 59.6                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |





| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_41695561  | Ca1                                     | 41695561                      | ATTTTTTTTT/ATTTTTTTTTTT                                       | TTCCAAAGTATTGTGG<br>GACACTT | TTGTTGGAGATAATTGA<br>AGCTGA    | 59.8                             | 964                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_41704419  | Ca1                                     | 41704419                      | CATAATAAT/CATAAT                                              | GGGGAATTTTTCATTT<br>GTGG    | TGTTTTGGTTTCAAGG<br>GACA       | 60.4                             | 311                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_41704503  | Ca1                                     | 41704503                      | CTTTTTTT/CTTTTTT                                              | GGGGAATTTTTCATTT<br>GTGG    | TGTTTTGGTTTCAAGG<br>GACA       | 60.4                             | 311                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_41705653  | Ca1                                     | 41705653                      | ATTTTTTTTT/ATTTTTTT                                           | CATCACGTAACATGA<br>CTTACCA  | TCCAATAATTTTCTC<br>TTTCG       | 59.8                             | 723                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_41709578  | Ca1                                     | 41709578                      | AGGGGG/AGGGG                                                  | TTGTGGAAGCAAGAGG<br>TGAA    | TCCCTCATCATATTT<br>GCC         | 59.4                             | 136                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_4171296   | Ca1                                     | 4171296                       | T/TCATTTTTAGCTTA                                              | CAACAAAACGCGCTAA<br>TGAC    | CGAGATTTTGAGGCAT<br>GTTG       | 59.4                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_41718814  | Ca1                                     | 41718814                      | T/TG                                                          | GGGTCGAATGTCGATT<br>CTGT    | TCATCTCTCAGCCCCA<br>CTCT       | 59.9                             | 156                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_41721873  | Ca1                                     | 41721873                      | ATTTT/ATTT                                                    | TGGTGAGTAAGAAATT<br>CAAGGGA | TGACAATCAAAGTAAAA<br>TGAGTCAAA | 60.0                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_417847    | Ca1                                     | 417847                        | CCAAAGCAA/CCAA                                                | TAAGGGTAAGGCCACC<br>AAAG    | AACCGTTATACGGCAA<br>CGAC       | 59.1                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_417899    | Ca1                                     | 417899                        | AAAAAG/A                                                      | ACCAAAGCAAGCGTTT<br>TAGG    | GTTTTGGCGAGTCCAT<br>CATT       | 59.4                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                         |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_41852137  | Ca1                                     | 41852137                      | ATTTTT/ATTTTT                                                 | TGACCGAAATGTTAAAGCG     | AACATTGTGAATGATCTCGTCA    | 58.8                             | 300                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_41949447  | Ca1                                     | 41949447                      | ATATTTTATTTTATTTT/ATATTTTATTTTATTTTATTTT                      | TGTTTTGTAAAAGTGTGCAGAA  | TTGTTTCCACTCATGCGAAG      | 58.9                             | 851                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_4196063   | Ca1                                     | 4196063                       | TCTACT/TCT                                                    | GCTGCAAAATGCAAACTGA     | TGGAACGAGGAATTGGAGTC      | 60.0                             | 694                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_41998443  | Ca1                                     | 41998443                      | CG/CGG                                                        | CCATTTTCTCACGTGCTTTC    | ATCCCTCTATTGGTGGTCC       | 59.7                             | 339                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_42053807  | Ca1                                     | 42053807                      | CGTTGTTGTTGTTGTTGTTGT/CGTTGTTGTTGTTGTTGTTGT                   | GGGATCTTTTGGCTGATGA     | CTCATCTCGCCATTGTTTT       | 60.0                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_42057802  | Ca1                                     | 42057802                      | ATTTTTTTT/ATTTTTTTT                                           | CGGTTAAAAACGTCGCAAAAT   | TTTGATACGTGTACTCAACCGAA   | 60.0                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_4214755   | Ca1                                     | 4214755                       | CTTTTTTTTTT/CTTTTTTTTTT                                       | TTTTGGTCCACATCAAGCTG    | GTATAATTGGTGGCCCGATG      | 59.7                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_42168404  | Ca1                                     | 42168404                      | TCC/TCCC                                                      | CCAATCGATTCCGTCAGTT     | TGGTGATTGTGTGGGAATTG      | 59.9                             | 207                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_42206966  | Ca1                                     | 42206966                      | G/GATGCT                                                      | AGACTCCGATACCACACCA     | GGGAAAATCATGTTTATCACAAATC | 58.0                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_42209181  | Ca1                                     | 42209181                      | GAAA/GAAAA                                                    | TTTTTCCCCCTTATGGTGAG    | GCGAGCATGAGAAGTTGTTG      | 58.9                             | 319                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                               | Forward primers (5'-3')       | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------|-------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                             |                               |                               |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_43467858  | Ca1                                     | 43467858                      | CTTTTT/CTTTTT                                                                                                               | GAGATTTAGAACCATC<br>AAATTGTCA | GCAACCTGCCATCCAT<br>ACTT      | 58.6                             | 603                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_43534972  | Ca1                                     | 43534972                      | CTTTTTTTTT/CTTTTTTTTTTT                                                                                                     | GTTGTTTGCCTTTTCC<br>CCTA      | TGTGTTAAATCCACCG<br>CAAA      | 60.0                             | 460                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_43550360  | Ca1                                     | 43550360                      | ATTT/ATT                                                                                                                    | TGCAGAGTAATTCGGT<br>TTGTTTT   | GGCATTAAAGCCTCAAA<br>TCCA     | 60.1                             | 458                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_43595794  | Ca1                                     | 43595794                      | AAAGAAGAAGAAGAAGAAGAA<br>GAAGAA/AAAGAAGAAGAAGAAGAA<br>GAAGAAGAAGAAGAA                                                       | GGAAGCCTGGAATGAC<br>ACAT      | TTCAATTCGATTTTGA<br>CCC       | 59.9                             | 555                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_43662427  | Ca1                                     | 43662427                      | TCAC/TCACAC                                                                                                                 | TCACGTCACAACACTC<br>CACA      | CGCGTCAGAGGTAGGA<br>AAAG      | 59.7                             | 382                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_43687147  | Ca1                                     | 43687147                      | TAA/TA                                                                                                                      | TGTGGCTAAGATTAGA<br>ATCCCAT   | TTGATGCAAACGTAATT<br>CATAAAGA | 59.0                             | 586                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_43690044  | Ca1                                     | 43690044                      | AATATATATATATATATATATAT/A<br>ATATATATATATATATATATAT                                                                         | AGACATATGTTGCTG<br>GCCT       | TGAGTTTGTTTGAGAG<br>GATTTGTT  | 59.7                             | 781                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_43911901  | Ca1                                     | 43911901                      | GTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATT/GTTATTATTATTATTATTATT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATT | TGAGGGACTGGATTCA<br>GGAG      | GGCGTGTTCTTTGTTT<br>GGTC      | 60.2                             | 578                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_43986145  | Ca1                                     | 43986145                      | AA/AATA                                                                                                                     | CCTCTTTGGTTCCATG<br>TGCT      | TGATGTGTTGTCTTG<br>GGGA       | 60.1                             | 385                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_44247311  | Ca1                                     | 44247311                      | GTTTTTTTTT/GTTTTTTTTT                                                                                                       | TTCTCCAGACTCTAGC<br>CCGA      | AGCTTCTCAGTAGGGG<br>GCTC      | 60.1                             | 592                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                      | Forward primers (5'-3')        | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------|--------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                    |                                |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_44248190  | Ca1                                     | 44248190                      | AATATATATATATATATATAT/AA<br>TATATATATATATATAT                                                      | GCTCACTGACAATGGC<br>TTCA       | CAACAATGGAGGAAGG<br>AGGA | 60.0                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_44368738  | Ca1                                     | 44368738                      | GATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAA/GA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAATAA | TTGTAACCCCCGAATT<br>GTTG       | AGAGGCAACAAGAAC<br>CGAA  | 59.8                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_44406344  | Ca1                                     | 44406344                      | TAA/TA                                                                                             | TGCAGAAATCTCATCA<br>AGCG       | GTGCCACTGACTTGTG<br>CAAT | 60.1                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_44467151  | Ca1                                     | 44467151                      | GTTT/GTTTT                                                                                         | ATGCAGCTCAAAAACA<br>GCCT       | GGTTCACCCAAAGATG<br>GCTA | 60.0                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_44650256  | Ca1                                     | 44650256                      | T/TC                                                                                               | TCGTTTGCCTCATTGG<br>ATTA       | AGGGAGGACGAAAATG<br>ACCT | 60.1                             | 444                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_44745225  | Ca1                                     | 44745225                      | A/AC                                                                                               | TCCGGATATAGTCCTG<br>CCAC       | TCCTTGTGAACGACTT<br>GGTG | 59.9                             | 632                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_44776081  | Ca1                                     | 44776081                      | AATATATATATATATATATATAT<br>ATATATATATATATAAATATATAT<br>ATATATATATATATATATATATATA<br>TATATATATATATA | TGGAATACCATATATT<br>TACGTTTTCA | TGACGGATCCTTTCTT<br>GACA | 59.1                             | 795                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_44808505  | Ca1                                     | 44808505                      | GAAAAAAAA/GAAAAAAAAA                                                                               | GAAATGAGCTGCACAC<br>CAGA       | TAAGGCATGCAAAGGT<br>TGGT | 60.0                             | 383                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_44847252  | Ca1                                     | 44847252                      | ATCTGATGTTCTGATG/ATCTGATG<br>TCTGATGTTCTGATG                                                       | TGTTTTCTGCCTTTTG<br>CCT        | AAAATCCAACAATCTCC<br>CCC | 59.9                             | 274                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_44847313  | Ca1                                     | 44847313                      | TATAATAATAATAATAATA/TATA<br>ATAATAATAATAATA                                                        | TGTTTTCTGCCTTTTG<br>CCT        | AAAATCCAACAATCTCC<br>CCC | 59.9                             | 274                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                   | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                 |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_4485491   | Ca1                                     | 4485491                       | CATATATATATATATATA/CATATATA<br>TATATATATATA                                                                     | TTTGATGTTGTTGGAG<br>ATGAAA | TGCCATGCATCAGTTG<br>TTTT  | 58.1                             | 792                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_44921329  | Ca1                                     | 44921329                      | ACTT/AGGATGCTGATCTTCTT                                                                                          | CCTCAAACGATTTTCTG<br>GGA   | CTTCCCAATGCGTGA<br>AGAT   | 60.0                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_44943657  | Ca1                                     | 44943657                      | CTATATATATATATATATATATATAT<br>ATATATATATATATATATATAT/CTAT<br>ATATATATATATATATATATATATATA<br>TATATATATATATATATAT | CATACCATGCATCCCA<br>ACAA   | TACTCGTTGCTCTCGTT<br>CCC  | 60.2                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45057162  | Ca1                                     | 45057162                      | CATAAA/CATAAATAAA                                                                                               | TTGCTTGAATAGGCAA<br>TGGA   | ACGTCGACGACATCAA<br>AGTG  | 59.3                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45057964  | Ca1                                     | 45057964                      | CAAA/CAA                                                                                                        | AAACTAGATTATGGCC<br>TGCG   | TGCTCGCAATTAACA<br>TGC    | 57.0                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45098064  | Ca1                                     | 45098064                      | GTTTTTTTTT/GTTTTTTTTT                                                                                           | AAGCCACTGTTAATCC<br>ACGC   | TGCTAGGGCACAACTC<br>TCCT  | 60.1                             | 125                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45124635  | Ca1                                     | 45124635                      | GTATATATATATATATATATATATA/G<br>TATATATATATATATATATATATATA                                                       | TCCGAGACACAAGACC<br>AACA   | TTACGAACACAATTGTT<br>GCCA | 60.3                             | 836                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45232358  | Ca1                                     | 45232358                      | T/TAGCAATAATG                                                                                                   | GTTAAGCCCCGATCAA<br>TGAA   | CATCCCCCTCTTTAAC<br>CAT   | 59.9                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45238172  | Ca1                                     | 45238172                      | T/TGACA                                                                                                         | ATTCTTTTGGAGCGC<br>AGAA    | CCAATTAGGTTTACGG<br>CGAA  | 60.0                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45246034  | Ca1                                     | 45246034                      | C/CGTCTTGTT                                                                                                     | CGATTTCGCTTTTAGC<br>ATCC   | CAATTGCGATATTATGG<br>GGG  | 59.8                             | 253                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                            | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                                          |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_45251376  | Ca1                                     | 45251376                      | C/CCTATGA                                                                                                                                                                | CTAGCTCTGGGTTCTGA<br>GTGG | ATCCGACTAGTTCCGG<br>GTTT | 60.0                             | 247                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45392704  | Ca1                                     | 45392704                      | ATTT/ATTTT                                                                                                                                                               | GGGGGCTCTTCATTTT<br>TCTC  | CACAGTTTCATCGCTC<br>CTCA | 60.0                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45395070  | Ca1                                     | 45395070                      | AT/A                                                                                                                                                                     | CACGAACGACAGAAGA<br>ACCA  | CCTCAGATGAGAGCCA<br>GGAC | 59.9                             | 481                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45443277  | Ca1                                     | 45443277                      | GTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAGTAATAGTAATAATAA<br>ATAATAATAATAACAATAATAATAAT<br>AATAATAATAATAATAGTAATAGTAA<br>TAATAATAATAATAATAATAATAATA | CCCACATTCATGACGT<br>GTTT  | CTTAGAGGTGGGAAC<br>GTGA  | 59.8                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45497101  | Ca1                                     | 45497101                      | TTTTTTTTTT/TTTTTTTTTTTTT                                                                                                                                                 | AGTATAAGTGGGGCCG<br>TGTG  | TGGATTGTGCCAATTT<br>TCA  | 59.9                             | 237                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45535603  | Ca1                                     | 45535603                      | GAAAAAAAAA/GAAAAAAAAA                                                                                                                                                    | GTTTAGGGTTGCTCAT<br>GGGA  | TTTGGAAGACTTTCGG<br>GTTG | 59.9                             | 318                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45609121  | Ca1                                     | 45609121                      | C/CT                                                                                                                                                                     | TCGCGTGAGAAAATAA<br>TCCC  | CGAACCCTCGGTAAAC<br>AAAA | 60.0                             | 295                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45609375  | Ca1                                     | 45609375                      | A/ATTACAAT                                                                                                                                                               | TTTTGTTTACCGAGGG<br>TTCG  | CAATGATCTTGAAGGC<br>ACCA | 60.0                             | 142                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45833155  | Ca1                                     | 45833155                      | CTTTTTTTTT/CTTTTTTTTTT                                                                                                                                                   | TGTGGCATTGGACCAA<br>CTTA  | GGGTAAAAACGGGTTG<br>GACT | 60.0                             | 981                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_45859437  | Ca1                                     | 45859437                      | G/GAATTTGGA                                                                                                                                                              | AGACCTGTGGTGTGAT<br>GCTG  | AAGAGAGGTCACTTTG<br>GCGA | 59.7                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)                | Forward primers (5'-3') | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|-------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                               |                         |                           |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_46088799  | Ca1                                     | 46088799                      | CTATATATATATATATATATATATATATATATATAT/CTATATATATATATATATATATATATATATATATATAT   | TAGTCCGTAAGTGGTGCCC     | GGGCTTTCCAAAGTGTATACC     | 60.0                             | 586                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_4612204   | Ca1                                     | 4612204                       | AATATATATATATATATATATATATATATATATATATATA/AATATATATATATATATATATATATATATATATATA | GCCATTGGGAATGACGACTT    | CGTTTTGCAACTTCCC AAC      | 59.9                             | 327                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_46178255  | Ca1                                     | 46178255                      | AATTTATAATTTAT/AAT                                                            | TCAAACATGCTCTGAATGCC    | AACCAATACATAAACATCACAGTGC | 59.8                             | 570                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_46186559  | Ca1                                     | 46186559                      | AGTGATTGGTTTGTGTGATTGGTTGTTG/AGTGATTGGTTTGTGTGTTTGTTG                         | AAAGCACACGATTTTCACCC    | TTCGGCATCTAGCACTTCCT      | 60.0                             | 775                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_46268212  | Ca1                                     | 46268212                      | TA/T                                                                          | AAACGCAATCCTTGAGTTCG    | CATGACTTGGATTGGTCTGTG     | 60.2                             | 226                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_46278771  | Ca1                                     | 46278771                      | ATGGCCTGGCCTGGCCTGGCCTG/ATGGCCTGGCCTG                                         | ACCTTCAGTCAGGGGCCTAT    | AAGTCTGGTCTGGCCTGAAA      | 60.0                             | 538                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_46283204  | Ca1                                     | 46283204                      | CA/CATA                                                                       | AGTGCCATGCCTAATGAAT     | CAATGGGCTTCTTACC TGGA     | 59.7                             | 425                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_46286614  | Ca1                                     | 46286614                      | CTTTT/CTTT                                                                    | CCAAGTTATGCTTGATCGCA    | CGAGAACCATCCTGCA TTTT     | 59.8                             | 820                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_46286661  | Ca1                                     | 46286661                      | GTAGGGATA/GTA                                                                 | CCAAGTTATGCTTGATCGCA    | CGAGAACCATCCTGCA TTTT     | 59.8                             | 820                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca1_P4_46352138  | Ca1                                     | 46352138                      | CACAAC/CACAACAAC                                                              | AGCGATGCATGTCTCAAGTG    | TGCCCTTCTTCTTTTCC TAGTG   | 60.0                             | 396                                           | INTERGENIC                                  | --                               | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_4647010   | Ca1                                     | 4647010                       | AATATATATATATATATATATATA/<br>AATATATATATATATATATATATA<br>ATA  | AAAAATACCACAACCTG<br>AATTAATGA | CATGTGAAATGTAGCC<br>AGTTGC | 57.4                             | 700                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_46491737  | Ca1                                     | 46491737                      | CAAG/CAAGAAG                                                  | GATGCATCTCACCAAG<br>GGTT       | CGGTGCAAACCTCTACG<br>TTCA  | 59.9                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_46500141  | Ca1                                     | 46500141                      | GCC/GC                                                        | GTAGCCAAAGGATTGC<br>CAAA       | ATGTGCAAGGAACCCG<br>TTAG   | 60.1                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_46507085  | Ca1                                     | 46507085                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                     | TCAATTTCTGCTCCG<br>GAAT        | TTCTTTGGGTTGCGT<br>TTAC    | 60.4                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_46523548  | Ca1                                     | 46523548                      | CAAAAAAAAAAAAAAAAA/CAAAAAA<br>AAAAAA                          | GTGGACAAACCTGCAT<br>TCCT       | ACCATGCACAGTTGCT<br>GAGA   | 60.0                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_46525859  | Ca1                                     | 46525859                      | GAAAAA/GAAAAAA                                                | CCCACCTGGATACAAG<br>GCTA       | AGTAGAGGGAGTTCCG<br>GTGC   | 59.9                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_46526481  | Ca1                                     | 46526481                      | CAAAAAA/CAAAAAAA                                              | TTAAATTCGAGGCG<br>AAAA         | ACATGGTTGTGGTGGT<br>GATG   | 59.7                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_46528558  | Ca1                                     | 46528558                      | CT/CTT                                                        | TTAAATTCCTCCTCG<br>GCT         | AACTCTGGGAACCTC<br>CTGT    | 60.0                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_46528735  | Ca1                                     | 46528735                      | GTGACAGCTGACAG/GTGACAG                                        | TTAAATTCCTCCTCG<br>GCT         | GGGGAACATCCCGT<br>TATT     | 60.0                             | 865                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_46539303  | Ca1                                     | 46539303                      | TTCAATCTTCATCAATCTTC/TTC<br>AAATCTTC                          | TCAAGCCAATCTTCCC<br>AAAC       | TCTGATGACAAAAGGG<br>GGAG   | 60.1                             | 757                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_46539360  | Ca1                                     | 46539360                      | CAAA/CAAAA                                                    | TCCCAAACAGCCTGAT<br>AACC      | CTGATGACAAAAGGGG<br>GAGA    | 59.9                             | 744                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_46633354  | Ca1                                     | 46633354                      | GTATATATATATATATATAT/ATAT<br>ATATATATATATATAT                 | CGACATGGCTCTGATA<br>CCAA      | TCAGACCGCCTTTACC<br>AATC    | 59.7                             | 615                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_46662012  | Ca1                                     | 46662012                      | AAT/AATAT                                                     | GCATTTACGTCGATATT<br>TATGAGTG | TCAGCCAAAAAGCTGA<br>TGTG    | 59.1                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_46798111  | Ca1                                     | 46798111                      | CCCTAAACCTAAACC/CCCTAAACC                                     | AAACCTGAAGCCCTAC<br>ACCA      | TTAGGGTTTCGGGATA<br>AGGG    | 59.6                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_46896717  | Ca1                                     | 46896717                      | AATATATATATATATATA/AATATA<br>TATATATATATATATA                 | CACGATGCATTGGTG<br>AGGT       | TCGTTCAATAACCTTTT<br>TCTTGG | 59.4                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_46900592  | Ca1                                     | 46900592                      | ATTT/ATTTT                                                    | GATGCCTTGACCATCC<br>TTGT      | TGGGTACACGCATATT<br>AACCAA  | 59.9                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_47016631  | Ca1                                     | 47016631                      | ACTCTCTCTCTCTCT/ACTCTCTCTC<br>TCTCTCT                         | ATTGCCTCTCAGTCGC<br>GTTA      | AAAATTCGACATCGTGA<br>GGG    | 60.9                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_47048638  | Ca1                                     | 47048638                      | TG/T                                                          | TAGCACCAGACCATTC<br>TCCC      | CAATTGAAGGCCCAAA<br>ACAT    | 60.1                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_47161229  | Ca1                                     | 47161229                      | TAGAG/TAG                                                     | TCTGCAATGAAAGCAA<br>ACACA     | AGTTTTGGCTCCCTATC<br>GGT    | 60.4                             | 829                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_47186820  | Ca1                                     | 47186820                      | ATTTTTTTTT/ATTTTTTTT                                          | CTCACTCTTAAACCAG<br>CCGC      | GTCTGCCACGTCACCT<br>TTTT    | 60.0                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_47346271  | Ca1                                     | 47346271                      | TA/TAA                                                        | CAGTCACACTAGCGAC<br>CGAA | GAACCCAAGGCTTTGT<br>CGTA  | 60.0                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_47373127  | Ca1                                     | 47373127                      | T/TTGTTGC                                                     | CAGCAGCAAGAGCCAT<br>GTTA | GCCATTCCTCTACCA<br>CCAA   | 60.2                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_4742142   | Ca1                                     | 4742142                       | TAAA/TAA                                                      | GACCGCGTAGATGTGG<br>AACT | GGATGAGACCTCTAC<br>TTGCC  | 60.1                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_47455633  | Ca1                                     | 47455633                      | GAAAAAAAA/GAAAAAAAA                                           | TTGGGGTCAGTCAAC<br>ACAA  | CGGTGAAATAGGTATG<br>CCAAA | 60.0                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_47580436  | Ca1                                     | 47580436                      | ATTTTTTTTTTT/ATTTTTTTTTT                                      | AAATGGTGAGGGGTGA<br>AGTG | CGACCCTTGGCTAATT<br>CAAA  | 59.8                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_47580698  | Ca1                                     | 47580698                      | ATTTTTTTTTTT/ATTTTTTTTTT                                      | TTTGAATTAGCCAAGG<br>GTCG | TCGATTCGAAATGGAT<br>GTCA  | 60.1                             | 615                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_47626582  | Ca1                                     | 47626582                      | ATTT/ATTTT                                                    | CATGATGATGGTTGCT<br>TTGC | CTTGCGCTACCATGTG<br>AAGA  | 60.1                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_47630703  | Ca1                                     | 47630703                      | TAAAAAGAAAAAGAAAAAGAA/TAA<br>AAAGAAAAAGAAAAAGAAAAAGAA         | CGTGTCCGGCAAAGTA<br>AAAT | GTGATGCACGCAGTAA<br>TTGG  | 60.0                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_47630977  | Ca1                                     | 47630977                      | AC/ACC                                                        | GGCCTTCCATCGTGAA<br>TAA  | TTTCGAATTCAGAACT<br>GCC   | 59.9                             | 916                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_47730180  | Ca1                                     | 47730180                      | GATATATATATATATATA/GATATA<br>TATATATATATATA                   | TGCGTATCTTAGGAAT<br>GCGA | GGCTAGACGAGTTCGA<br>CGAC  | 59.4                             | 321                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                 |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_4776428   | Ca1                                     | 4776428                       | GAAAAAAAA/GAAAAAAAA                                                             | CTAACTCGCCAACAAT<br>GCAA   | TTTCACAAAGAAGAA<br>CCGC    | 59.9                             | 829                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_47908081  | Ca1                                     | 47908081                      | CCTCTCTCTCTCTCTCTCTCT/CCTC<br>TCTCTCTCTCTCTCTCTCTCT                             | ACCTTTTTCCTTCACTT<br>GCG   | CCAACCCCTTTTCCCAA<br>AAT   | 59.4                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_47969192  | Ca1                                     | 47969192                      | GTTTTTTTT/GTTTTTTTTT                                                            | AAATGAAGATGCGAC<br>CAACT   | TTTCGCTTGTGCAAT<br>GTTT    | 58.7                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_4801141   | Ca1                                     | 4801141                       | GAAAAAAAA/GAAAAAA                                                               | AATCAAAGTGCCAAA<br>ATGC    | GCTATTCACACCCCT<br>CAAA    | 59.9                             | 902                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_48055075  | Ca1                                     | 48055075                      | GTATATATATATATATATATATAT<br>ATATATA/GTATATATATATATATA<br>TATATATATATATATATA     | TGACACTCGCATCTTT<br>GTGA   | GGCCATATCCGAAAC<br>ATTG    | 59.0                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_48114146  | Ca1                                     | 48114146                      | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATAT                           | TGATTGTTGTTGGGCC<br>ACTA   | TTTGTTCTCCATTTTGC<br>TTTTG | 60.0                             | 807                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_48114666  | Ca1                                     | 48114666                      | TTATATATATATATATATATATATA<br>TATATATA/TTATATATATATATAT<br>ATATATATATATATATA     | CAAAAGCAAAATGGAG<br>AACAAA | GGTCTTGCGATGACTT<br>CCAT   | 59.3                             | 365                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_48201393  | Ca1                                     | 48201393                      | AATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATA<br>TATATATATATATATATATAT | TTCTCCGTGTTTTCAT<br>TCC    | TGGCGTTTGAGAATTAT<br>ACGTG | 59.9                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_48206332  | Ca1                                     | 48206332                      | GTATATATATATATAT/GTATATAT<br>ATATATATATAT                                       | TAGTGTGTAACCCGTG<br>CGTC   | TCATGCAAAATCAAAG<br>AAATGA | 59.6                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_48236817  | Ca1                                     | 48236817                      | TAA/TA                                                                          | TGGGTGTTGCCCATAT<br>ATCA   | TTTGATCCATTTCAAT<br>TGATT  | 59.6                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                           |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_4971192   | Ca1                                     | 4971192                       | T/TC                                                                                      | CGCCATGTACAATGAA<br>ATGC   | GGAGTTGGGTCTTTGG<br>TGAA    | 60.0                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_4974908   | Ca1                                     | 4974908                       | ATTTTTTTTTT/ATTTTTTTTTT                                                                   | ATGGGTTAACGAAAA<br>GCCC    | TTAATCCCAAGCTCCAC<br>CAG    | 60.2                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5139845   | Ca1                                     | 5139845                       | TTTCTTCTTCTTCTTCTTCTTCT<br>TCTTCTTCTT/TTTCTTCTTCTTCTTCT<br>TCTTCTTCTTCTTCTTCTTCTT         | ACGTCTGAATCGGATT<br>TTGC   | CCCAGAAGAAGATGGA<br>GCTG    | 60.1                             | 306                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5180264   | Ca1                                     | 5180264                       | CTAATAATAATAATAATAATAAT<br>AATAATAATAAT/CTAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAAT | ATGCATGGAGCTATAA<br>GCCG   | TTCAAAGTTGAATAAC<br>CCTTCTC | 60.2                             | 684                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5273611   | Ca1                                     | 5273611                       | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATATA<br>TATATAT                         | TGCATTAATTTTAAAA<br>CGTCAA | TGTTGCCACGGTTGT<br>TAAA     | 59.5                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5351086   | Ca1                                     | 5351086                       | CAAA/CAA                                                                                  | TGTGGCAGACAGCCAA<br>CTAA   | TTTGGCAATCGAAAATT<br>GTG    | 60.4                             | 607                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5393125   | Ca1                                     | 5393125                       | AGTGT/AGT                                                                                 | GGCAATTCAGAATGGT<br>GTGTT  | GAGGCCATGTCAAGGA<br>AGTT    | 59.9                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5417726   | Ca1                                     | 5417726                       | GTTTTTTTTT/GTTTTTTTTT                                                                     | GGAGTGGTGAAGTGTG<br>GCTT   | TTCCCCATCAATTATTT<br>GCC    | 60.2                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5417880   | Ca1                                     | 5417880                       | GATCA/GA                                                                                  | GGAGTGGTGAAGTGTG<br>GCTT   | TTTCAACTCACTATGCG<br>CCC    | 60.2                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5420246   | Ca1                                     | 5420246                       | GTTAATT/GTT                                                                               | CCCATATGCAACTCCT<br>TGGT   | CACCAACAACATTTAGA<br>GGCAA  | 59.8                             | 213                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')     | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|-----------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                  |                             |                                 |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_5426267   | Ca1                                     | 5426267                       | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATATAT            | ACCAACCGACCCACTT<br>GATA    | TCAAACACACGAGATG<br>GTCC        | 60.2                             | 317                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5428904   | Ca1                                     | 5428904                       | TCACA/TCA                                                        | TTAATGGGTAGGTGGG<br>TGGA    | TTTTCAGCGGTGTCAC<br>TGAG        | 60.0                             | 839                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5428960   | Ca1                                     | 5428960                       | GTT/GTTT                                                         | AGAATGAGGTTCTGAG<br>CCGA    | TTTTCAGCGGTGTCAC<br>TGAG        | 60.0                             | 807                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5437282   | Ca1                                     | 5437282                       | CATATATATATATATATATATA/CA<br>TATATATATATATATATATA                | TGCAATGTTAATTAAGC<br>GGG    | GAATGCATTGTGATG<br>GGTG         | 58.7                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5454590   | Ca1                                     | 5454590                       | TA/TATAA                                                         | GTGTTCGGAAAAGGAC<br>GTGT    | AATGGTCCCAGTTCAA<br>CCAC        | 60.0                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5455204   | Ca1                                     | 5455204                       | TTGTT/TTGTTAATGTT                                                | TGGTTGAACTGGGACC<br>ATTA    | GGCATCAACAACAGCA<br>AGAA        | 58.8                             | 300                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5484309   | Ca1                                     | 5484309                       | ATATTATTATTATTATTATTATTA<br>TT/ATATTATTATTATTATTATTA<br>TTATTATT | CGAAATTTTGATTGAGA<br>AAGTGG | CGCGCGATGCATAGTA<br>TAAA        | 60.0                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5500920   | Ca1                                     | 5500920                       | CTAT/CTATAACGTCATAT                                              | GGAAGGGAATCGATGA<br>GAAA    | TATTCATTGGTTGGGG<br>GAAA        | 59.1                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5530672   | Ca1                                     | 5530672                       | CTTTTTTTTTTTTT/CTTTTTTTTT                                        | TGGATTTCTCAATGCC<br>TTCC    | GGAAAAAGCCAAGAGA<br>AGCA        | 60.0                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_5872810   | Ca1                                     | 5872810                       | TTATATATATATATATATAT/TTAT<br>ATATATATATATATAT                    | GTAAGCTTCTTGCGAC<br>CACC    | TGAAATGACTATAATTT<br>TGATCGAATG | 59.9                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                    | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                  |                            |                              |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_5875747   | Ca1                                     | 5875747                       | TTAATTTAAATT/TTAATTTAAATTAA<br>ATAATTTAAATT                                                      | TGATGGATGTCCTGGA<br>AACA   | CATCCATGCAAAAGCA<br>GAGA     | 59.9                             | 504                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_5948606   | Ca1                                     | 5948606                       | AA/AATA                                                                                          | GCGTATAAAAAGGAAC<br>CAAAGC | TAGAGCCGCAGCTGAT<br>TTTT     | 59.2                             | 450                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_6071071   | Ca1                                     | 6071071                       | TTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAA/TTAATAATAATAATAATAAT<br>AATAATAATAATAA | AAGAGAGATCGTGACC<br>GTTACA | GCGGTTAACGAATACG<br>CAAT     | 58.9                             | 853                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_6129000   | Ca1                                     | 6129000                       | CTTTTT/CTTT                                                                                      | CGTCATGTATCTTGGT<br>CGGA   | TGTTTAACACATTAACA<br>TGACCCA | 59.5                             | 556                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_6129831   | Ca1                                     | 6129831                       | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATAT                                              | TCTTGGACGAGTTTTT<br>CAACA  | TTAAACCGACACGGA<br>AAGG      | 58.4                             | 579                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_6134198   | Ca1                                     | 6134198                       | ATAT/ATATAAAATTAT                                                                                | TGGCAAATATTGCGAG<br>TGAA   | TGTGGGGCCAAGACAT<br>AAAT     | 60.2                             | 600                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_6138299   | Ca1                                     | 6138299                       | AT/ATT                                                                                           | GGCAGCATGTTCTTGA<br>TTTTT  | CCGATTGTTGATCGAG<br>GTTT     | 59.1                             | 846                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_6149449   | Ca1                                     | 6149449                       | CTTTT/CTTTTT                                                                                     | CTGAATATTGAGGCC<br>ATCC    | CTTCGGTTGCTAAAAG<br>AGAGC    | 59.3                             | 393                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_6157606   | Ca1                                     | 6157606                       | A/AT                                                                                             | TGGAGTGTCAATTGAGG<br>ACCA  | GGAACGTTACATGACC<br>GGAA     | 60.1                             | 789                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_6157953   | Ca1                                     | 6157953                       | AC/A                                                                                             | TGGTTTGTCAATCCGG<br>TCAT   | ATGTCTCATTATGCTC<br>CCC      | 61.2                             | 359                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_6158400   | Ca1                                     | 6158400                       | TAAAA/TAAAA                                                   | GGGGAGCATGAATGAG<br>ACAT    | AAACCGCGACAATTTAA<br>TCTC  | 59.9                             | 387                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6163758   | Ca1                                     | 6163758                       | G/GTTTCTTAAATACAAA                                            | TCTTTCATGTAGGATG<br>CGATAAA | ATGGAACCTTCCACTC<br>ATGG   | 58.8                             | 767                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6164122   | Ca1                                     | 6164122                       | TAG/T                                                         | GTTGTGTATGGGTCTT<br>CCCCG   | TGACGGAATTACAACG<br>CAAA   | 60.2                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6178179   | Ca1                                     | 6178179                       | ATTTTAATTTTAATT/ATTTTAATT                                     | AATTTTGGCATGCGAC<br>TACC    | TTTCCTTCCAATATCT<br>GCC    | 60.0                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6202713   | Ca1                                     | 6202713                       | CTTTTT/CTTTTTT                                                | CGCTTCCTTCTCACAC<br>CACA    | AAAAGGCAATACATCCA<br>ATCAA | 60.0                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6203281   | Ca1                                     | 6203281                       | GTTTTTTTTT/GTTTTTTTTT                                         | CTCCTTGAGTTTGTAG<br>ACACGA  | TCGATTATGCGTAGGG<br>AAGG   | 59.5                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6216689   | Ca1                                     | 6216689                       | CT/CTAT                                                       | TTTGGAATGCACATCC<br>TCCT    | GGGATCAAGGGTTGAG<br>TGAA   | 60.5                             | 254                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6267078   | Ca1                                     | 6267078                       | GAAA/GA                                                       | TTTCTTGCACTGGTTT<br>GTGC    | TGGGTCCCTCATTGTA<br>CTCC   | 59.9                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6267684   | Ca1                                     | 6267684                       | GT/GTTT                                                       | GGAGTACAATGAGGGA<br>CCCA    | GCCGCGGTATTATTCC<br>TACA   | 59.8                             | 384                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6279594   | Ca1                                     | 6279594                       | ACAACCTCAACCTCAACCTCAAC/AC<br>AACCTCAAC                       | ATCCGACGGTAACAGA<br>AACG    | CAAAGGAGAAATGAAG<br>CCCA   | 60.0                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_6293009   | Ca1                                     | 6293009                       | TAAAAA/TAAAAAA                                                | TGTGGTTCAAAGCAGATTCG      | CATCGATCAGTGTGTGTTTGG      | 59.8                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6307014   | Ca1                                     | 6307014                       | ATTTTT/ATTTTTT                                                | ATTGATGACACGTGGA<br>GGGT  | CGAAAAACACATTCGAA<br>GAGC  | 60.2                             | 826                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6311323   | Ca1                                     | 6311323                       | T/TCACGA                                                      | CGGAGAACCAATCACT<br>CACA  | GTTGAGCCGAGGCAAC<br>TATG   | 59.7                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6313076   | Ca1                                     | 6313076                       | CG/C                                                          | CCGCAAAATGAAATTAA<br>GGGA | GGGAAACATTCTCACA<br>TTTGC  | 59.9                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6313907   | Ca1                                     | 6313907                       | T/TC                                                          | GGAGTCTTGTGTCATG<br>TGCAA | TTCACGTGCTTTTAAAT<br>TTGTG | 59.7                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6342773   | Ca1                                     | 6342773                       | TG/T                                                          | AGGGTCATGGGTGTCA<br>CAAT  | AGCACATCCACCTTCC<br>ATTC   | 60.1                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_63669     | Ca1                                     | 63669                         | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATAT             | AAGGGCGAAGATAAAT<br>CGGT  | AAACCTGACGGGAAC<br>ATTG    | 59.9                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6374330   | Ca1                                     | 6374330                       | AAAGAAGAAGAAGAA/AAAGAAGAA<br>GAA                              | CAAAATGATGGACACC<br>CTTG  | TCCATCTTGGACCAAT<br>CTCA   | 58.8                             | 291                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6376706   | Ca1                                     | 6376706                       | TTGGATAAATTGTGGATAAATTGTG/<br>TTGGATAAATTGTG                  | GCTCGTCCAATATTTA<br>CGCA  | CCCAGCAGTGAAGCAA<br>ACTT   | 60.1                             | 379                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6404378   | Ca1                                     | 6404378                       | ATTTTTTTT/ATTTTTTTTTT                                         | AATTGCATTTTATGTCC<br>GCC  | TGTTGCAGGTTCTGAG<br>ATCG   | 59.8                             | 858                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                     | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                                   |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_6472948   | Ca1                                     | 6472948                       | TAA/TAAA                                                                                                                                                          | TGGCAGTTTCATTGT<br>CGTC   | TCTTCATCCCCAACCTT<br>CAC   | 59.7                             | 830                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6559705   | Ca1                                     | 6559705                       | CATATATATATATATATATA/CATATA<br>TATATATATATATATA                                                                                                                   | GGGTCAAACCTTGG<br>AAAT    | TCCTCGTGTTCACTTTC<br>GC    | 60.0                             | 910                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6714588   | Ca1                                     | 6714588                       | ATTTTTTTTTTT/ATTTTTTTTTTTT                                                                                                                                        | TTTGGGGCCCTCTCT<br>TTAT   | GCAGTGAAGCTCCCTG<br>ATTCT  | 59.9                             | 678                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_6972063   | Ca1                                     | 6972063                       | CTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTAT/CTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTAT | GTTTTCGTTCCTCCTC<br>CCC   | CCGGTGCAATTTAACC<br>TTGT   | 60.1                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7017413   | Ca1                                     | 7017413                       | ATTTT/ATTT                                                                                                                                                        | GCTTTGCCTTAAAAAC<br>CAGC  | CGAGCATGGTCAAGAG<br>TTTT   | 59.8                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7103961   | Ca1                                     | 7103961                       | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAAT/AAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAAT                                      | CAAGGCCCAAACCAA<br>CTAA   | CTTATGGACATTGGGG<br>TTGG   | 60.0                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7215414   | Ca1                                     | 7215414                       | AA/AACA                                                                                                                                                           | AACCCCAACTACAAG<br>GTCC   | CAATTTGACAAGCCCC<br>CTAA   | 60.1                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7274145   | Ca1                                     | 7274145                       | AATATATATATATATATATATAT<br>A/AATATATATATATATATATAT<br>A                                                                                                           | TGAATGAACTTTATCC<br>TGCCA | CAGCGTGAACGACTTC<br>AAAA   | 59.6                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7423109   | Ca1                                     | 7423109                       | TTCTCTCTCTCTCTTTCTCTCTCT<br>CTCTCT/TTCTCTCTCTCTCTCTT<br>TCTCTCTCTCTCTCT                                                                                           | CGGTTTTGACAAATG<br>GTTT   | ATGGCCATGTCTGACT<br>CGTT   | 57.5                             | 345                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7582813   | Ca1                                     | 7582813                       | CATATATATATATATATATATATA<br>TATATATATATATATAT/CATATAT<br>ATATATATATATATATATATATATA<br>TAT                                                                         | CTCCAGTCGATGAGAT<br>TCAAA | TGTTGAAATCCATTCA<br>TTAGCA | 57.9                             | 769                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)      | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                    |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_7618300   | Ca1                                     | 7618300                       | AGGTGTCTAG/A                                                       | GAAGAGGCCACATGGT<br>TCAT  | CCAAGCATCATCACCA<br>AATG     | 59.9                             | 743                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7635339   | Ca1                                     | 7635339                       | ATGTCATCCCT/AT                                                     | GCACGCGTTTTCAATG<br>TAGA  | AAATGTCATCCCTCAG<br>CGAC     | 59.9                             | 207                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7635551   | Ca1                                     | 7635551                       | GAAAAA/GAAAA                                                       | TGTCATGTCTATCCCTC<br>TGGA | GCCCTTTCACATGGAT<br>CAAG     | 60.0                             | 250                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7642434   | Ca1                                     | 7642434                       | TA/TAA                                                             | TGCCACACAAAAATCTT<br>GGA  | TAACTACGCTTGTGG<br>GGTC      | 60.1                             | 219                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7648479   | Ca1                                     | 7648479                       | ATTTTT/ATTTTTT                                                     | TGCCAAGACAGCTGAA<br>AGTG  | GACAAATGGAAGTGCT<br>GGGT     | 60.2                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7657426   | Ca1                                     | 7657426                       | ATT/AT                                                             | CAGCCTCCTCAAATCA<br>GCTT  | AATGATTGGGGAACAT<br>TGGA     | 59.6                             | 765                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7661306   | Ca1                                     | 7661306                       | CTT/CTTT                                                           | AGTGTGAGCTTCTTTT<br>CCGC  | CACGAAATGAATAACA<br>GACATTGG | 59.6                             | 266                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7668769   | Ca1                                     | 7668769                       | TAAAA/TAAAAA                                                       | TTGACCATCCTCTTCG<br>ATCC  | TAAGCAACACGCAAAG<br>AACG     | 60.0                             | 297                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7672846   | Ca1                                     | 7672846                       | AAACACTCCTACCTCCAACACTCCT<br>ACCTCCAACAC/AAACACTCCTACCT<br>CCAACAC | TAAGCCCCATGTTTGA<br>GACC  | GGCCTGATGCTGTCAA<br>CTTT     | 59.9                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7677005   | Ca1                                     | 7677005                       | TCA/T                                                              | TTGCGAATGTCGACCT<br>TAAA  | TGAATTTTGTTCGATT<br>TCATT    | 59.3                             | 870                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_7678204   | Ca1                                     | 7678204                       | C/CATT                                                        | TCACGCACCTTCATACC<br>AATCA  | CATGAGCAATCACGGT<br>TTTG  | 60.1                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7679519   | Ca1                                     | 7679519                       | TCAC/TCACCAC                                                  | ACCCACACAAACCTAC<br>CTCG    | GGAAAAAGCCAAGGAC<br>ATGA  | 59.9                             | 762                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7679708   | Ca1                                     | 7679708                       | AGGG/AGG                                                      | ACCCACACAAACCTAC<br>CTCG    | GGAAAAAGCCAAGGAC<br>ATGA  | 59.9                             | 762                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7702136   | Ca1                                     | 7702136                       | ACA/ACATGCA                                                   | TTGAGATATTGATTTGC<br>ATCACA | ATGCCCTTGCAGAGCT<br>AGAA  | 58.2                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7705518   | Ca1                                     | 7705518                       | A/AG                                                          | AAGGTCAAGTTGAGTT<br>GGGG    | TTCATTGGCCCTAAAA<br>TTG   | 59.0                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7713699   | Ca1                                     | 7713699                       | TAAAAAAAA/TAAAAAAAAA                                          | TGTGACAATCATCGTC<br>GTCT    | TGTTTTGGATGGAAGA<br>TTTGC | 57.6                             | 652                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7720463   | Ca1                                     | 7720463                       | C/CT                                                          | TCAAAATTTTCAACCAA<br>AACCC  | ATCGGTCCAACGGTTA<br>TGTC  | 60.1                             | 845                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7721034   | Ca1                                     | 7721034                       | CTTTT/CTTT                                                    | CATAACCGTTGGACCG<br>ATTG    | GTTTTGCCATTGGTGC<br>TTTT  | 60.2                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7726229   | Ca1                                     | 7726229                       | CAAAAAAAAA/CAAAAAAAAA                                         | TTTAGTGCCCGAGAGG<br>AAGA    | TTTGAGTCCCAACCAAA<br>GGA  | 59.9                             | 394                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7726361   | Ca1                                     | 7726361                       | GAATAAATAAA/GAATAAA                                           | TTTAGTGCCCGAGAGG<br>AAGA    | TTTGAGTCCCAACCAAA<br>GGA  | 59.9                             | 394                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_7726541   | Ca1                                     | 7726541                       | AT/ATATATATATATGT                                             | GCGTGATCCATCATT<br>GACA       | GGAAATTGCTCAAACT<br>CACG | 60.5                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7745366   | Ca1                                     | 7745366                       | A/ATAT                                                        | TGGAGAAACTCTTCCG<br>CTGT      | ACTTTGGGGAGAGGCT<br>TTGT | 60.0                             | 175                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7750166   | Ca1                                     | 7750166                       | ATTT/ATTTT                                                    | TTGCAATAGGCGTTGA<br>AGTTT     | AGGTCAAGGGTTGGGC<br>TACT | 59.8                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7750284   | Ca1                                     | 7750284                       | AAAGAA/AAA                                                    | TTGACAATAGAATCGAT<br>CAAAAACA | AGGTCAAGGGTTGGGC<br>TACT | 59.9                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7763628   | Ca1                                     | 7763628                       | ATGAAA/ATGAAAATCTGTGAAA                                       | CAGCTCCTCCCAACAT<br>CATT      | AGCTGCAGTGTGTAT<br>GCCA  | 60.1                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7775058   | Ca1                                     | 7775058                       | C/CCTTAAT                                                     | AGCCCAACCCTTGACC<br>TAAT      | GCACGGAAACAACATG<br>TGAC | 59.8                             | 838                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7782299   | Ca1                                     | 7782299                       | AG/A                                                          | TTGTGCGAAAAGAGGAA<br>GTGCT    | CAAGACACACCTTGG<br>GATT  | 59.1                             | 448                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7783146   | Ca1                                     | 7783146                       | TAAA/TAA                                                      | AATTCAAGCCAAATGC<br>CATC      | CTGTGTTTTTGCCTCA<br>ACG  | 59.9                             | 834                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7783374   | Ca1                                     | 7783374                       | GAAAAAAAA/GAAAAAAAAA                                          | ACAAATGCTGAAATT<br>GCCA       | CTGTGTTTTTGCCTCA<br>ACG  | 59.2                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7786618   | Ca1                                     | 7786618                       | CAAAAAAAAA/CAAAAAAAAA                                         | CCAATGAGGGAGAAGG<br>TTCA      | TTAAATTGCTACCCAC<br>GCC  | 60.0                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_7824017   | Ca1                                     | 7824017                       | AT/ATT                                                        | AAGAATGGTGGACACT<br>TGCC  | ACCCATGTGGCTACTG<br>GAAG | 60.0                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7824410   | Ca1                                     | 7824410                       | TTTTTT/TTTTTCTTTTT                                            | TGGTTCATGGGTTTT<br>GGAT   | AAAATTGGCCCACAAT<br>TAGG | 60.0                             | 123                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7858563   | Ca1                                     | 7858563                       | AATATATATATAT/AATATATAT                                       | AAAAACAAATGCAATC<br>GATCA | TTTTCATGCGTTCCTC<br>TTT  | 58.1                             | 233                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7865713   | Ca1                                     | 7865713                       | C/CT                                                          | TGCACTCACTCCAACA<br>AACA  | CAAAGCATACCAACCA<br>CAGC | 58.8                             | 799                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7888288   | Ca1                                     | 7888288                       | TC/TCC                                                        | GCTTTC AAGCCAGACC<br>AGAC | TTTGAGCGGAGAAGT<br>AATGA | 60.0                             | 274                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7913832   | Ca1                                     | 7913832                       | GAGAAGAAGAAGAAG/GAGAAG<br>AAGAAGAAGAAGAAG                     | ACACTTGCAAAAATGA<br>GGGG  | TCACTCCTCTTCTCCCC<br>AAA | 60.0                             | 370                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7914166   | Ca1                                     | 7914166                       | T/TG                                                          | TGCATAGGTTGTTGTG<br>GGAA  | GACGAGAGGTTGGAGA<br>CTCG | 60.0                             | 939                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7914415   | Ca1                                     | 7914415                       | T/TC                                                          | TTTGGGGAGAAGAGGA<br>GTGA  | GACGAGAGGTTGGAGA<br>CTCG | 59.8                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7929432   | Ca1                                     | 7929432                       | T/TTA                                                         | ATATCCGCAAGCTGAA<br>TCGT  | GGTTTGAACCTCCAC<br>AAGA  | 59.7                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7929572   | Ca1                                     | 7929572                       | CCATCTCATC/CCATCTCATCTCATC                                    | ACTTACTGTTTCAACGC<br>GGG  | GGTTTGAACCTCCAC<br>AAGA  | 60.2                             | 325                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_7933054   | Ca1                                     | 7933054                       | TTTAATTA/TTTA                                                 | TCCTGCATAACACCATT<br>GGA   | CCTTCACAAACTTGAAG<br>GACC | 59.9                             | 883                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7933130   | Ca1                                     | 7933130                       | TG/TGG                                                        | TCCTGCATAACACCATT<br>GGA   | CCTTCACAAACTTGAAG<br>GACC | 59.9                             | 883                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7947164   | Ca1                                     | 7947164                       | T/TA                                                          | AACGATTTTTCACGCTT<br>GCT   | CAATGATTGGAATTTG<br>GAGGA | 59.9                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7959222   | Ca1                                     | 7959222                       | TAAAAAAAA/TAAAAAAAAA                                          | AGTGCCAAGAAGACTT<br>CCGA   | TAATTGACACCAAGCC<br>ACGA  | 60.0                             | 444                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7959979   | Ca1                                     | 7959979                       | GTTT/GTTTATTA AAAAGGATTT                                      | TCGTGGCTTGGTGTC<br>ATTA    | GGTCGCCAATTTTGGT<br>TATG  | 60.1                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7960391   | Ca1                                     | 7960391                       | ATTT/ATTTT                                                    | CCTAGGGTAACCGTG<br>CTCA    | CCTCTCCTGCCTTAGT<br>CCCT  | 60.1                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7961218   | Ca1                                     | 7961218                       | CAAA/CAAAGAAAAA                                               | TTGAGTTTTGGAGGG<br>AGAA    | GAAGGGAAGGAAGGA<br>GATGG  | 59.6                             | 171                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7965606   | Ca1                                     | 7965606                       | CTTTT/CTTT                                                    | TGCTTGTGAATAAATC<br>ATCGCA | TGGTCCATTATTAGGT<br>GGG   | 60.5                             | 344                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7981639   | Ca1                                     | 7981639                       | AATATATA/AATATA                                               | GAAGCCATGGAAGTGT<br>TGGT   | TCCTCCCGAGGGATAT<br>TACC  | 60.0                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7984637   | Ca1                                     | 7984637                       | TAAAAA/TAAAAAAA                                               | TTGATTGCTTGCCATTA<br>TGC   | TGGTTTTGCCCATATG<br>GTTT  | 59.7                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_7994670   | Ca1                                     | 7994670                       | ACT/A                                                         | TTAACGTGCCACCTTC<br>ACAA     | ACTTCATGGGCATGGG<br>TTAG     | 60.1                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7995701   | Ca1                                     | 7995701                       | ATTAAATGAGTGTTAAAT/ATTAAAT                                    | GCGTAAGTTATGCATG<br>CCAAT    | GGTGCAAGGGAAGAAA<br>ATGA     | 60.0                             | 902                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7995766   | Ca1                                     | 7995766                       | CAAAAAA/CAAAAAAA                                              | GCCAATTGCGGTAGC<br>TGT       | GGTGCAAGGGAAGAAA<br>ATGA     | 59.9                             | 887                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7995820   | Ca1                                     | 7995820                       | CTATA/CTATATATA                                               | TTGTTTTGTGAATAAAA<br>ATCCCTT | GGTGCAAGGGAAGAAA<br>ATGA     | 58.1                             | 492                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_7996602   | Ca1                                     | 7996602                       | CTTTT/CTTTT                                                   | TCATTTTCTCCCTTGC<br>ACC      | TTCTCAAGCACCAAGC<br>ACAC     | 60.1                             | 926                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8000567   | Ca1                                     | 8000567                       | TT/TTAT                                                       | CCAACCTTCACACTC<br>GTTT      | TGACACCAAACCTCAGT<br>CCTTG   | 60.0                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8003639   | Ca1                                     | 8003639                       | AC/A                                                          | TTGGTCATCTCCAAAG<br>GTCC     | GGACACAAAATATAATT<br>GAGCCA  | 59.9                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8003853   | Ca1                                     | 8003853                       | TAT/TATATATAAAT                                               | TGATAATTTCTTGCCCA<br>TTTTTC  | TGACATTTTAACTCAAG<br>AGACCGA | 58.1                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8003954   | Ca1                                     | 8003954                       | CCCTATGTT/C                                                   | TGATAATTTCTTGCCCA<br>TTTTTC  | TGACATTTTAACTCAAG<br>AGACCGA | 58.1                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8004049   | Ca1                                     | 8004049                       | AAT/AATATATAT                                                 | GGCTCAATTATATTTTG<br>TGTCCC  | TCATGATATTATGCACC<br>GGG     | 58.8                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                   |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_8004353   | Ca1                                     | 8004353                       | AAAT/AAATAAT                                                      | TCGGTCTCTTGAGTTA<br>AAATGTCA | TGGAAGGGATCTCAAT<br>TTGC   | 60.2                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8017826   | Ca1                                     | 8017826                       | AAAGA/AAAGAAGAAGAAGAAGA                                           | TGTGCTATATTCGGTT<br>GGCA     | TCAGTCAAACCATCGA<br>ACCA   | 60.1                             | 156                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8018022   | Ca1                                     | 8018022                       | G/GAAACAT                                                         | TGTTTGGTTCGATGGT<br>TTGA     | TGTATTGGGCCAGTTT<br>CACA   | 59.9                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8018283   | Ca1                                     | 8018283                       | GAAA/GAA                                                          | TGTTTGGTTCGATGGT<br>TTGA     | TGTATTGGGCCAGTTT<br>CACA   | 59.9                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8020277   | Ca1                                     | 8020277                       | ATTT/ATTTGTTT                                                     | TCGCGGTGAATATCAC<br>AAGA     | GTCGATTCAAGTTGGC<br>GAAT   | 60.2                             | 756                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8021607   | Ca1                                     | 8021607                       | AT/ATT                                                            | CGTCCACCCTCACCTA<br>CCTA     | TGCCAACAAATCTTCTG<br>AAAAA | 60.0                             | 939                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8031450   | Ca1                                     | 8031450                       | TAAAAAA/TAAAAAAA                                                  | ATCTTCTTTTGTGGG<br>GCCT      | CTTGGCAGATCTCGAG<br>TATGAA | 59.9                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8031692   | Ca1                                     | 8031692                       | TTA/TTATA                                                         | ATCTTCTTTTGTGGG<br>GCCT      | CTTGGCAGATCTCGAG<br>TATGAA | 59.9                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8031727   | Ca1                                     | 8031727                       | CG/C                                                              | ATCTTCTTTTGTGGG<br>GCCT      | CTTGGCAGATCTCGAG<br>TATGAA | 59.9                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8033091   | Ca1                                     | 8033091                       | TTCTCTCTCTCTCTCTCTCTCTC/<br>TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC | GCTTTTACAACATGGA<br>CGCA     | GGAAGGGAATGAAGGT<br>GTGA   | 59.7                             | 171                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_8033455   | Ca1                                     | 8033455                       | CTTTTTTTTT/CTTTTTTTTTTT                                       | TCACACCTTCATCCCT<br>TCC    | CCCAGGAGAAGAAAAT<br>CGTG | 59.9                             | 766                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8041307   | Ca1                                     | 8041307                       | T/TG                                                          | CGGCGGCAATTGTTAT<br>AAGT   | CAATTTCAAGCAAAATC<br>GCA | 60.0                             | 890                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8041662   | Ca1                                     | 8041662                       | TAAC/TAACATTAAAC                                              | CCCTTCATTGGAGATG<br>TTCC   | TTGGGGACACTAAGAG<br>GTGG | 59.3                             | 866                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8053901   | Ca1                                     | 8053901                       | TCTCTG/TCTCTGCTCTG                                            | CTCCAATGTGTCCCA<br>CCTT    | GTTGTAAATTGCACGG<br>GTCC | 59.8                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8062841   | Ca1                                     | 8062841                       | T/TGATGATAA                                                   | TCGGTTCACGTACTAC<br>CAATGA | TGTTGCTCTTGCCATAC<br>TGC | 60.4                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8090497   | Ca1                                     | 8090497                       | ATTTTT/ATTTTTT                                                | GAGGGGCTACCACCA<br>ATTC    | TGCATCCAACATCTTCA<br>TCC | 60.7                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8091150   | Ca1                                     | 8091150                       | CA/CAA                                                        | TGGCTAACGTTCAATT<br>GCAG   | TCGAAACAACCTCCAC<br>ACAA | 59.9                             | 202                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8091521   | Ca1                                     | 8091521                       | TTTAAAA/TTTAAAAATTAAAA                                        | GTTTGTGTGCATGTCA<br>CCGC   | TGAAACTCTGGCGAAG<br>ATGA | 60.0                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8094210   | Ca1                                     | 8094210                       | AAAT/AAATAAT                                                  | GCCAACTGTCCCAAG<br>ACAC    | TGGCTTTGTGGTACAT<br>TGGA | 60.6                             | 340                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8107780   | Ca1                                     | 8107780                       | T/TTGAAATC                                                    | CTTTGTGCAATTGGG<br>TGTG    | CTGCTGAGTTGCCTGT<br>ACCA | 60.0                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                    | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                  |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_8116992   | Ca1                                     | 8116992                       | ATTTTTTTTT/ATTTTTTTT                                                                             | TGTGTGTGAAGGGAT<br>TTCTAACC | CAATCGAACGAGACGA<br>GTCA    | 59.3                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8248772   | Ca1                                     | 8248772                       | ATTTTTTTTT/ATTTTTTTTTT                                                                           | TGCAACATGAATTGA<br>AAGGA    | ATAGTCGGGAATGCAA<br>CCTG    | 59.1                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8319139   | Ca1                                     | 8319139                       | TGGGCGCG/TGGGCGCGCTCGGGC<br>GCG                                                                  | CCCAAGTCCCAAGAG<br>TCAA     | CAAAGACCCGGAACC<br>AAAT     | 60.1                             | 292                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8327619   | Ca1                                     | 8327619                       | AATATATATATATATATATATATAT<br>ATATATATATAAATATATATATATAT<br>ATATATATATATATATATATATATA<br>TATATATA | AATAGCTCCCGCAAGT<br>TTGA    | CATGACATCTTTCAATC<br>CAATCA | 59.8                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8340429   | Ca1                                     | 8340429                       | TAAAAAAAA/TAAAAAAAAA                                                                             | TGGACAAATCCATATC<br>GTCTG   | GTGCACCGACGTGCT<br>AAAA     | 59.4                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8415684   | Ca1                                     | 8415684                       | TA/TAA                                                                                           | AGAAATGTGATGCAAG<br>AGGAAA  | GGGTCAAGATGAGAGA<br>GCCA    | 58.8                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8430467   | Ca1                                     | 8430467                       | TT/TTATTATTATTAT                                                                                 | AGGTCATGGGCTGGAT<br>GTAG    | ACCCTTTCACTGCGCT<br>CTTA    | 60.0                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8590076   | Ca1                                     | 8590076                       | TAAAAAAAA/TAAAAAAAAA                                                                             | TCCTTGAAGCTTTGCC<br>ACTT    | TCCATATCTTGCGACAT<br>GCT    | 60.0                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_8836170   | Ca1                                     | 8836170                       | ATTTTTTTTTTT/ATTTTTTTTTTTT                                                                       | GTAGAGCCTGACTTTT<br>GCCG    | GGGGTTTAGCACGACT<br>GTGT    | 60.0                             | 722                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_89785     | Ca1                                     | 89785                         | ATTTTTTTTTTT/ATTTTTTTTTTTT<br>TT                                                                 | CACGAGTTGACATTC<br>ACGG     | TCCATCAAGATCATTC<br>CAGC    | 60.2                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                 |                            |                             |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_9130103   | Ca1                                     | 9130103                       | TTATATATATATATATATAT/TTAT<br>ATATATATATATATAT                                                   | GGGTCAAATTCGTTG<br>ACCAT   | TACGGGTCAAGACAGG<br>TTCG    | 61.0                             | 550                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_9223996   | Ca1                                     | 9223996                       | TAAAAAAAAA/TAAAAAAAAA                                                                           | AATGGATTCTTCCGCT<br>CAAA   | ACAGAACGGTGCGTTG<br>TAAA    | 59.6                             | 489                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_9225279   | Ca1                                     | 9225279                       | GTTTTTTT/GTTTTTTT                                                                               | AGGATTCCACAGATCA<br>GCGT   | TCAATTCACAAAGTTG<br>AGGG    | 59.7                             | 646                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_9233850   | Ca1                                     | 9233850                       | GTTTTTTTTTTTT/GTTTTTTTTT                                                                        | TGAGTTCTTTGAATTT<br>GCGTG  | GTTGCGTCTAGCAACT<br>TTCTG   | 60.3                             | 637                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_9286959   | Ca1                                     | 9286959                       | GAAAAAAAAA/GAAAAAAAAA                                                                           | TAGTTGGGGCCATATC<br>CAAA   | TGGAACGCTACACGC<br>TATG     | 60.1                             | 631                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_9322441   | Ca1                                     | 9322441                       | TTATATATATATATATATATATATA<br>TATCTATATATATATAT/TTATATATA<br>TATATATATATATATATCTATATAT<br>ATATAT | TGCCTTTTCGTTTTCAA<br>TTC   | AACGGTTGAGCAATGA<br>ATCC    | 57.9                             | 442                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_9516400   | Ca1                                     | 9516400                       | AATATATATATATATATATATATAT<br>ATATATATATAT/AATATATATATATA<br>TATATATATATATATATATATATAT<br>ATAT   | ACATTGAACCCTAATC<br>GCGT   | TGATGATAAACCGAGG<br>GGAG    | 59.5                             | 412                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_9681529   | Ca1                                     | 9681529                       | CTATATATATATATATA/CTATATATA<br>TATATATATA                                                       | GGATGTTATGACGTGC<br>CAAA   | TTGAACAATATCAATGC<br>ACAACA | 59.4                             | 310                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_9686315   | Ca1                                     | 9686315                       | TTATTATTATTATTA/TTATTATTATT<br>ATTAATATTATTATTATTA                                              | TCAAATGCTTTAATGGC<br>TCAGA | TTTTTAGTTTGAAGACC<br>TTTGTC | 59.9                             | 446                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca1_P4_9830366   | Ca1                                     | 9830366                       | AATATATATATATATATATA/AATATA<br>TATATATATATATATA                                                 | TCCAGGATGTGTTACC<br>ATGAA  | CTATCCGGCTTTTGG<br>ATCA     | 58.8                             | 575                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                  | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_9867623   | Ca1                                     | 9867623                       | AATATATATATATATATATATAT/A<br>ATATATATATATATATATATATAT                                                                          | GCCAAATATGTGTGC<br>TTTTCG   | TTCTGTCGTCACAGAG<br>GACG  | 59.5                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_9871519   | Ca1                                     | 9871519                       | ATT/A                                                                                                                          | CTTAGTCCACGTGCAA<br>ACGA    | AAAGTGCGGGCCAATA<br>TCTA  | 59.9                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_9965386   | Ca1                                     | 9965386                       | CATATATATATATATAT/CATATATAT<br>ATATATATAT                                                                                      | TGGAATCAACTAATCAT<br>GGTGG  | GATGAAAAGAGGGAGG<br>AGGG  | 59.7                             | 824                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_9965836   | Ca1                                     | 9965836                       | CAAAAAAAAA/CAAAAAAAAAAAAA                                                                                                      | CCCTCCTCCCTCTTTT<br>CATC    | CACCACCTCATCCTCT<br>GTG   | 60.0                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca1_P4_9995156   | Ca1                                     | 9995156                       | C/CG                                                                                                                           | TTGTATTTTGGGGCCA<br>TTGT    | TGCAAGTGACAATTTG<br>ATCG  | 60.1                             | 934                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_10013835  | Ca2                                     | 10013835                      | ATTTTTTTTT/ATTTTTTTTT                                                                                                          | TACTCACCCAAATCCG<br>CTTC    | TAGACCCTCATCCTCAT<br>CCG  | 60.1                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_10081600  | Ca2                                     | 10081600                      | CAAAAAAAAAAAAA/CAAAAAA<br>AAAAA                                                                                                | TTTTGATTGATTGATGA<br>TGGG   | TGCAAAATTCACCTCAC<br>GAA  | 58.3                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_10149284  | Ca2                                     | 10149284                      | AATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTA/AATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTA | GGCTAAAAGTCTCCG<br>AGTTCA   | TTCTACGTATCTCCC<br>GGTG   | 59.9                             | 822                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_10169628  | Ca2                                     | 10169628                      | CAAAAAA/CAAAAAA                                                                                                                | TCATAATGAGCAGCGT<br>ATCTTCA | TGCCTAATCGATTGCA<br>CATT  | 59.9                             | 691                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_1023421   | Ca2                                     | 1023421                       | TTATATATATATATATA/TTATATA<br>TATATATATATA                                                                                      | TCCACGTCTAAAGCC<br>ATTG     | ACAAGACAGACCCTTTT<br>GACA | 60.1                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                              | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                            |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_1024227   | Ca2                                     | 1024227                       | CAATAAAATAAAATAAAATAAA<br>ATAAAATAAAAT/CAATAAAATAA<br>AAATAAAATAAAATAAAATAAA<br>ATAAAATAAT | TTGTCAAAGGGTCTG<br>TCTTG    | TGACTGCCGCACATT<br>AGAG     | 57.8                             | 411                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_1033751   | Ca2                                     | 1033751                       | CATTTATTA/C                                                                                | TGTGTGATTTTCAATAG<br>TCACCG | AAGTTAAGGGACCACG<br>GGAT    | 59.9                             | 845                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_10362435  | Ca2                                     | 10362435                      | TAA/TA                                                                                     | GAGGGGTAGCGAGG<br>GTAAG     | CCCACACAAAGTCAT<br>GAAA     | 60.1                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_10388305  | Ca2                                     | 10388305                      | TTTTAAATTTATTAAATTTATT/TTT<br>TAAATTTATT                                                   | TCTCCTTAGCGGCTAT<br>TCCA    | TTGACCGAATGAGATT<br>GTTAGA  | 59.9                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_10411790  | Ca2                                     | 10411790                      | TCGAACTTAC/TC                                                                              | TAGCTGCAGCAAGAAG<br>CAAA    | GGTTTCATATTCGAACC<br>CGAG   | 60.0                             | 882                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_1074412   | Ca2                                     | 1074412                       | ATTT/ATTTTTTT                                                                              | CCTCCTCGGTCTCTTC<br>TCCT    | AAATTGAGTTTCAAAAC<br>CACCAA | 59.9                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_1074830   | Ca2                                     | 1074830                       | CATAT/CAT                                                                                  | CTTGGTGGTTTTGAAA<br>CTCAAT  | TCGATTATGCGTAGGG<br>AAGG    | 58.2                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_1075762   | Ca2                                     | 1075762                       | ATTTTTTTTTTT/ATTTTTTTTTT                                                                   | TTAGCCGCGACAATA<br>ATTC     | CTGTACTCACGTCAGG<br>CTGC    | 60.1                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_10763562  | Ca2                                     | 10763562                      | CAAAAA/CAAAA                                                                               | CTATAGCATCGAAAAG<br>CGGC    | AGTGTGGCTAGGTCG<br>ATGC     | 60.0                             | 121                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_10777745  | Ca2                                     | 10777745                      | TGAA/TGAATTGTCGAA                                                                          | CCTCGAGTTTGCATCC<br>TCTC    | TTACATTGTTCAATCGT<br>CGAAA  | 60.0                             | 725                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                       | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                     |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_10779124  | Ca2                                     | 10779124                      | TTA/TTACATA                                                                                         | CACTTTTCTTATGCACG<br>GCA     | GCAGCGAGTAGGAGAA<br>ATGC    | 59.9                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_10890760  | Ca2                                     | 10890760                      | CTTTTTT/CTTTTT                                                                                      | TGGCAAATCGATTGAA<br>ACAA     | TACATCAACGAAGATC<br>GCCA    | 60.1                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_10914293  | Ca2                                     | 10914293                      | GAAAAAAA/GAAAAAAA                                                                                   | GCACTCAAAGAATGCG<br>ATCA     | GCATTTCATGTTGTGT<br>TGC     | 60.0                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_10928556  | Ca2                                     | 10928556                      | ATTTTTTT/ATTTTTTTT                                                                                  | CATCCGTGGTCCCTTA<br>ACTT     | GCTAAATTACATTCGTG<br>GTCCC  | 58.9                             | 370                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_10948001  | Ca2                                     | 10948001                      | ATTA/ATTACACTGACGTTA                                                                                | TGATTCTTGATCATGTT<br>GTTTTCA | CCATCCTCACTCCAAA<br>GACAA   | 59.5                             | 702                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_1107319   | Ca2                                     | 1107319                       | ATAATA/ATAATAATATTAATA                                                                              | AAAAGTTTTGTGCACCT<br>CCA     | ATGCCATGGTTGTGGA<br>ACTT    | 58.3                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_11085781  | Ca2                                     | 11085781                      | AATATATATATATATATATATATAT<br>ATATATATTTATATATATATAT/AATA<br>TATATATATATATATATATATTTAT<br>ATATATATAT | TTTGGTTTTGAACTCG<br>GAGG     | CACCGTAGTGTGGTGG<br>TGAG    | 60.1                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_11294573  | Ca2                                     | 11294573                      | CAAAAAAAAA/CAAAAAAAAAAAAA                                                                           | AGCACATTGATCACGT<br>CCAA     | TCTTATTCAACCGCAC<br>CCA     | 60.1                             | 343                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_11320069  | Ca2                                     | 11320069                      | A/AC                                                                                                | ACCAAGGCATCGTCAA<br>AATC     | CCGATGCACTTATACTT<br>CAAAGA | 59.9                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_11347624  | Ca2                                     | 11347624                      | TTATATATATATATATATA/TTATA<br>TATATATATATA                                                           | AATACCTCCACGGTC<br>CTTT      | CAACAAATTGCTGCCTT<br>GTG    | 59.7                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                     |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_11497600  | Ca2                                     | 11497600                      | AG/A                                                                | TGATGAATGGTTGTGG<br>CACT  | ACGGGGTGTACATTG<br>TGGT   | 60.0                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_11671380  | Ca2                                     | 11671380                      | G/GT                                                                | CCACTAGGTACCCAC<br>TCCA   | ATAGCCGGTGGTGCTG<br>TATC  | 59.8                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_11716435  | Ca2                                     | 11716435                      | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATA<br>TATATATAT | CACAGTCCGCATGTG<br>CTAT   | TGCACTGACAGGGAAA<br>TCAA  | 59.7                             | 857                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_11722953  | Ca2                                     | 11722953                      | AATATATATATATA/AATATATATA<br>TATATATA                               | TTTGAATGGCGACTT<br>TCTT   | AATTGGCATTTCGAAC<br>TGG   | 57.5                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_11829316  | Ca2                                     | 11829316                      | TTATATATATATATATATATATA/T<br>TATATATATATATATATATA                   | TTCCCTCAACAATTT<br>CAA    | CTCAAGGCCTTCACC<br>TTTT   | 58.0                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_11998730  | Ca2                                     | 11998730                      | AA/AATAATA                                                          | AGCTCCACGTCTGCTT<br>TTGT  | CAACGCTTGCCATCAA<br>TTAG  | 60.1                             | 474                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12040519  | Ca2                                     | 12040519                      | ATT/AT                                                              | CCACATCAACCAAAA<br>GCTG   | GTGAGGTGGCATTGCA<br>GAGT  | 59.2                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12041702  | Ca2                                     | 12041702                      | GTTTTTTT/GTTTTTTT                                                   | TCATCCTTTCTCCCCTC<br>TCA  | GAGGAGAGGTCCACAT<br>CAGC  | 59.7                             | 768                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12048675  | Ca2                                     | 12048675                      | AATAATTTATAATTTATA/AATAATTT<br>ATA                                  | CAAACATGCTGATGTG<br>GACC  | CCATTGGTAAATGGCT<br>AACAA | 60.0                             | 278                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12167727  | Ca2                                     | 12167727                      | GTATATATATATATATATA/GTATA<br>TATATATATATATATA                       | AAGGTCGTAAGCTTGT<br>CGATG | TAGCACCGTAGCGGAG<br>AGAT  | 59.4                             | 715                                           | INTERGENIC                                        | --                                  | --                    | --  |





| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_12933106  | Ca2                                     | 12933106                      | A/AT                                                          | AGGTTGAAAGAAGCCC<br>CACT    | ATCGGTTGTTGGTGA<br>AATG   | 60.1                             | 834                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12933573  | Ca2                                     | 12933573                      | CACCAACCAACC/CACCAACC                                         | TCATTGACAAGGAAAG<br>AACATGA | CGAATTGGTTTTGGGA<br>TTTG  | 59.6                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12934202  | Ca2                                     | 12934202                      | AAA/AAACAA                                                    | AGAAAGCAAGCAAATC<br>CCAA    | TTCCAACACCTCACGAT<br>TCA  | 59.8                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12934953  | Ca2                                     | 12934953                      | TTCTATCTATCTATCTATCTAT<br>C/TTCTATCTATCTATCTATCTA<br>TCTATC   | TGCCTCAAAAATCTGG<br>TGTG    | CTGCTCCAAACTGATC<br>ACGA  | 59.7                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12937651  | Ca2                                     | 12937651                      | ATTTT/ATTTT                                                   | GATTGCTTTCCTCTATG<br>CCG    | GTTTTGGCGTTGGTT<br>CACT   | 59.8                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12939688  | Ca2                                     | 12939688                      | AATATATA/AATATA                                               | TTTTGGTGTTGAGGGT<br>GTCA    | TTAATCAAAGCGGCAA<br>AAGAA | 60.0                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12941200  | Ca2                                     | 12941200                      | CAAAA/CAAA                                                    | TGTGCTTCTTCCTGATT<br>TTGG   | GGCCAAAGACGGATAT<br>GGTA  | 60.2                             | 888                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12941800  | Ca2                                     | 12941800                      | T/TA                                                          | CATATCCGTCTTTGGC<br>CATT    | CCTTGAACAATTTGGG<br>CAGT  | 59.8                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12946880  | Ca2                                     | 12946880                      | A/AC                                                          | AACTACGGCATAACAA<br>CCGC    | TTGAAAGTCCACATTG<br>GAAAG | 60.0                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12947970  | Ca2                                     | 12947970                      | G/GT                                                          | TGCTTTTATGAGCATT<br>CGGG    | CGACTTCAAATCCCTTC<br>GAG  | 60.1                             | 777                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_12952557  | Ca2                                     | 12952557                      | ACATATCATATCA/ACATATCA                                        | AAAGCATTTTATCCCCA<br>CCA     | TTTTTCATCTCACTCTC<br>TCCCA   | 59.4                             | 787                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12952944  | Ca2                                     | 12952944                      | TGTCATGATT/TGTCATGATTGTAGT<br>CATGATT                         | TGGGAGAGAGTGAGAT<br>GAAAAA   | ACGGATGTCTAATCCG<br>TTGG     | 58.9                             | 308                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12960292  | Ca2                                     | 12960292                      | GT/GTTAT                                                      | TTCATACATCCAATCGT<br>GGTTT   | CCACAAGAAGCAACAC<br>AAGC     | 59.2                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_12963805  | Ca2                                     | 12963805                      | ATTTTTTTTTTT/ATTTTTTTTTT                                      | TGATTGTGCTATCTTAC<br>CTTTGGA | GATCCCATCAAACCA<br>CCAG      | 60.0                             | 867                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_13230836  | Ca2                                     | 13230836                      | GTATATATATATAT/GTATATATATAT<br>ATAT                           | TTCGGAAGTCCATCGG<br>TATC     | AAAAGTTTCAAACACAT<br>GTAAACA | 59.9                             | 891                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_13284989  | Ca2                                     | 13284989                      | TGG/TGGG                                                      | GTCGGCTGTCGGTTGT<br>TATT     | GGTCTGAGGTGGTTTA<br>ACGC     | 60.0                             | 803                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_13639596  | Ca2                                     | 13639596                      | TAATTAATAAAAT/TAAT                                            | AAGCCAGCCGCATGTA<br>AATA     | TTCACCTCCTCTGCATC<br>TTTCA   | 60.6                             | 788                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_13748106  | Ca2                                     | 13748106                      | GTATTATTATTATTATT/GTATTATTA<br>TTATTATTATT                    | TTATGGAGCCACCAAA<br>GGAC     | TCTAATCAAGCAAGCA<br>CCCC     | 59.9                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_13757790  | Ca2                                     | 13757790                      | AATATATATATATATAT/AATATAT<br>ATATATATATATAT                   | TTTTCTCGTATGGGTA<br>GTTTTGTT | CAAGATGCTGTTCTCG<br>TTCG     | 58.3                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_13853423  | Ca2                                     | 13853423                      | CAAAAAA/CAAAAAA                                               | CATTGCCAGTATGCGA<br>CATC     | AAGGTCCACAAAGAGC<br>CTCC     | 60.1                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_13923559  | Ca2                                     | 13923559                      | ATGCAGCTTTCTAAA/ATGCAGCTTT<br>CTAAATTCTGCAGCTTTCTAAA          | TTTGACCAAAACCTTG<br>GAGG       | CAGGGCGGTACAAACC<br>TTTA | 59.9                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_13956607  | Ca2                                     | 13956607                      | ATT/ATTATTT                                                   | TGAAATTTGTGATTAG<br>TTGCTTAAAA | AAACAAGTTGGTGGTG<br>GAGC | 59.6                             | 686                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_13957739  | Ca2                                     | 13957739                      | TGG/TG                                                        | ATTATCCCCACCCCA<br>CTAC        | TTTCAAAAACGGTGGT<br>GTGA | 59.8                             | 755                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_13957855  | Ca2                                     | 13957855                      | TACA/TACACA                                                   | GCTCCACCACCACTT<br>GTTT        | CAGCTACGCACAATGG<br>CTAA | 60.0                             | 196                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_14069182  | Ca2                                     | 14069182                      | GAAAAAAAAAAAAA/GAAAAAAAAAAAA<br>AA                            | TTCATAAGGGATTTTTC<br>TTCAACA   | TGTTCAACCCTCGAAG<br>ATCA | 59.1                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_14192522  | Ca2                                     | 14192522                      | GAAAAAAAAAAAAA/GAAAAAAAAAAAA                                  | TACAAATTGGATGCGG<br>TTGA       | CCCTCTGCAATGTCGG<br>TAAT | 59.9                             | 755                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_15154581  | Ca2                                     | 15154581                      | ATTT/ATT                                                      | GTTAGAACTGGGCCCA<br>ACAA       | AAATTTTCCCTGTACCC<br>CCA | 60.0                             | 884                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_15157427  | Ca2                                     | 15157427                      | AGAGC/AGAGCGACGAGC                                            | CAGAGCAATCGGAGAA<br>GAGG       | GGGGTTCTTCAAATT<br>GGGT  | 60.1                             | 203                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_15168662  | Ca2                                     | 15168662                      | ACGCGCGCGCGCGC/ACGCGCGCG<br>CGC                               | GGGGATTGTTGGAAT<br>GATG        | CAGATTCGGAGAGCTT<br>TTGG | 60.0                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_15190617  | Ca2                                     | 15190617                      | TTTTATCTTTATC/TTTTATC                                         | AGCCTCCAATATTAG<br>GCC         | AACGGTGGATGCATGT<br>ATGA | 59.6                             | 799                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)                                                                               | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                              |                         |                         |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_15307192  | Ca2                                     | 15307192                      | AATATATATATATATATATAT/AATATATATATATATATATATATAT                                                                                              | ACGGTGGGCTGTATT TTGA    | GCAACCCTTTCATTGT GGAT   | 60.4                             | 638                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca2_P4_15313880  | Ca2                                     | 15313880                      | ATATTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTATA<br>TTATTATTATTATT/ATATTATTATTA<br>TTATTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATT | GCAAAAAGCAGCGCAA TAAT   | ACGAATCTAACGGTGG TTGC   | 60.4                             | 360                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca2_P4_15343692  | Ca2                                     | 15343692                      | CTTTTTTTTT/CTTTTTTTTTT                                                                                                                       | AAGGGGAAACTTTGAC CGAC   | ACAATTTTAAACCGTTG CCG   | 60.3                             | 725                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca2_P4_15363492  | Ca2                                     | 15363492                      | AGCAG/AGCAGCACAGAATAATGCA G                                                                                                                  | GTTTTGGTCCATTTGAT GGC   | CTGCATTTTGATGTGCT GCT   | 60.2                             | 594                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca2_P4_15589036  | Ca2                                     | 15589036                      | ATTT/ATTTT                                                                                                                                   | ATACGCCTCAACAAAAT GGC   | CTGCTTTGCTTGATTCC GTT   | 60.0                             | 376                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca2_P4_15598813  | Ca2                                     | 15598813                      | TA/TAA                                                                                                                                       | GGAGGCGCATTAGATA TGGA   | GCCTCGTGAGTTGCAT CATA   | 60.0                             | 518                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca2_P4_15653418  | Ca2                                     | 15653418                      | TAAAAAAAAA/TAAAAAAAAA                                                                                                                        | CGTCACTGTTTCTCC CCAT    | GGTCATGGGTTACGA ATCT    | 60.0                             | 869                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca2_P4_15700651  | Ca2                                     | 15700651                      | ATTTTTTTTTT/ATTTTTTTTTT                                                                                                                      | GTGACTCCAACATGAC CCCT   | CCAATGCATTCCATTCA ACA   | 59.8                             | 743                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca2_P4_15778128  | Ca2                                     | 15778128                      | G/GGATGGA                                                                                                                                    | GATGGATGAAAAAGAG GCAA   | ATCTTAAGCCCCTTCC CAAA   | 60.0                             | 788                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca2_P4_15812866  | Ca2                                     | 15812866                      | TAAAAAAAAA/TAAAAAAAAA                                                                                                                        | CATTGGCGGAGCTTTA CAAT   | CCATGGCCACTTCAAG ATTT   | 60.1                             | 298                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                           | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                         |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_15920758  | Ca2                                     | 15920758                      | GTATATATATATATATAT/GTATATAT<br>ATATATAT                                                                                                 | TTCGGAAGTCCATCG<br>TATC   | GCAAATGCTCCCCTAA<br>TTGA  | 59.9                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_16003270  | Ca2                                     | 16003270                      | AAT/A                                                                                                                                   | GGTACACTTCCGGCAA<br>GAAA  | AAGAGAGGTCACITTTG<br>GCGA | 60.1                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_16296988  | Ca2                                     | 16296988                      | TAAAAAAAAA/TAAAAAAAAA                                                                                                                   | GAGGGAGGTGTGTAGT<br>CCCA  | GCGTTGTGTATCCTC<br>CGTT   | 60.0                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_1640062   | Ca2                                     | 1640062                       | ATTTTTTTTT/ATTTTT                                                                                                                       | AGATCATGTGCAAAAA<br>GGGG  | AGTAACCGTGAGGGAA<br>CGTG  | 59.9                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_16419363  | Ca2                                     | 16419363                      | GCT/GCTCT                                                                                                                               | TGAACCTCTCAGCCGA<br>ACCT  | TCACACGACTTTTGCT<br>GGAG  | 60.0                             | 135                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_16496636  | Ca2                                     | 16496636                      | GTCAAAC/GTCAAACAAAAGGACT<br>ATTCAAAC                                                                                                    | TATGGACTTTGTGGTG<br>GCAA  | TTGGCACGTACTCCCA<br>TACA  | 60.0                             | 441                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_16514436  | Ca2                                     | 16514436                      | AC/A                                                                                                                                    | TGTGCTGGAAGGCAC<br>ATAG   | GTCTCCCCCACTACAG<br>TCCA  | 59.9                             | 812                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_16650133  | Ca2                                     | 16650133                      | ATTTTTTTTT/ATTTTTTTTTTT                                                                                                                 | ACAGGCTCCCGTTTTA<br>TG TG | AAACGCAATCCTTGAG<br>TTCG  | 60.0                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_16938931  | Ca2                                     | 16938931                      | CTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATT/CTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATT | GAAAGCGCTTCCGTTT<br>ACAG  | ACAGCCACTGCCCAAG<br>TATC  | 60.0                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_17061321  | Ca2                                     | 17061321                      | TAATATATA/TAATATATAAATATATA                                                                                                             | TTTGCTCGGAAGCTT<br>TTTA   | AGGAAGAGTGGAGTTG<br>CGAA  | 60.0                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                         | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                       |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_17368826  | Ca2                                     | 17368826                      | A/ATTTATTTTtaggg                                                                      | TGACATATCCGCTATG<br>AACGA | ATCCATCAACGCTTTC<br>ACC   | 59.2                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_17388033  | Ca2                                     | 17388033                      | GTT/GTTT                                                                              | TGGACACGACGGTGAA<br>ATAA  | GTCGGCCACAAGAAGA<br>CAAT  | 60.0                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_17491578  | Ca2                                     | 17491578                      | CATATATATATATATATATATATAT<br>TA/CATATATATATATATATATATAT<br>TA                         | AGTTGGTCCCCTAGAA<br>CCGT  | CGGTGAATCCTTTACG<br>GAGA  | 59.9                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_17994837  | Ca2                                     | 17994837                      | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATAT<br>TAT                        | TGTGGCCCTATGTACT<br>GCTG  | TTGGAAGGAGCCCTTA<br>CCTT  | 59.7                             | 799                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_18223174  | Ca2                                     | 18223174                      | TTAATAATAATAATAATAATAAT<br>AATAATAATAATAA/TTAATAATAATA<br>ATAATAATAATAATAATAATAA      | CTCAGGATGCGACTTG<br>TTGA  | AAGTGATTTGTGGGTG<br>ATTGG | 60.0                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_18225715  | Ca2                                     | 18225715                      | A/ATATAT                                                                              | GCCATTCCAAATGTTT<br>GCTT  | TGGCTAATAACGATTTC<br>CCG  | 59.9                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_18343132  | Ca2                                     | 18343132                      | T/TGGCGACAACATA                                                                       | TCAAATGAATGGTTTGA<br>GCG  | TCCCTCCTTCACAAAT<br>TGG   | 59.7                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_18496873  | Ca2                                     | 18496873                      | AATATATATATATATATATATATAT<br>ATATATATATAT/AAATATATATATAT<br>TATATATATATATATATATATATAT | AAAAATCCCACGTTTGT<br>CCA  | TAAGTTGTGCGAGAA<br>GTGC   | 60.2                             | 914                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_1853896   | Ca2                                     | 1853896                       | AATATATATATATATATATATATAT<br>ATATATATATATATATATATATATAT<br>T                          | TGAGTCCGCTTCCCAA<br>TTAC  | TTGAGCACGACTTTTTG<br>CAC  | 60.1                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_1856734   | Ca2                                     | 1856734                       | ATT/AT                                                                                | TCCCACTTTCACGTA<br>CACA   | AACCATTGAAGCAAC<br>CGTC   | 60.0                             | 709                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                           |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_18833380  | Ca2                                     | 18833380                      | TAAAAAAAAA/TAAAAAAAAA                                                     | TCGAAAAATCCCTTGA<br>AAAAGA | GGACCTATCAAGTGAG<br>CTTGTG  | 60.0                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_18859929  | Ca2                                     | 18859929                      | TTATATATATATATATAT/TTATAT<br>ATATATATATAT                                 | AAAACAAGCGATCCAT<br>TTGC   | GGTGCTTTGGGGTGTA<br>AAGA    | 60.1                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_18870465  | Ca2                                     | 18870465                      | GAAAAAAAA/GAAAAAAAA                                                       | TTGCTCCGATTCTATC<br>CTTCA  | TTGATCCTGCCATCTTG<br>TCA    | 59.8                             | 766                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_18957648  | Ca2                                     | 18957648                      | CNNNNNNNNN/CNNNNNNNNN                                                     | CACAAAAACCAACCTG<br>CCTT   | CGTTGTCTCTTTATTG<br>ACGATG  | 60.0                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_19132671  | Ca2                                     | 19132671                      | AATATATATATATATATAT/AAT<br>ATATATATATATATAT                               | CGGTGAATCCTTTACG<br>GAGA   | CTCCTTTCCCTCCACA<br>CAA     | 60.1                             | 142                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_1919646   | Ca2                                     | 1919646                       | TC/TCTCC                                                                  | TTGAAGCGATGTGGTT<br>GAAG   | CCAAAACAACTATGCC<br>CGTT    | 59.8                             | 339                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_19219016  | Ca2                                     | 19219016                      | ATTTT/ATTT                                                                | CCCGTGAGATCCTCCT<br>AACA   | TGAATCTACGGCTTTCT<br>GGG    | 60.1                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_19384298  | Ca2                                     | 19384298                      | GGAGAGAGAGAGAGAGAGAGA<br>GAGAGAGAGAG/GGAGAGAGAGAG<br>AGAGAGAGAGAGAGAGAGAG | TGGTTTGGTCAATTTG<br>AGGC   | GAAGCCCAAGTTCCAA<br>ATGA    | 60.9                             | 679                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_19387244  | Ca2                                     | 19387244                      | TTATATATATATATAT/TTATATAT<br>ATATATATATAT                                 | CGACATTGTAGCACCC<br>CTTT   | TTTAGATCCCTTGAC<br>GACC     | 60.0                             | 191                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_1941868   | Ca2                                     | 1941868                       | TTATATATATATATATAT/TTATAT<br>ATATATATATATAT                               | CCGTTACTGCGTCCTA<br>TGGT   | CAATGTCAAAAGTTGG<br>TCTCTGA | 60.0                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                          |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_19437057  | Ca2                                     | 19437057                      | TTATATATATATATAT/TTATATATAT<br>ATATATAT                       | GAATTTAAGGCGTTTC<br>GGGT      | CTTGGTCTAACCCTCA<br>CCCA | 60.3                             | 351                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_19589028  | Ca2                                     | 19589028                      | GATATATATATATATATATATATA<br>TA/GATATATATATATATATATATA<br>TA   | AATGTGAATCCACCA<br>GGAA       | GTCTTTTACAGCGCTTT<br>GGC | 60.2                             | 533                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_19603206  | Ca2                                     | 19603206                      | ACC/AC                                                        | GAGTCCGTAGGAGTAG<br>GGGG      | AATTGAACTTGACGTC<br>GCC  | 60.0                             | 537                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_19616982  | Ca2                                     | 19616982                      | TC/TCC                                                        | AGCTTACCATCCACAA<br>ACGG      | AAAAGTCTGCGACGCT<br>TGTT | 60.0                             | 347                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_19705772  | Ca2                                     | 19705772                      | GAAAA/GAAAAA                                                  | TATTTTGGATTTTGGCT<br>CGG      | AGGAAGAGTGGAGTTG<br>CGAA | 59.9                             | 475                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_19727969  | Ca2                                     | 19727969                      | AATTTATTTATTTATTTATTTT/A<br>ATTTATTTATTTATTTATTT              | GGCGACTCCATTGAAT<br>TTGA      | TTCTTAGCATTGGGAT<br>TGC  | 61.0                             | 833                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_19791685  | Ca2                                     | 19791685                      | C/CG                                                          | TAGGCCATTTTCGTCC<br>TCAC      | AATCCAATGACACAAAC<br>GCA | 60.1                             | 392                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_20175480  | Ca2                                     | 20175480                      | GATATATATATATATATA/GATATA<br>TATATATATATATATATA               | TTTCAGAGTGCTGTG<br>GTTAGCA    | GATCTGAGGTGTCATG<br>GGCT | 60.0                             | 669                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_20348649  | Ca2                                     | 20348649                      | AATATATATATATATATAT/AAAT<br>ATATATATATATATATAT                | TTCTGTGGTTTACAAAT<br>TCAATACA | GGTCGAAATTGGTGTT<br>GGTC | 59.7                             | 664                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_20353586  | Ca2                                     | 20353586                      | T/TG                                                          | TCTCCCTCCTTCCTCC<br>ATT       | CATTAAGAGGTTCCCC<br>CTCC | 60.0                             | 844                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                          | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                        |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_20474785  | Ca2                                     | 20474785                      | GAAAA/GAAAAA                                                                                                           | ATACTGGCTCGGAGGC<br>TTTT | CGTAGCGTGGTAGTGA<br>GCAA  | 60.2                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_20689303  | Ca2                                     | 20689303                      | AATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATATA<br>TATAT                                                      | CCCCTAAATTCGAGG<br>ACAA  | TTCACACATGGGTCAA<br>ACTCA | 59.9                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_20715795  | Ca2                                     | 20715795                      | T/TCATCA                                                                                                               | GACATTGCATTTTGA<br>CACG  | AAATGGATTTTACGCCAA<br>TCG | 60.0                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_21001173  | Ca2                                     | 21001173                      | CATATATATATATATATATATATA<br>TATA/CATATATATATATATATATA<br>TATATATATATA                                                  | TCAATGCGGTCTCTGA<br>AGTG | CCCACAGTCGATGTTG<br>TTTG  | 60.0                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_210507    | Ca2                                     | 210507                        | TATAATAATAATAATAATAATAAA<br>TAATAATAATAATAA/TATAATAATAA<br>TAATAATAATAATAATAATAATAA<br>ATAATAA                         | CATTGTCAAACCTTCG<br>CTCA | CCATGGTTTCTTTGCTT<br>GTT  | 59.8                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_21312312  | Ca2                                     | 21312312                      | GTTTTTT/GTTTTTTTT                                                                                                      | TATCAGAGTTCTCCCC<br>ACCG | AGAAACCACAACGCAA<br>CACA  | 60.1                             | 356                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_21314611  | Ca2                                     | 21314611                      | AG/AGG                                                                                                                 | CAAACCCTTTCAAGGT<br>GCAT | GCACTGCCCAAGAAT<br>TTTA   | 60.0                             | 443                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_21330368  | Ca2                                     | 21330368                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AA/AAATAATAATAATAATAATAAA<br>TAATAATAATAATAATAATAATAA<br>ATAATAA | ACAAACAAGTTGAGCA<br>CCCC | ATGAACGAAAGACGTG<br>ACGG  | 60.0                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_21631180  | Ca2                                     | 21631180                      | CATATATATATATATATATATATA<br>T/CATATATATATATATATATATAT                                                                  | ACGCACCATCTTGTA<br>AGGG  | ATCGACGCGTAGTTTC<br>AAGG  | 60.0                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_21672716  | Ca2                                     | 21672716                      | ATT/AT                                                                                                                 | TGATGCCGTGCCATAA<br>ATAG | TAACCTTGCCTTTGGG<br>TGAG  | 59.5                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                              |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_2169056   | Ca2                                     | 2169056                       | C/CG                                                                                                         | AACCTCTCCAAGAGGA<br>TCGG   | GGAGAGTGAAACGGAT<br>GGAA    | 60.6                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_21695019  | Ca2                                     | 21695019                      | CAAAAAAAAA/CAAAAAAAAA                                                                                        | TGCCTCTGATTCCTTT<br>CAGA   | TCTGTGCTCTCAAATG<br>GTGC    | 59.9                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_21695844  | Ca2                                     | 21695844                      | GTTATTATTATTATTATTATTATT<br>ATTAATATTATTATTATTATTA/GTTA<br>TTATTATTATTATTATTATTATTA<br>TTAATATTATTATTATTATTA | GATGAAATTCAGGCTC<br>GCTC   | TTGACAAGGGAAAACC<br>TTGC    | 59.9                             | 444                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_21717164  | Ca2                                     | 21717164                      | TA/T                                                                                                         | GGTAGAGGCAGGCCAT<br>ATCA   | GATTGTGAGGGATTT<br>TTCAGC   | 60.1                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2174282   | Ca2                                     | 2174282                       | ATTTTTTTTTTTT/ATTTTTTTTTTT                                                                                   | TGACATCCATCTTATGT<br>GGGTC | GGTCTACTCATGTTGA<br>AAGACGC | 59.7                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2178973   | Ca2                                     | 2178973                       | CATAAAATAAAATAAAATAAA/CATA<br>AAATAAAATAAAATAAAATAAAATAA<br>AA                                               | CCTTATTTACGGCAA<br>GTCG    | TTGGGTTAGGGAAAGT<br>CGTG    | 60.6                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_21804816  | Ca2                                     | 21804816                      | AT/ATAAGT                                                                                                    | CGCCATAGACCATTTGG<br>AAAC  | TCCATTGATCACACAAC<br>GGT    | 60.3                             | 860                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_21943275  | Ca2                                     | 21943275                      | AGCGCG/AGCG                                                                                                  | GCAGATTGGAAGGTG<br>TGGT    | ACAATCAGCACGCAAG<br>AATG    | 60.0                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_22196471  | Ca2                                     | 22196471                      | TTGAGTTTGGGGTTGTGA/TTGA                                                                                      | CCAACAAGGACCCAAA<br>GCTA   | ATTTTCGCATCTTTTG<br>CGT     | 60.1                             | 871                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_22301472  | Ca2                                     | 22301472                      | CCAATCGATTGGG/CCAATCGATTG<br>GGCAATCGATTGGG                                                                  | CCCGTGAGATCCTCCT<br>AACA   | TTAAGTCAGGGGCTCA<br>GGAA    | 60.1                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                       | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                     |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_22468520  | Ca2                                     | 22468520                      | CAAAAAAAAA/CAAAAAAAAA                                                                               | TGGCCATGTGCATTGT<br>TTAT | AGGCATCAACGCCTAA<br>ATTG | 59.8                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_22483205  | Ca2                                     | 22483205                      | AT/A                                                                                                | CGTGCCACTTTTCTCT<br>AGGC | AGATCATGTGCAAAA<br>GGGG  | 60.0                             | 369                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_22495551  | Ca2                                     | 22495551                      | TAAAAAAAAA/TAAAAAAAAA                                                                               | TGTTTTGCCGTTCTCT<br>CCTC | AAGAACTTCTCCAATG<br>CGG  | 60.4                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_22533042  | Ca2                                     | 22533042                      | CATATATATATATATAT/CATATAT<br>ATATATATATATAT                                                         | GGTTGTCGCACCAAT<br>TTCT  | GCAAAAGTGTCCCCAC<br>AAGT | 60.0                             | 395                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_228183    | Ca2                                     | 228183                        | GTTTTTTTTT/GTTTTTTTTT                                                                               | TTCGAAACGTTGGATG<br>AATG | GCAACCATCTGACCA<br>GTGA  | 59.5                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_22939976  | Ca2                                     | 22939976                      | TATTTAAATTTAA/TATTTAAATTTAA<br>ATTTAA                                                               | GCACCCACAAAGTAGG<br>CATT | CTCGGCCTCAATACTT<br>GCAT | 60.0                             | 893                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2301289   | Ca2                                     | 2301289                       | CATATATATATA/CATATATATATATA                                                                         | TGCAAAATCAAGCGAA<br>TGAG | TTTTTGCAAGTCTACCC<br>AGG | 60.0                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_23030877  | Ca2                                     | 23030877                      | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTAT/ATATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTAT | GCGAGTGTGGAGGTT<br>TGAT  | CACGCTTGAGTCCTGT<br>TTCA | 60.1                             | 851                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_23050911  | Ca2                                     | 23050911                      | AATG/AATGGTCTATTGGCTTATG                                                                            | TATGGGGATCGGAAAT<br>CAAA | ACAATCGAAATTTAGG<br>CCG  | 60.1                             | 907                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_23192749  | Ca2                                     | 23192749                      | TCA/TCACAACA                                                                                        | GCCGAATAAAACCCTC<br>ACAA | AGCTGTATTGGGCCTC<br>CTTT | 59.9                             | 319                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                              |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_23193466  | Ca2                                     | 23193466                      | TA/T                                                                                         | CCACAAATGCTCATCG<br>TGAC   | TTTGACGCCACAAAAG<br>ACAG  | 60.1                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_23243854  | Ca2                                     | 23243854                      | AAATAATAATAATAATAATAATA<br>ATAATAAT/AAATAATAATAATAATA<br>TAATAATAATAATAATAAT                 | TTTCATGATAATTTTGG<br>AGGGA | CGGCTTTACACCACCT<br>GTTT  | 58.4                             | 252                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2324553   | Ca2                                     | 2324553                       | GATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAA/GATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAA | GTTCAAAAGGAGCTTG<br>ACCG   | AGAGGCAACAAGAAC<br>CGAA   | 59.9                             | 315                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_23360931  | Ca2                                     | 23360931                      | ATTTTTTTTT/ATTTTTTTTT                                                                        | GAGTTGGAATGGCGGT<br>AAAA   | TGTCAGCCAACCCCTC<br>TTCT  | 59.9                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_23496145  | Ca2                                     | 23496145                      | TTATATATATATATATAT/TTATAT<br>ATATATATATATATAT                                                | GTTTTGTAGTGGCCCC<br>AAAG   | CTTTCAAACGGCGAC<br>TTTC   | 59.5                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_23509535  | Ca2                                     | 23509535                      | AAAACTTAAACTTAAACTTA/AA<br>AAACTTAAACTTA                                                     | CCCTCTGAATTTTTGT<br>TTTCC  | CCCACACCTCGACTA<br>AAGA   | 59.0                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2354894   | Ca2                                     | 2354894                       | ATT/ATTT                                                                                     | CCTTCCCCAGATCCTT<br>AACC   | TGTAGTGGGTAATTTG<br>AGCCG | 59.8                             | 866                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2356056   | Ca2                                     | 2356056                       | ATTCAAC/ATTCAACTTTTCAAC                                                                      | GAAAGCGCAGCTACTT<br>TTCG   | ACGATTCCCACTCA<br>CACA    | 60.3                             | 918                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_23695824  | Ca2                                     | 23695824                      | ATT/AT                                                                                       | AATGGTTTTACGCCA<br>AAGT    | TCTCCCTCCCTCCTTCA<br>TTT  | 59.5                             | 817                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_23792320  | Ca2                                     | 23792320                      | GGAGTAAGAGAGTAA/GGAGTAAGA<br>GAGTAAGAGAGTAA                                                  | TCAGAAATCCCTGATCC<br>CAAG  | GCAACCAGGAGGCAAG<br>TCTA  | 60.0                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                  |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_2383872   | Ca2                                     | 2383872                       | CTTTTTTTTTTT/CTTTTTTTTTT                                         | TGGCCGCAAGAAAAT<br>AATC   | TTCCACCAACAAGGA<br>AAGG  | 60.0                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2388005   | Ca2                                     | 2388005                       | GTTTTTTTTT/GTTTTTTTTT                                            | GCCAACAACGTTACGA<br>GCTA  | CTTGCTAAATGCCCA<br>CTTC  | 59.0                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_23887857  | Ca2                                     | 23887857                      | TG/T                                                             | TCTAAGTGGTTGCC<br>TTGG    | TCATGGCAATGCAGA<br>TGAT  | 60.1                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_23932608  | Ca2                                     | 23932608                      | TAAATTAATGAATAAAATTAA/TAA<br>ATTAAT                              | AAGGCATCCAATCAA<br>GCAC   | CTCAAGATTTAGCGC<br>CGTC  | 60.1                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_23986096  | Ca2                                     | 23986096                      | TTATATATATATATATATA/TTATA<br>TATATATATATATATA                    | CAAAATTTCAAACAA<br>ACCCG  | GCACGACAAACACCTC<br>AAAA | 60.6                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_23989802  | Ca2                                     | 23989802                      | AAAAACAAAACAAA/AAAAACAAA<br>CAAAACAAA                            | AATTCGTTGAGCCGT<br>CTAGT  | AGCACGGGGAGTATGA<br>GAAA | 60.1                             | 421                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_23990182  | Ca2                                     | 23990182                      | AAAAACAAAACAAA/AAAAACAAA<br>CAAAACAAA                            | TCTCATACTCCCGTG<br>CTTT   | ATCCCTACACCAGAT<br>GCAC  | 59.7                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_24078993  | Ca2                                     | 24078993                      | ATATTATTATTATTATTATTATTA<br>TT/ATATTATTATTATTATTATTA<br>TTATTATT | CGCATGAGAAATTGTG<br>CCTA  | ATTGCAACCGCAACCA<br>TACT | 59.8                             | 883                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_24124699  | Ca2                                     | 24124699                      | ATTTTTTTTTTTTT/ATTTTTTTTTT<br>TTT                                | ATATATCGGGGTTTCAT<br>GGCA | CCATGCTTCACCTTG<br>GTAT  | 60.0                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_24251584  | Ca2                                     | 24251584                      | ACCCCC/ACCCCCC                                                   | GATTGCTTTCTGGGTG<br>GAAA  | TGATCAACCCTTGGTG<br>TGAA | 60.1                             | 652                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)        | Forward primers (5'-3')      | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                      |                              |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_24252139  | Ca2                                     | 24252139                      | TAA/TAAGAAA                                                          | GATCCTCAAATCGACCTCCA         | TGTCACCATTGGTCTC<br>CAAA  | 60.0                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_24349766  | Ca2                                     | 24349766                      | AATTTAATT/AATTTAATTATATTTAA<br>TT                                    | TCTTCACGCCAAGAAG<br>AAAAA    | AAAAACGATTGCGAAT<br>GGAG  | 60.0                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_24393200  | Ca2                                     | 24393200                      | G/GAAGATA                                                            | TCCTAGAACATGCATC<br>ACGC     | TACCCTTTGCTAGCCC<br>CTTT  | 59.8                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_24393621  | Ca2                                     | 24393621                      | CAAAAA/CAAAA                                                         | AGGGGCTAGCAAAGG<br>GTAAA     | GCTCAAGGTGACAAGC<br>CTTC  | 60.1                             | 344                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_24538889  | Ca2                                     | 24538889                      | ATATTATTATTATTATTATTATTA<br>T/ATATTATTATTATTATTATTAT<br>TATTATTATTAT | GGAGGACATGCAAATG<br>AGGT     | GTGGTTTGCAAGGCTAT<br>GGAT | 59.9                             | 829                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_24597882  | Ca2                                     | 24597882                      | C/CAGAAAAATCA                                                        | TTATTCGGGCCTGTCA<br>AAAC     | ATGGCGTTTACCCAAG<br>ACTG  | 59.9                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_24943194  | Ca2                                     | 24943194                      | A/AATT                                                               | AACCCCTCCAAGAAC<br>GACT      | AGGGCCCCACTAACTC<br>CTTA  | 60.0                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_24943252  | Ca2                                     | 24943252                      | CTTT/CTT                                                             | AACCCCTCCAAGAAC<br>GACT      | AGGGCCCCACTAACTC<br>CTTA  | 60.0                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_25241576  | Ca2                                     | 25241576                      | GATATATATATATATATATATATA<br>TATATATATA                               | TATTTTGATTTTGGCT<br>CGG      | AAATGGAGGAAGGAGG<br>GAGA  | 59.9                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_25427657  | Ca2                                     | 25427657                      | TTATATATATATATATATATATATA<br>TATAT/TTATATATATATATATATA<br>TATATATAT  | TGTTGTTGAAGATGAA<br>ATATTGGC | TTTGCGCTAGTGAAGT<br>TGACA | 60.2                             | 723                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                           |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_25458560  | Ca2                                     | 25458560                      | ATTTTTTTTT/ATTTTTTTTT                                                                     | CAAATTTAATGGCACA<br>GGGG    | AATTGGAGTGTGTGAT<br>TCGC  | 60.2                             | 957                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_25527401  | Ca2                                     | 25527401                      | GATAATAATAATAATAATAATAA<br>TAATAATAA/GATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAA | ACCCTTCAATTTTCGACA<br>TGC   | CCAATTGGAATTTGCAA<br>CAA  | 59.9                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_25529860  | Ca2                                     | 25529860                      | CTTT/CTTTTT                                                                               | AGCAGCCCAAGCAAGA<br>CTTA    | TCATGCCGATTGATAG<br>AGGTT | 60.2                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_25554310  | Ca2                                     | 25554310                      | TTGTGTGTGTGTGT/TTGTGTGT<br>GT                                                             | ATGCGGCAGGTATGAG<br>AACA    | ATATCAACGCCCTTTTG<br>CAT  | 61.6                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_25593755  | Ca2                                     | 25593755                      | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATA<br>TATATAT                         | AACCCGTTTTGATTGA<br>GTGC    | TGCGAAATTAGGCCTC<br>CATC  | 60.0                             | 466                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_25663538  | Ca2                                     | 25663538                      | TAAAAAAAAAAAAA/TAAAAAAAAAA<br>A                                                           | TGCTCTGACTCTCCAA<br>TTTCTTC | GGGATTGGACTGCCTA<br>GCTT  | 60.0                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_25737290  | Ca2                                     | 25737290                      | TAAAAAAAAAAAAA/TAAAAAAAAAA                                                                | GGTCGTCTGTTGGGTT<br>GTCT    | GTCGACGGCGAGAAGA<br>ATAA  | 60.0                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_25795167  | Ca2                                     | 25795167                      | GAATTTTAAATTTTAA/GAATTTT<br>TAAATTTTAAATTTTAA                                             | AGCCACGGCTCTAAG<br>ATCA     | TTGGTTTCATTGTTTG<br>CATTT | 60.0                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_25911445  | Ca2                                     | 25911445                      | GAAAAAAAAAAAAA/GAAAAAAAAAA                                                                | TTTCCCGACTTGGTCC<br>TTTA    | TGCGCTTAAAGACAGG<br>GAGT  | 59.5                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2607354   | Ca2                                     | 2607354                       | AATATATATATATATATATATAT/A<br>ATATATATATATATATATATATAT                                     | GGATATTGGGGATGGC<br>CTAC    | CCCATGTGATGAGCTA<br>CCCT  | 60.4                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_26102860  | Ca2                                     | 26102860                      | TAAAAAAAAA/TAAAAAAAAA                                         | ACGTATGGTTACCGT<br>CACA    | AGCGATCCCTCCGTT<br>ATTT    | 59.1                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_26111863  | Ca2                                     | 26111863                      | AATATATATATATATATATATAT/ATATATATATATATATATATATAT              | ATGCGTACATCAAGG<br>TGGT    | GGCTCATATATTTGCAT<br>TCACG | 60.3                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_26504489  | Ca2                                     | 26504489                      | CAA/CAAAA                                                     | CCGACGTCCAGTCAGA<br>ATTT   | CTCAATTGGACACCGT<br>TCCT   | 60.1                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_26531031  | Ca2                                     | 26531031                      | TA/T                                                          | AGAGATCTGTGCAGCC<br>GAGT   | GCACTCAATTTGGGA<br>AAAA    | 60.2                             | 746                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_26693813  | Ca2                                     | 26693813                      | TAAAAAAAAA/TAAAAAAAAA<br>AAA                                  | GCACACATGCAGAAAG<br>GAGA   | TCCAATCTCGAAAAA<br>CACTG   | 60.0                             | 629                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2671437   | Ca2                                     | 2671437                       | TAAAAAAAAA/TAAAAAAAAA                                         | TAATTCAGCCAAGGAA<br>GCCA   | GGAAACGCAAAAGGA<br>ATCA    | 60.7                             | 235                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_26811414  | Ca2                                     | 26811414                      | TAAAAAAA/TAAAAAAA                                             | GGGCTTGTTTGATTGT<br>GTTTT  | GGCTCCATTCTTTGCT<br>CTTG   | 59.0                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_26823619  | Ca2                                     | 26823619                      | AATA/AA                                                       | TGGCGACATATTTTG<br>GTGA    | TATGCGGCTGCCTATT<br>TTTC   | 59.9                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_26914055  | Ca2                                     | 26914055                      | ATTTTTTTTT/ATTTTTTTTTTT                                       | AGGTTTGAACCGTCAC<br>CAAC   | TTTGCATGTTCAATCAC<br>TCCA  | 59.9                             | 255                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2692293   | Ca2                                     | 2692293                       | ATTTTTTTTT/ATTTTTTT                                           | AAAGGTGATGAAGCAG<br>ATTTGA | TGGTGTCTCTCTTCT<br>CTAATCG | 60.1                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_27143098  | Ca2                                     | 27143098                      | AA/AACA                                                       | CGTTCATTTATTGTTGG<br>GGC     | GGGTTTTGGTAGCCAA<br>CTCA      | 60.2                             | 200                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_27261925  | Ca2                                     | 27261925                      | AATGCA/AA                                                     | CCAGTCCTCACACCCT<br>TGTT     | TGAATTTTCCAACGGTC<br>ACA      | 60.0                             | 356                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2744252   | Ca2                                     | 2744252                       | TAAAAAAAAA/TAAAAAAAAA                                         | TTCCAAATACGCAACC<br>ACAA     | TTCTTGCCTTTCATGTT<br>CCA      | 60.0                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_27506078  | Ca2                                     | 27506078                      | AATATATATAT/AATATATATAT                                       | GGCGTAAGGATGGA<br>AACA       | ACCTCAATTTCTCGGC<br>TCA       | 59.9                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_27544148  | Ca2                                     | 27544148                      | CATATATATATATATATATATAT/C<br>ATATATATATATATATATATATAT         | CCAGCAAATTCCTGCA<br>TTCT     | TGCACGGATGGATCAT<br>AAAA      | 60.2                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_27612199  | Ca2                                     | 27612199                      | TA/T                                                          | CCACATGATCACTCAT<br>AAATATCG | AAAAATGGATTGACATA<br>AATTGAAA | 58.4                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_27642027  | Ca2                                     | 27642027                      | TAA/TA                                                        | ACCCCATTTTGTTGTG<br>GTGT     | TGCTTGGCTATGGCAT<br>AAGA      | 60.0                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_27679281  | Ca2                                     | 27679281                      | AATATATATATATATA/AATATATA<br>TATATATATATATATA                 | TGGTCATTTGTCTTG<br>CTGC      | AAGGGTCAATTCAACG<br>GTGT      | 59.8                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_27776478  | Ca2                                     | 27776478                      | GTTTTTTTTT/GTTTTTTTTT                                         | CAATGAACCTGGTCAA<br>CCCC     | GCCCATGTCTGCATAG<br>TAACAA    | 60.2                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_27776538  | Ca2                                     | 27776538                      | TAAAAAA/TAAAAA                                                | CAATGAACCTGGTCAA<br>CCCC     | GCCCATGTCTGCATAG<br>TAACAA    | 60.2                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                          |                           |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_27800362  | Ca2                                     | 27800362                      | ATTTTT/ATTTTTT                                                          | ATAACCCACCTTTCAT<br>CCC  | CCCTTGATTATCCATGC<br>ACC  | 59.9                             | 821                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_27802687  | Ca2                                     | 27802687                      | TTATATATATATATATATATATATA<br>TATATAT/TTATATATATATATATATA<br>TATATATATAT | TTTGTCAGCACTTCCA<br>TCG  | TCACACCAAAATGAAAT<br>CACG | 59.8                             | 540                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_27896998  | Ca2                                     | 27896998                      | GAAAAA/GAAAAAA                                                          | CTGCCACTTCTTCCC<br>TCAC  | GGCTGACACACACACA<br>CACA  | 59.8                             | 531                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_28009782  | Ca2                                     | 28009782                      | TTATATATATATATATAT/TTATAT<br>ATATATATATATATAT                           | TGGCAATGTGGTACTG<br>GAGA | GGAAGTCCGAATTTC<br>AATG   | 60.1                             | 206                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_28037628  | Ca2                                     | 28037628                      | AATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATA<br>TATATAT       | CTAGTGTTGCACGGGT<br>CAAA | CATAACGAATTCTCCCA<br>CCG  | 59.8                             | 768                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_28235085  | Ca2                                     | 28235085                      | GTTTTTTTTT/GTTTTTTTTTTT                                                 | TCCAAATAGCGACTTC<br>CCAC | TCCAAATGTTACAGCCA<br>GCTC | 60.1                             | 567                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_28235280  | Ca2                                     | 28235280                      | AATATATATATATATATATA/AATATA<br>TATATATATATATATA                         | TCCAAATAGCGACTTC<br>CCAC | ACAATCCTCAAATGCG<br>GAGA  | 60.1                             | 701                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_28235432  | Ca2                                     | 28235432                      | AATATATATATATATATATA/AATA<br>TATATATATATATATATA                         | TCCAAATAGCGACTTC<br>CCAC | GCTGCATGTTCTTATG<br>CTCG  | 60.1                             | 849                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_28262473  | Ca2                                     | 28262473                      | GAA/GAAAA                                                               | CTGAGACACGGCGACA<br>ATAA | ATCGGAGCAATTCTGC<br>ATTC  | 59.9                             | 305                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_28365177  | Ca2                                     | 28365177                      | AATATATATATATATATATATAT/A<br>ATATATATATATATATATAT                       | TCGGTCTCCTCATTTG<br>ATCC | GGGCCACATGTAATGC<br>TTCT  | 60.0                             | 768                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_28396846  | Ca2                                     | 28396846                      | ATATTTTT/ATTATTTTT                                            | TGGGCCCACTTAATC<br>CATA      | CATGTCCAAAACAAAT<br>CAATCA | 60.1                             | 337                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_28464989  | Ca2                                     | 28464989                      | AAAA/AAAAATAAAA                                               | TCATCGCAGGTGTACC<br>ATGT     | AACATTGCACCGGTTT<br>GATT   | 60.0                             | 414                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_28465231  | Ca2                                     | 28465231                      | CAAAA/CAAAA                                                   | TCATCGCAGGTGTACC<br>ATGT     | GGTATCAGAGCCACC<br>ATGT    | 60.0                             | 908                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_28465620  | Ca2                                     | 28465620                      | A/AT                                                          | AGCTCCATTGCAAAA<br>CACC      | GCAATCCCACAGGTA<br>TGCT    | 60.1                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_28482218  | Ca2                                     | 28482218                      | CATA/CATATA                                                   | TCCATAGAATTAATGGT<br>CCCC    | TTTGCTTTATCAAGCCA<br>CCC   | 57.7                             | 198                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_28556774  | Ca2                                     | 28556774                      | GAAAAAAA/GAAAAAAA                                             | TCCTAGCAAATCCAC<br>ACGA      | GACAATGAAATTGGGG<br>TTGG   | 59.3                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_28569281  | Ca2                                     | 28569281                      | T/TC                                                          | CATCTGTAATGATGCG<br>CCAC     | GA CTGGACGTAACCCA<br>CGTT  | 60.1                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_28614815  | Ca2                                     | 28614815                      | AATATATATATATATA/AATATATA<br>TATATATATATA                     | ATTCCACATCCACAA<br>GGAA      | GCAGTGCAGCAACAGA<br>AAAA   | 60.2                             | 441                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_286502    | Ca2                                     | 286502                        | TAAAAAAA/TAAAAAAA                                             | AATAGGCTGCCACAAG<br>AGGA     | TGGACACGACGGTGAA<br>ATAA   | 59.8                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2881711   | Ca2                                     | 2881711                       | CTTTTGTTACTCTTT/CTTTGTTACT<br>CTTTTGTTACTCTTT                 | TTCATTTTCATCAATTCG<br>ATCCTT | GGCAATGCCACCGTAA<br>AATA   | 59.8                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                 |                             |                              |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_28873803  | Ca2                                     | 28873803                      | GTTTT/GTTTT                                                                     | GGCAGGCAACAAGACA<br>AAAT    | TCCGTGCATGCCATAA<br>TCTA     | 60.1                             | 656                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_28981150  | Ca2                                     | 28981150                      | TAAAAA/TAAAAA                                                                   | TGTTTAGGGATCAAAA<br>CTGAGGA | CAAAGGTATGTATAAGT<br>GGGGAAA | 60.0                             | 454                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_29089904  | Ca2                                     | 29089904                      | CTAAATTTTTAAATTTT/CTAAATTT<br>TTTAAATTTTTTAAATTTT                               | TCATAATCACCCCT<br>CCTTT     | TGGTGAAACAATTCAAA<br>CGC     | 59.7                             | 644                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_29142241  | Ca2                                     | 29142241                      | TAAAAAAAAAAAAA/TAAAAAAAAA                                                       | CAACTCGATTCAACCA<br>GGGTA   | TCCCTACAAGATGGCA<br>TGAA     | 60.0                             | 670                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_29156803  | Ca2                                     | 29156803                      | ACG/A                                                                           | ACATGACATTTTGCCG<br>ATGA    | GTCATGTGGCTTTGGT<br>GTTG     | 59.9                             | 544                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_29184413  | Ca2                                     | 29184413                      | GAAAAAAAAA/GAAAAAAAAA                                                           | TGGTGGGTGATTGCTG<br>ATTA    | AAGATTGGAACCTGGG<br>CCTT     | 59.9                             | 435                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_29212961  | Ca2                                     | 29212961                      | TTATATATATATATATATATATATATA<br>TATATATAT/TTATATATATATATATA<br>TATATATATATATATAT | TAGTTTGTAACCCGTG<br>CGTC    | CAAAAAAAGACATGGT<br>GTTGGA   | 58.7                             | 273                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_29215176  | Ca2                                     | 29215176                      | T/TTTGATATTCTCTC                                                                | ACGGTTGAGAATTGAG<br>TGGC    | CGCACACCTCTAACAA<br>CCAA     | 60.1                             | 508                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_29220253  | Ca2                                     | 29220253                      | GATATATATATATATATATATA/GA<br>TATATATATATATATATATA                               | AGGCATGGTGTTGGAG<br>TCAT    | CTAGTTCGTAACCCGT<br>GCGT     | 60.4                             | 253                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_29220546  | Ca2                                     | 29220546                      | GATAATAATAATAATAATAATAA<br>TAATAAT/GATAATAATAATAATAA<br>ATAATAATAATAATAAT       | CACGTGTCAAACCTGC<br>CAAT    | GTAACCGTTGGAGCAC<br>CACT     | 59.6                             | 534                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_29239999  | Ca2                                     | 29239999                      | AAT/A                                                         | GGCTGCTGATCCTGTT<br>CTTC   | CTGACGGACGGACTCA<br>TTTT  | 60.0                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29240150  | Ca2                                     | 29240150                      | TC/TCACC                                                      | CTTAGAGCATCTCCAA<br>CGGC   | GAAGCATCGTTCCTTC<br>CTGA  | 60.0                             | 134                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29240273  | Ca2                                     | 29240273                      | ATTTTTTTTT/ATTTTTTTT                                          | CTTAGAGCATCTCCAA<br>CGGC   | CAACGGTGAACTCAAT<br>ATGGG | 60.0                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29240382  | Ca2                                     | 29240382                      | TCCC/TCC                                                      | CTTAGAGCATCTCCAA<br>CGGC   | CCTTGCACTATCATTTT<br>CGGA | 60.0                             | 803                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29240470  | Ca2                                     | 29240470                      | T/TCAC                                                        | CTTAGAGCATCTCCAA<br>CGGC   | TGTCCTTGTTCCCTTG<br>CACT  | 60.0                             | 838                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_292468    | Ca2                                     | 292468                        | ATTTTTTTTT/ATTTTTTTTT                                         | GGAAGGAACGGTGCTT<br>CATA   | TTTTGCTCCAACGGTG<br>AACT  | 60.1                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29252004  | Ca2                                     | 29252004                      | GTT/GT                                                        | TCAAAGGTGCACTCTT<br>GCTATT | TGGCTTCCGGAAGAC<br>TAAA   | 59.0                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29348083  | Ca2                                     | 29348083                      | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATATAT         | TTTTCCAACACCAGAG<br>TCCC   | GATGCCTCATCGTGGA<br>GATT  | 59.9                             | 629                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29356033  | Ca2                                     | 29356033                      | CTTTTTTTTTTT/CTTTTTTTTTT                                      | TGAAGTCAACCCGTCA<br>ACTG   | AGGTGCAATTCATCT<br>ACCG   | 59.7                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2941126   | Ca2                                     | 2941126                       | AATATATATATA/AATATATATATATA                                   | CAAACCCATTGGTCCC<br>TTTA   | CGTGTATATACGCACA<br>CCCAA | 59.7                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                         | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                       |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_29417303  | Ca2                                     | 29417303                      | TACA/TAACA                                                                                                            | CCCAGAAATCGATTAG<br>GCAA  | TCAACGTTTCGTTTGGT<br>TCA    | 60.0                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29423510  | Ca2                                     | 29423510                      | TAA/TAAAA                                                                                                             | TGCCAACAAAAATACAT<br>GCAA | TGGAGGCTATCACCAA<br>TGTTT   | 60.0                             | 846                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29444244  | Ca2                                     | 29444244                      | ATTTT/ATTTT                                                                                                           | AAATCCGACTGTCTAA<br>CCCG  | TTTTCTCCTCCAATTA<br>GTCCAA  | 59.1                             | 826                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29445825  | Ca2                                     | 29445825                      | TGTCTAACCCGTCTAACCCG/TGTC<br>TAACCCG                                                                                  | TCACCCACACTCTCAA<br>TCCA  | CCCTACCTAGGGGTGG<br>ACAT    | 60.1                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29445927  | Ca2                                     | 29445927                      | AACCCGAACCC/AACCCGAACCCAC<br>CCGAACCC                                                                                 | TGCTTAACCCGTCTAA<br>CCCG  | CCCTACCTAGGGGTGG<br>ACAT    | 60.0                             | 138                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29466835  | Ca2                                     | 29466835                      | CC/CCTC                                                                                                               | TAAACAGATCCCGAA<br>TGCC   | GCATGTTTGAGAGGGG<br>AGAA    | 59.9                             | 130                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2955850   | Ca2                                     | 2955850                       | GGGCCGG/GGG                                                                                                           | CCGTCCAACCTTCATTC<br>CATT | CACCACAAATTCGATG<br>ACG     | 59.8                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29677109  | Ca2                                     | 29677109                      | ATTTTTT/ATTTTTT                                                                                                       | TGCAACGAGTTAAGTG<br>TCCAA | CAAATTTAACGACCAGA<br>TGTGTG | 59.4                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29722067  | Ca2                                     | 29722067                      | TTATATATATATATATATATATATATA<br>TATATATATATATATATATAT/TTATA<br>TATATATATATATATATATATATATAT<br>ATATATATATATATATATATATAT | CCTCCCTCGTGTGAGA<br>TGTT  | TCGTGCAACTCTTAAAT<br>CCAA   | 60.1                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2975267   | Ca2                                     | 2975267                       | GAAAAAAA/GAAAAAAA                                                                                                     | TTCACGACTTGAAAG<br>GACC   | TGATCGCCATTGATTG<br>AGAA    | 60.1                             | 750                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_29787158  | Ca2                                     | 29787158                      | CATATATATATATATATATATA/CATA<br>TATATATATATATATATATA           | TATTGCACTTGCCGTA<br>CCAA    | TTAGCAAAACGTTCCG<br>TTCC   | 60.1                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2982838   | Ca2                                     | 2982838                       | TAAAAA/TAAAA                                                  | TCCCGAACGTTCCAGAT<br>TAGC   | CCCCATTGATTATCGA<br>ACAA   | 60.2                             | 272                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29829814  | Ca2                                     | 29829814                      | AAT/AAATAT                                                    | CTTTTCGTCGGAGTTT<br>GTCC    | TCGTCCTCTGTTTCT<br>CGT     | 59.7                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29829940  | Ca2                                     | 29829940                      | TT/TTTCGAAAAAAT                                               | CTTTTCGTCGGAGTTT<br>GTCC    | TCGTCCTCTGTTTCT<br>CGT     | 59.7                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2984623   | Ca2                                     | 2984623                       | CATTA/CA                                                      | TGCCAAACCAATGTCT<br>TCTT    | GAGTCTCATGTCTCAA<br>CGAGGA | 58.2                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29847360  | Ca2                                     | 29847360                      | CTTTTTTTTTTT/CTTTTTTTTTT                                      | AACGTTCTCCGTTTTTC<br>AGC    | GTGCGTCATGCAAATA<br>TGGT   | 59.4                             | 838                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2984806   | Ca2                                     | 2984806                       | T/TG                                                          | TTTGCTCCGGTCTAAG<br>AAAGA   | GAGTCTCATGTCTCAA<br>CGAGGA | 59.1                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29850746  | Ca2                                     | 29850746                      | TTATATATATATATATATATAT/TT<br>ATATATATATATATATAT               | TCCACCTAAGACCCTA<br>AAAGAAA | TTCTTTGGCTCCTCCTC<br>GTA   | 58.4                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29855866  | Ca2                                     | 29855866                      | AATAATTATAATTTAT/AATAATTTA<br>T                               | TCAATATTCCGATTGC<br>GTGA    | CGACGAAACAAAACAT<br>GGAA   | 60.0                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29884511  | Ca2                                     | 29884511                      | ATGTGTGT/ATGTGTGTGT                                           | GCTCAAGTATGGGCAA<br>AAGC    | TGGGGTCATCCAAATT<br>CAGT   | 59.9                             | 457                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')        | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|--------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                 |                                |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_29887425  | Ca2                                     | 29887425                      | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>ATATA | TTCGTTTGAAAACCT<br>AGCAA       | TACGACCTACCGAAGC<br>AACA   | 59.1                             | 708                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2995772   | Ca2                                     | 2995772                       | AAAGTA/AA                                                       | TGTGAACTTTTATGCAT<br>GGC       | TGTTGCGTTGGTCCTT<br>AGAA   | 57.2                             | 279                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2996172   | Ca2                                     | 2996172                       | ATTT/ATT                                                        | TTCTAAGGACCAACGC<br>AACA       | GTATGATCGATTATGC<br>GCGA   | 59.3                             | 434                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29962779  | Ca2                                     | 29962779                      | G/GC                                                            | AGCCAACGGACCACTA<br>ACAC       | TTGCCATTCTTCTCG<br>TCT     | 60.0                             | 237                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29962869  | Ca2                                     | 29962869                      | TAACAACAA/TAACAA                                                | TGGAAGCCATGATTAG<br>GAGG       | TCTCCATTCTGTTGTG<br>ATG    | 60.0                             | 182                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_29963169  | Ca2                                     | 29963169                      | TGG/TGGG                                                        | TGGAAGCCATGATTAG<br>GAGG       | TGGAATCAGAGAGGGA<br>CGTT   | 60.0                             | 876                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2996523   | Ca2                                     | 2996523                       | ATTT/ATT                                                        | CTCGAGTCGGTGTTGT<br>GATG       | TTCTTCACGATCATCCA<br>TGC   | 60.3                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_2996631   | Ca2                                     | 2996631                       | CAAAAAAAAA/CAAAAAAAAA                                           | CTCGAGTCGGTGTTGT<br>GATG       | TTCTTCACGATCATCCA<br>TGC   | 60.3                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3000587   | Ca2                                     | 3000587                       | ATTTTTTT/ATTTTTT                                                | CCTGTCATTCTAATTA<br>CGTGTTTTG  | TGTGAGACCATTTAAC<br>CCATCA | 60.2                             | 999                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3000644   | Ca2                                     | 3000644                       | ATTTTTTT/ATTTT                                                  | TGATTCAATTGTGAAGT<br>TTTAATGTG | GGAGAAACATCACGTT<br>GACC   | 59.4                             | 949                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                               | Forward primers (5'-3')        | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------|--------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                             |                                |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_3002705   | Ca2                                     | 3002705                       | TGG/TG                                                                                      | TGCAACGATTACCACA<br>TGAA       | TTTGTCTTTTGGTCTG<br>CCT    | 58.5                             | 340                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3004734   | Ca2                                     | 3004734                       | CA/CAA                                                                                      | GGTTGTTTCATCCAACC<br>CCTA      | GAACGAGTTCATGTGG<br>CCTT   | 59.6                             | 871                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30050486  | Ca2                                     | 30050486                      | CAGAAGAAGAAGAAGAAGAAG<br>AA/CAGAAGAAGAAGAAGAAGA<br>AGAAGAA                                  | AATCGGAGAAATGAAG<br>CCCT       | TTGAAATGAAGGTGG<br>GGTC    | 60.0                             | 157                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3005264   | Ca2                                     | 3005264                       | AATATACATATA/AATATA                                                                         | ATCATTAAATCGTCGAC<br>CCCA      | AAAGCGTTTTTGTCA<br>CACC    | 60.2                             | 797                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3005316   | Ca2                                     | 3005316                       | TAAAAAAAA/TAAAAAAAA                                                                         | ATTGATGGGCCAACAG<br>ATTT       | AAAGCGTTTTTGTCA<br>CACC    | 59.2                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3005699   | Ca2                                     | 3005699                       | C/CT                                                                                        | AAACCACAATGGAGGC<br>CTAA       | CGAGAATTAATTGGAG<br>GCCA   | 59.4                             | 729                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30095996  | Ca2                                     | 30095996                      | TAAAAAAAA/TAAAAAAAA                                                                         | CATTCCCGCTACATTTT<br>GGT       | GGAGAGAGGCCAATTT<br>TTCA   | 59.8                             | 226                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30096276  | Ca2                                     | 30096276                      | TA/TAAA                                                                                     | CATTCCCGCTACATTTT<br>GGT       | GAAGCTGCTTGTGTGC<br>CATA   | 59.8                             | 876                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30096869  | Ca2                                     | 30096869                      | CATATATATATATATATATATATA<br>TATATATATATAT/CATATATATAT<br>ATATATATATATATATATATATATA<br>TATAT | CATTGCAGGTGCTATG<br>GTTG       | TTCTCTTATGAAGCGG<br>AGGA   | 60.1                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30125989  | Ca2                                     | 30125989                      | TAAAAA/TAAAAA                                                                               | TTCCAATTATGGTGAG<br>TAATGATTTT | TTGTGAGCATGAGAAG<br>TTGTTG | 59.3                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_3016406   | Ca2                                     | 3016406                       | AC/ACGAGC                                                     | TCGTTGTGTCATCTA<br>TCCG   | GCAGCGTTTATCTCTC<br>CCA   | 60.7                             | 366                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30165012  | Ca2                                     | 30165012                      | T/TGA                                                         | TTGTTGTGACATCGAA<br>CGTCT | CAACAATTTCTCATGCT<br>CGC  | 59.2                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3016524   | Ca2                                     | 3016524                       | GAAAAAAAA/GAAAAAAAAA                                          | TGGGAGAGATAAAACG<br>CTGC  | TCTTTCACAACTCAAA<br>AGTGC | 60.4                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30173035  | Ca2                                     | 30173035                      | GAAAAAAAA/GAAAAAAAAA                                          | CGAGTCTCAAACGGT<br>TGAA   | TCCCCCTGATTTTGT<br>TTG    | 58.9                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30174020  | Ca2                                     | 30174020                      | CTT/CTTT                                                      | TTATCCCGCATATTG<br>GACT   | AGTCCTTGGGACCGAA<br>AAGT  | 59.3                             | 227                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3019431   | Ca2                                     | 3019431                       | CTT/CTTT                                                      | TTCAACCATCAACATT<br>TGACC | TGCTTTGTTTGCAAAAT<br>GGT  | 59.7                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3020730   | Ca2                                     | 3020730                       | CAAAAAAAAA/CAAAAAA                                            | GTGAGGATTTGCAAGA<br>CGTG  | ATGTTGGTATGCGTTG<br>TTGA  | 59.3                             | 625                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3021004   | Ca2                                     | 3021004                       | TAAAAAAAA/TAAAAAAAAA                                          | ATCAACAACGCATACC<br>AACA  | ATTCGGAACGTTTTC<br>CAG    | 57.5                             | 380                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3021370   | Ca2                                     | 3021370                       | CACTA/CA                                                      | TGCAAAACGTTCCGA<br>AATA   | TCAAAAATTGATTCCA<br>CCCA  | 59.2                             | 241                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3022598   | Ca2                                     | 3022598                       | AGTGGTC/A                                                     | TCCTGAAACAAATGCA<br>CCAA  | TGAGAACTTTCGAGT<br>CGGG   | 60.1                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_3025547   | Ca2                                     | 3025547                       | GAAAAAAAAA/GAAAAAAAAA                                         | TCAAAATAATACCGACC<br>CCG   | AAAAACGAGGCGATGA<br>CAAT  | 59.7                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30282909  | Ca2                                     | 30282909                      | GAAAAAAAAA/GAAAAAAAAA                                         | TGCATAATTGTCCATG<br>CGAT   | CCATAATTGTTTTGCA<br>GTCCA | 59.9                             | 378                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3028297   | Ca2                                     | 3028297                       | TAAAAA/TAAAA                                                  | TCAGTTAATCCCAACT<br>GCAA   | ATGCACCAAGTGCAAC<br>TGAG  | 59.6                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3029534   | Ca2                                     | 3029534                       | ATAAT/A                                                       | ACCGCTCTATTAAGGG<br>CGAG   | TCCATCGCAATTGAATA<br>ATGA | 60.7                             | 765                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3029555   | Ca2                                     | 3029555                       | TAAAA/TAA                                                     | ACCGCTCTATTAAGGG<br>CGAG   | TCCATCGCAATTGAATA<br>ATGA | 60.7                             | 765                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3031259   | Ca2                                     | 3031259                       | ATTTTT/ATTTTT                                                 | TCAATTGCGATGGATA<br>GAGAAA | AATTGGTGTACCGATT<br>GCGT  | 59.7                             | 647                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3031554   | Ca2                                     | 3031554                       | C/CCAAAATATCT                                                 | CATCTTGTCATCAAA<br>GGA     | GGTGTACCGATTGCGT<br>ATCC  | 59.5                             | 279                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3031875   | Ca2                                     | 3031875                       | AG/A                                                          | TTGGATACGCAATCGG<br>TACA   | ATGCACTTGCAAGACC<br>TTTT  | 60.0                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3032103   | Ca2                                     | 3032103                       | T/TTTAA                                                       | TTGGATACGCAATCGG<br>TACA   | ATGCACTTGCAAGACC<br>TTTT  | 60.0                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3033174   | Ca2                                     | 3033174                       | CTTTTTT/CTTTTT                                                | GATCCAATGCTCAGTC<br>ATGC   | GCACCATCATTTGACC<br>CTTC  | 59.2                             | 619                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_3033231   | Ca2                                     | 3033231                       | TAAAA/TAAAA                                                   | GATCCAATGCTCAGTC<br>ATGC     | GCACCATCATTTGACC<br>CTTC   | 59.2                             | 619                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3033295   | Ca2                                     | 3033295                       | CAAAAAAAAA/CAAAAAAAAAA                                        | GATCCAATGCTCAGTC<br>ATGC     | GCACCATCATTTGACC<br>CTTC   | 59.2                             | 619                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3033478   | Ca2                                     | 3033478                       | CAAAAAAAAA/CAAAAAA                                            | GATCCAATGCTCAGTC<br>ATGC     | CCTCCATTCCTGGTCA<br>ATGT   | 59.2                             | 927                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30340535  | Ca2                                     | 30340535                      | TAAAA/TAAAA                                                   | TTTGCATCGATGATCG<br>TAATTT   | GATCTCGAGTTTGAGT<br>TCAGGA | 59.5                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30340851  | Ca2                                     | 30340851                      | TA/TAA                                                        | TGTCTTATCCTGAACTC<br>AAACTCG | ATTGGTCAACCACCC<br>AAAA    | 59.8                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30341034  | Ca2                                     | 30341034                      | TAA/TAAA                                                      | TGTCTTATCCTGAACTC<br>AAACTCG | ATTGGTCAACCACCC<br>AAAA    | 59.8                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30343224  | Ca2                                     | 30343224                      | CT/CTT                                                        | TGGATGCGTAGCAGAT<br>TAGAGA   | CGTCACTTGGTCACTT<br>GGTG   | 60.0                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30344280  | Ca2                                     | 30344280                      | AAATGAA/AAA                                                   | TTTAAGAGCCCGTGA<br>AATG      | GGTCCCAACCAAGTA<br>TGAA    | 60.1                             | 789                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30352286  | Ca2                                     | 30352286                      | TG/TAACG                                                      | TAAAAAGTGGTTCGGT<br>TCGG     | TTATTTTCCCTTTTGG<br>CCC    | 60.0                             | 826                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30352364  | Ca2                                     | 30352364                      | ATTTTTTT/ATTTTTT                                              | TAAAAAGTGGTTCGGT<br>TCGG     | TTATTTTCCCTTTTGG<br>CCC    | 60.0                             | 826                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30359357  | Ca2                                     | 30359357                      | A/ATTC                                                        | TCACAAGGTTCCCTCT<br>CCAG  | TCCTTCATCTTCAACCA<br>AAACA | 60.2                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30375925  | Ca2                                     | 30375925                      | GTTT/GTT                                                      | TAGCCACCCCAAAAAT<br>CAAA  | AAGAGGGTGAAAGAAA<br>GGGTG  | 60.3                             | 288                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30384877  | Ca2                                     | 30384877                      | TTATAT/TTAT                                                   | TGCATTGCAGCATAAC<br>AACTT | GTGTTGGGCCAAATCA<br>AAAT   | 59.4                             | 185                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30385121  | Ca2                                     | 30385121                      | A/AAT                                                         | TGATTTGGCCCAACAC<br>CTAT  | GCAAATACAAAGGACC<br>GTCAA  | 60.2                             | 381                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30385586  | Ca2                                     | 30385586                      | CAA/CAAA                                                      | TTGACGGTCCTTTGTA<br>TTTGC | ACAGAAAATGTCGTCC<br>CTGC   | 60.0                             | 384                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30393573  | Ca2                                     | 30393573                      | CT/CTT                                                        | TCCCAACAGGAATGA<br>AACC   | AGTGCAAGCATCATGG<br>AGAA   | 59.8                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30393592  | Ca2                                     | 30393592                      | ATTTTTTT/ATTTTTT                                              | TCCCAACAGGAATGA<br>AACC   | AGTGCAAGCATCATGG<br>AGAA   | 59.8                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30393638  | Ca2                                     | 30393638                      | TAAAAAAAAA/TAAAAAAAAA                                         | TCCCAACAGGAATGA<br>AACC   | AGTGCAAGCATCATGG<br>AGAA   | 59.8                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30393886  | Ca2                                     | 30393886                      | TC/T                                                          | ATTCTCCGATTTTCCC<br>CAT   | TGTTTTCAGTGCAAGC<br>ATCA   | 59.6                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30394906  | Ca2                                     | 30394906                      | CAAAA/CAAAA                                                   | GAGAGAGGGGCAAGG<br>TCAC   | AGGCTTTTGTGTTGTT<br>GGG    | 59.8                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30394922  | Ca2                                     | 30394922                      | AA/AATATA                                                     | GAGAGAGGGCAAGG<br>TCAC       | AGGCTTTTGTGTGTT<br>GGG      | 59.8                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30395203  | Ca2                                     | 30395203                      | CATATATATA/CATATATATATA                                       | CCCAACAACAACAAA<br>GCCT      | AAACCAGCATGACAAA<br>AGCA    | 60.0                             | 289                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30397553  | Ca2                                     | 30397553                      | TAAAA/TAAAAA                                                  | TCTTTTTCATTCCAACC<br>CTCA    | CCGAAAGTGTGGGTCT<br>CTTC    | 59.5                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30399984  | Ca2                                     | 30399984                      | CATATATATATATATAT/CATATAT<br>ATATATATAT                       | AGGTGGGCCATTACT<br>TGAT      | AGTGGAGGACCACTTC<br>CTCA    | 60.6                             | 836                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30401507  | Ca2                                     | 30401507                      | TT/TTGT                                                       | GCATCACAAAGGGTTT<br>TTGG     | TCGATGCGAATACAAC<br>TAAATCA | 60.3                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30401609  | Ca2                                     | 30401609                      | AACAAAAATA/AA                                                 | GCATCACAAAGGGTTT<br>TTGG     | CATATGAAAGTTTGGC<br>CACG    | 60.3                             | 828                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30401833  | Ca2                                     | 30401833                      | ATTT/ATT                                                      | GGTCGAGTTTGCAATG<br>ATGA     | TGACCACAAGTTGCCA<br>AAAA    | 59.7                             | 761                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30431126  | Ca2                                     | 30431126                      | AATATATATATATATATATA/AA<br>TATATATATATATATA                   | TTGACAATAATTTTCT<br>CGAGTTGA | ACCAACGTTGCACCAA<br>GATT    | 59.2                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30433128  | Ca2                                     | 30433128                      | TAAAAAAAA/TAAAAAAAAA                                          | GAAATTGCATTTATCTC<br>CCCC    | TTACAGTTAAGGGCCA<br>ACCG    | 59.6                             | 737                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30433806  | Ca2                                     | 30433806                      | CTTTT/CTTTT                                                   | CGGTTGGCCCTTAAC<br>GTAA      | TCCTCAAACCAAAATG<br>GTC     | 60.0                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30439365  | Ca2                                     | 30439365                      | GAAAAAAAAA/GAAAAAAAAA                                         | CCAAGTTCAACACTCA<br>TATGCC  | ATGGAGAATTCAGCCC<br>AACA      | 59.5                             | 406                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30444678  | Ca2                                     | 30444678                      | CATATAT/CATATATAT                                             | CACTAGTGATGCCGTG<br>ATGC    | GCGCTAGATGGCAAGG<br>TAAG      | 60.3                             | 457                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30445438  | Ca2                                     | 30445438                      | TTTTAAATTTA/TTTTAAATTTAA<br>ATTTA                             | CTGAACCGAACCGGTT<br>TTTA    | TTGTTGCGATCGATATA<br>TTTTTG   | 60.0                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30445916  | Ca2                                     | 30445916                      | TAAAAA/TAAAAA                                                 | CAAAATATATCGATCG<br>CAACAA  | AATTGAAAGCTGCATT<br>GGCT      | 59.0                             | 406                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30447122  | Ca2                                     | 30447122                      | CATATATATATATAT/CATATATATAT<br>ATATATATATATATAT               | TGGTGACACACAATACA<br>ATCAAA | CAAGGCCGAGAAGACA<br>AAAG      | 59.9                             | 225                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30447611  | Ca2                                     | 30447611                      | A/AT                                                          | CTTTTGTCTTCTCGGC<br>CTTG    | CGTGCTCATCTCCATT<br>GTTG      | 60.0                             | 891                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30447653  | Ca2                                     | 30447653                      | AC/A                                                          | CTTTTGTCTTCTCGGC<br>CTTG    | ATCTCCTCAGCATTGTC<br>GCT      | 60.0                             | 943                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30459901  | Ca2                                     | 30459901                      | A/AT                                                          | GGAGTGGGCACTCAAC<br>TTTT    | CACACTTCTCACCCCC<br>ACTT      | 59.2                             | 219                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30460218  | Ca2                                     | 30460218                      | AATATAT/AATAT                                                 | ATCATGAAAGTGGGG<br>TGAG     | TGAAACCGATCAAATC<br>CACA      | 59.8                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30461229  | Ca2                                     | 30461229                      | AG/A                                                          | TCCATTCAATCAAGA<br>CGTG     | TTTTTGTCTCACATTGA<br>TTGTCTTT | 59.5                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30461396  | Ca2                                     | 30461396                      | CTTTTTTT/CTTTTTTTTT                                           | AAAAGAAGTGGTTGT<br>CCGC    | AAACGATGCTTATCC<br>GTGAA    | 59.2                             | 929                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30462677  | Ca2                                     | 30462677                      | ATAAATT/ATAAATTGACTATTAAATT                                   | GAAATTTAAAAAGCGT<br>GCGG   | AACAAACCTAGTGCC<br>ATGC     | 59.7                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30463432  | Ca2                                     | 30463432                      | TAAAAAAAAA/TAAAAAAAAA                                         | ATTCTCAACCTTGGT<br>GTGC    | AGTGTTTGTTGGGAG<br>GTGG     | 60.0                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30464150  | Ca2                                     | 30464150                      | CTT/CTTT                                                      | CCACCTCCCAACAA<br>CACT     | GGCAAGTTGCTTTTAC<br>CAAAAC  | 59.9                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30464334  | Ca2                                     | 30464334                      | ATCT/AT                                                       | CCACCTCCCAACAA<br>CACT     | GGTGTCATGGCTTCTA<br>CATT    | 59.9                             | 792                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30476467  | Ca2                                     | 30476467                      | CAAAAAAAAA/CAAAAAAAAAA                                        | AGCAATGTGGCATGCA<br>TAAA   | GGGAATGTTTGTGAA<br>TGTCG    | 60.1                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30481523  | Ca2                                     | 30481523                      | TTTAAAAAAT/TTTAAAAAATATGTTA<br>AAAAAT                         | GTTGGCTCCCAAGAC<br>ACAT    | TCGATTTTCATTAAAGT<br>GTTGGA | 60.0                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30481983  | Ca2                                     | 30481983                      | ATATTATTT/ATATTATTTAAATTATT<br>ATTT                           | TCAATGCATGGAAAT<br>AATCTCT | TGGTCCTCATCCATCA<br>AACA    | 57.8                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30484744  | Ca2                                     | 30484744                      | GG/GGACG                                                      | ACATGAGACCGTCAAT<br>GCAA   | CGAAAAATCAAAATAAC<br>ATCGC  | 60.1                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30484802  | Ca2                                     | 30484802                      | A/ATT                                                         | ACATGAGACCGTCAAT<br>GCAA   | CGAAAAATCAAAATAAC<br>ATCGC  | 60.1                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30485065  | Ca2                                     | 30485065                      | AC/A                                                          | CACAACTTCTTCAGTC<br>CTGTGG | TAAGAAAATTGGGGTG<br>GCAG  | 59.8                             | 889                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30490084  | Ca2                                     | 30490084                      | ATTTTTTTTTTTTTT/ATTTTTTTTTT<br>T                              | CCCCCTACTACTTGAC<br>GATCC  | TTCCCAAATGCAATTTT<br>TCC  | 59.8                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30490349  | Ca2                                     | 30490349                      | TA/TTAA                                                       | GGAAAAATTGCATTG<br>GGAA    | GTTGGCTTACACATTG<br>GGCT  | 59.8                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30490413  | Ca2                                     | 30490413                      | TTAAATAAAAA/TTAAAA                                            | GGAAAAATTGCATTG<br>GGAA    | GTTGGCTTACACATTG<br>GGCT  | 59.8                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30494831  | Ca2                                     | 30494831                      | GAAAAAAAA/GAAAAAAAAA                                          | TGAGAACGCCCATGTC<br>AATA   | TCTCTGGCAACCGTTC<br>TTCT  | 60.1                             | 404                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3049734   | Ca2                                     | 3049734                       | AGAT/A                                                        | CGATCTCATATGTGGG<br>GACC   | TGCAATCGAAAGAAGT<br>GTGG  | 60.2                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30514044  | Ca2                                     | 30514044                      | TAAAAAA/TAAAAA                                                | TTGAATGGTTTGTGAT<br>CCGA   | TCCATTGGAAGCATTG<br>ACTTC | 59.9                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30516125  | Ca2                                     | 30516125                      | GATATA/GATA                                                   | GAGATGAAAACGGATG<br>GGTG   | CATGACAATCATTGCA<br>GCC   | 60.3                             | 831                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30516532  | Ca2                                     | 30516532                      | GT/G                                                          | CACAAGGTTTGTGCAC<br>TGAAA  | CATGACAATCATTGCA<br>GCC   | 59.8                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30520425  | Ca2                                     | 30520425                      | GAAAAAAAA/GAAAAAAAAA                                          | TTGACGTAGGCTCTTG<br>GGTC   | ATGTCTGCTTCCATTG<br>CAC   | 60.0                             | 745                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30521356  | Ca2                                     | 30521356                      | TTC/TTGCTC                                                    | TAACAATTCCTCCGC<br>CAAG  | GCAGCCGTCTATGCTA<br>TTCA   | 60.1                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30522267  | Ca2                                     | 30522267                      | AATTAT/AAT                                                    | GAACAGTGGCAATTCA<br>TCCA | TTTTGGTGCCAAATTCT<br>TCTC  | 59.5                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30522321  | Ca2                                     | 30522321                      | ATTTTTTTT/ATTTTTT                                             | GAACAGTGGCAATTCA<br>TCCA | CGATGTGTGCATGCTC<br>TCTAA  | 59.5                             | 865                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30523254  | Ca2                                     | 30523254                      | AATAT/AATATGAATATAT                                           | TCATCGTTTGCAAGGT<br>TTTG | TAATGCATTCTATTGCT<br>GGC   | 59.7                             | 249                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30525393  | Ca2                                     | 30525393                      | TTA/TTATA                                                     | CAGCCACAGCATAGCT<br>TTCA | GACGTGTGTTGCTTTA<br>AGGG   | 60.2                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30526988  | Ca2                                     | 30526988                      | GAAAA/GAAA                                                    | CTCGTGAAGGATTAGG<br>TCGG | TTGCAACGCATCTCAAT<br>CTC   | 59.7                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30527039  | Ca2                                     | 30527039                      | TAAAAA/TAAAA                                                  | CTCGTGAAGGATTAGG<br>TCGG | TTGCAACGCATCTCAAT<br>CTC   | 59.7                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30527100  | Ca2                                     | 30527100                      | TAAAAAAAAA/TAAAAAAAA                                          | CTCGTGAAGGATTAGG<br>TCGG | TTGCAACGCATCTCAAT<br>CTC   | 59.7                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30549976  | Ca2                                     | 30549976                      | ATTTTTTT/ATTTTTT                                              | TTTCTTTATTCTCGGTG<br>GCG | GCTTGGATTAGGAAAA<br>ATCGAC | 60.2                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30550114  | Ca2                                     | 30550114                      | TAAAAAA/TAAAAA                                                | TTTCTTTATTCTCGGTG<br>GCG | TGCATTGCATCAAGCT<br>CAAC   | 60.2                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30550167  | Ca2                                     | 30550167                      | ACA/ACAGTCA                                                   | TTTCTTTATTCTCGGTG<br>GCG     | TGCATTGATCAAGCT<br>CAAC  | 60.2                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30550309  | Ca2                                     | 30550309                      | ATTTTT/ATTTTTT                                                | TTTCTTTATTCTCGGTG<br>GCG     | TGCATTGATCAAGCT<br>CAAC  | 60.2                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30553119  | Ca2                                     | 30553119                      | T/TTAGAC                                                      | TTTTTATGAGGCGTGG<br>AAGG     | AAACTAACACACCCC<br>CGTG  | 60.1                             | 223                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30553379  | Ca2                                     | 30553379                      | GAAAA/GAAAAA                                                  | TTTTTATGAGGCGTGG<br>AAGG     | CCATGAACACGCCAA<br>CATA  | 60.1                             | 874                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30553679  | Ca2                                     | 30553679                      | TAAAAAA/TAAAAA                                                | TGCACCTTATCACTTG<br>GTAATCG  | TGTTTGCAGCTTCAAT<br>GAC  | 59.2                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30554237  | Ca2                                     | 30554237                      | AC/A                                                          | GTCATTGAAGCTCGCA<br>AACA     | ATGTTCCAAGGTTGGT<br>CTGC | 60.0                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30559073  | Ca2                                     | 30559073                      | AG/A                                                          | TGCATACAAAAGTCAC<br>CCCA     | AAAAATTATGGGCTTTG<br>GGC | 60.0                             | 982                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30559202  | Ca2                                     | 30559202                      | AT/ATT                                                        | CCCAACCACTTCATCA<br>ATCC     | AAAAATTATGGGCTTTG<br>GGC | 60.2                             | 750                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30559409  | Ca2                                     | 30559409                      | CT/CTT                                                        | GGAGAACTAAATTCA<br>CATGAGTGG | AAAAATTATGGGCTTTG<br>GGC | 60.3                             | 258                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30566132  | Ca2                                     | 30566132                      | AT/ATT                                                        | CAGAGACAAAAGAGGG<br>AACCA    | TTGTGTTGTTGTGTGT<br>GCG  | 59.3                             | 884                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30567133  | Ca2                                     | 30567133                      | TAAAAAAA/TAAAAAA                                              | AAATTACGCAACAATT<br>GGC     | GAAGCGCAACTAAAC<br>AAGC     | 59.8                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30574328  | Ca2                                     | 30574328                      | TAAAA/TAAAAAA                                                 | CCATTGAGGAGTGGAG<br>AACTTT  | CTTGTGTGTTCCCAAT<br>GCAA    | 59.6                             | 783                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30575439  | Ca2                                     | 30575439                      | ATCT/ATCTCT                                                   | GGTTGATTATGGTTTT<br>GGCG    | ATCCAAAGCAGCATCC<br>ATTG    | 60.2                             | 862                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30575554  | Ca2                                     | 30575554                      | T/TC                                                          | TGCAAAACGAGGTGTG<br>GTCT    | ATCCAAAGCAGCATCC<br>ATTG    | 60.4                             | 457                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30585501  | Ca2                                     | 30585501                      | CTTTTTTTT/CTTTTTTTTTT                                         | GAAACGGTTGGAAGGT<br>TGAA    | ATCAAAATATCTTTCG<br>CGG     | 59.9                             | 305                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30623473  | Ca2                                     | 30623473                      | T/TGAA                                                        | TGACAAAAGGGTCAA<br>CGTG     | CCGCAATCAATTTAGC<br>GAAT    | 59.6                             | 686                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30624454  | Ca2                                     | 30624454                      | C/CT                                                          | TCATGAATGCAACGTG<br>GTTT    | TTTTGCTGTTTGTTTA<br>CGTCAT  | 60.0                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30624742  | Ca2                                     | 30624742                      | GTTTTT/GTTTTTTT                                               | TTGCTTGCAACACAAA<br>ACTTC   | TGAACCATTCATCACAA<br>AAAGAG | 59.0                             | 837                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30626190  | Ca2                                     | 30626190                      | T/TCA                                                         | TTGTCATTTTGATCATT<br>GATTCG | GGTGGTTTGTAAACAC<br>AGCAAA  | 59.8                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30635014  | Ca2                                     | 30635014                      | ATGTGTGTG/ATGTGTGTG                                           | TCGTGTGAGACGAAAA<br>ATCG    | CTCACCAGCTGCATCA<br>CATT    | 59.8                             | 367                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30642500  | Ca2                                     | 30642500                      | GAAAAAAAA/GAAAAAAAAA                                          | TGCAGTTGCCGACAAT<br>TTTAT   | TCCTCGGTAACCAAC<br>AAGC      | 60.5                             | 128                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_30647034  | Ca2                                     | 30647034                      | CAT/CATAT                                                     | TTGACGTACCCAACCA<br>TTGA    | CCCTCACTTAAGCCCA<br>CAAA     | 59.8                             | 443                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_30647302  | Ca2                                     | 30647302                      | AGGGGG/AGGGG                                                  | TTGACGTACCCAACCA<br>TTGA    | GGGCCTGTGGGTCTAC<br>TTTT     | 59.8                             | 759                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_30647346  | Ca2                                     | 30647346                      | A/AT                                                          | TTTGTGGGCTTAAGTG<br>AGGG    | GGGCCTGTGGGTCTAC<br>TTTT     | 60.1                             | 336                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_30647396  | Ca2                                     | 30647396                      | ATTTTTTTTT/ATTTTTTTTT                                         | TTTGTGGGCTTAAGTG<br>AGGG    | GGGCCTGTGGGTCTAC<br>TTTT     | 60.1                             | 336                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_30672819  | Ca2                                     | 30672819                      | CAAAAAAAAA/CAAAAAAAAA                                         | ATGGCATATCCGTGGG<br>TAAT    | TAGGCCCTAGGGACAA<br>TGTG     | 59.0                             | 834                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_30676386  | Ca2                                     | 30676386                      | GAAAAAAAA/GAAAAAAAA                                           | ATCCACCAACGTCCAA<br>GTTC    | CCTTGGTATGACCCTA<br>ATTCTT   | 59.8                             | 532                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_30676605  | Ca2                                     | 30676605                      | GAAAAA/GAAAA                                                  | GCTCCAGCAAAATAG<br>AAATGG   | TCATCAATCAACTACT<br>TACGCAGA | 60.1                             | 504                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_30676782  | Ca2                                     | 30676782                      | ACTAGC/ACTAGCTAGC                                             | GCTCCAGCAAAATAG<br>AAATGG   | TCATCAATCAACTACT<br>TACGCAGA | 60.1                             | 504                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_30676877  | Ca2                                     | 30676877                      | CAAAAAAAAA/CAAAAAA                                            | AAGGAATTAGGGTCAT<br>ACCAAGG | TCATCTACAACAAAAT<br>TGAACAAA | 59.6                             | 606                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30677085  | Ca2                                     | 30677085                      | TAAAAAAAA/TTATAAAAAAAAA                                       | TCTGCGTAAGTAGTT<br>GATTGATGA | TTGCGCCTTTTCAGTAT<br>TTTC     | 60.2                             | 668                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30678202  | Ca2                                     | 30678202                      | TA/T                                                          | AGCTAATTGTGGGCGA<br>AAAA     | TGGAAAAGGTTTTGGG<br>TTTG      | 59.7                             | 922                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30679907  | Ca2                                     | 30679907                      | GTTTTTT/GTTTT                                                 | AAAGCGAAATGATCAA<br>ACGG     | TTCCCTTCAAATTGTAG<br>CATGA    | 60.1                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30680775  | Ca2                                     | 30680775                      | AATATATAT/AATATAT                                             | GGGCTGACTATGGATT<br>TGGA     | TATTTGGCTGACGTGG<br>AACA      | 59.9                             | 225                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30690091  | Ca2                                     | 30690091                      | CT/CTTT                                                       | GCGGTGTTTGTTTGGG<br>TAGT     | GGAGCACACAGATGCG<br>AATA      | 59.9                             | 335                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30690274  | Ca2                                     | 30690274                      | A/AT                                                          | TTAGGGGAACGTGAAA<br>TTGG     | CGGTCACTGCACAC<br>ACAA        | 59.8                             | 444                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30690304  | Ca2                                     | 30690304                      | ACC/AC                                                        | GCGGTGTTTGTTTGGG<br>TAGT     | TGTACATTCAAATCAAA<br>CAAATTCA | 59.9                             | 825                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30690368  | Ca2                                     | 30690368                      | TAAAAAAA/TAAAAAAA                                             | TATTCGCATCTGTGTG<br>CTCC     | CGTGGTTGAGTAGATG<br>TGCC      | 59.8                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30690413  | Ca2                                     | 30690413                      | AT/ATAAATT                                                    | TATTCGCATCTGTGTG<br>CTCC     | CGTGGTTGAGTAGATG<br>TGCC      | 59.8                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30690532  | Ca2                                     | 30690532                      | CTATTTTATT/CTATT                                              | TATTCGCATCTGTGTG<br>CTCC     | CGTGGTTGAGTAGATG<br>TGCC      | 59.8                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30691545  | Ca2                                     | 30691545                      | CTAATAAA/CTAATAAATAATAAA                                      | CCACATTAGTCCATCA<br>CCGA    | ATCAAGGTCGGGAAT<br>AACC         | 59.4                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30703095  | Ca2                                     | 30703095                      | TT/TTATAAACT                                                  | AACGGGGGATTGAAGA<br>GATT    | CGCATACATACGGTGA<br>TTGC        | 59.8                             | 882                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30703318  | Ca2                                     | 30703318                      | AC/A                                                          | ACCCGCAGAATTTGCT<br>AAGA    | CGCATACATACGGTGA<br>TTGC        | 59.8                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30703947  | Ca2                                     | 30703947                      | ATTTTTTTTT/ATTTTTTTTT                                         | CCGTATGTATGCGTGA<br>CACC    | TCGAATTGGATTTCA<br>TATTTTC      | 59.9                             | 423                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30704638  | Ca2                                     | 30704638                      | TA/TAA                                                        | AAATTCAGTGCAACGC<br>ACAT    | CCCACTTGGATAACAA<br>TTCC        | 59.2                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30705361  | Ca2                                     | 30705361                      | GATATATATA/GATATATATATA                                       | TGCCACATTTTCCTTC<br>TTG     | GGATGAGGCTTTCAAT<br>TCTACG      | 58.7                             | 264                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30731994  | Ca2                                     | 30731994                      | AATGATGAT/AATGAT                                              | GGCCAAACTTGATTCA<br>AACC    | CGTCGACGATAGCATA<br>AGCA        | 59.4                             | 754                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30742309  | Ca2                                     | 30742309                      | CAGAGAGAG/CAGAGAGAGAGAGA<br>G                                 | CGTTGCGGTAACAAAC<br>AATG    | TTGAGAGAAAAGGCAGG<br>CTTA       | 60.0                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30742679  | Ca2                                     | 30742679                      | TAAAAAA/TAAAAAAA                                              | TGTTTGCTTCATTGCG<br>AGAG    | AAATTTGATGTAGAATA<br>TAACCCAAAA | 60.0                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30744544  | Ca2                                     | 30744544                      | TT/TTAT                                                       | CACCTATACATGCAAG<br>AGCAAAA | TCAACGAGCATGTGGA<br>AAAG        | 59.3                             | 920                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30765377  | Ca2                                     | 30765377                      | TAAA/TAAAAA                                                   | CATGCCATCTTGTAGG<br>GACA | TCATTTTCTCGCACGA<br>CAC     | 59.5                             | 678                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30783813  | Ca2                                     | 30783813                      | CTTTTTTT/CTTTTTTT                                             | AAGGACATGGTACCAC<br>CAGC | TGTGAACATGCGCGAT<br>TAACTGA | 59.9                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30794341  | Ca2                                     | 30794341                      | ATTTTT/ATTTTTT                                                | GAGTTGAATGCAGCTG<br>ACCA | CCAAAAACAAATTTTC<br>GGGA    | 60.0                             | 678                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30794400  | Ca2                                     | 30794400                      | CTTTTTTT/CTTTTTTT                                             | GAGTTGAATGCAGCTG<br>ACCA | TGCATTTCACTGGAGA<br>CGTT    | 60.0                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30794960  | Ca2                                     | 30794960                      | TTTTTATTTTATT/TTTTTATTTTATT<br>TATTTTATT                      | ACGTCTCCAGTGAAAT<br>GCAA | AGCCTTGATGTTGTTT<br>GCG     | 59.3                             | 506                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30795414  | Ca2                                     | 30795414                      | TAAAA/TAAA                                                    | GCAAAACATCAAGG<br>CTCA   | TGAAAAAGTTTTTGGT<br>CCCTG   | 59.8                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30795526  | Ca2                                     | 30795526                      | TTAATATAATAT/TTAATAT                                          | GCAAAACATCAAGG<br>CTCA   | TGAAAAAGTTTTTGGT<br>CCCTG   | 59.8                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30805003  | Ca2                                     | 30805003                      | T/TA                                                          | TGCTGAATTGGATAGA<br>GGGG | TTTTTGTTTGTGTACA<br>TTGTTTT | 60.0                             | 838                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30805135  | Ca2                                     | 30805135                      | CATTAATTA/CATTA                                               | CCTCATGGTGTGTGAT<br>TTGC | GCGAAAGCAAAATAGA<br>GTGGA   | 60.0                             | 880                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30806790  | Ca2                                     | 30806790                      | T/TA                                                          | GAAGTCAACATGTGCA<br>TGGG | TTTAAAAATTATGCGACG<br>GCA   | 60.0                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30841102  | Ca2                                     | 30841102                      | TCC/TCCC                                                      | TGACACTAGCTTGTGC<br>GGTC   | CCTAGCCAACATTGAA<br>GGGA   | 60.1                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30843280  | Ca2                                     | 30843280                      | AAATTAA/AAA                                                   | CCACAATCATTGGGAA<br>GTGA   | TGGATGAATAGGGGAT<br>TGCT   | 59.3                             | 305                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30844156  | Ca2                                     | 30844156                      | TTTAA/TTTAATTAA                                               | TCCACACTCTGTAGG<br>TTGCAT  | CAGAATCAGCACGCAA<br>ACAT   | 59.7                             | 854                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30844625  | Ca2                                     | 30844625                      | A/AG                                                          | ATGTTTGC GTGCTGAT<br>TCTG  | ATGTCATGACCGCATG<br>ATTG   | 59.9                             | 387                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30846242  | Ca2                                     | 30846242                      | T/TG                                                          | CCTTTGCGAACTTGAA<br>GACC   | TCCTCCCTCTTG CAGG<br>TTTA  | 59.9                             | 815                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30846291  | Ca2                                     | 30846291                      | CAAA/CAA                                                      | CCACCTGGATCTGAGT<br>GTGA   | TCCTCCCTCTTG CAGG<br>TTTA  | 59.7                             | 761                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30847431  | Ca2                                     | 30847431                      | AA/AATAGTTA                                                   | CCAATCTTGTGGAGTG<br>CTCA   | TCCTCCATCATCTCATG<br>TTACC | 59.8                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30848508  | Ca2                                     | 30848508                      | TTGATAAT/TTGATAAATGATAAT                                      | TTGAAGGACCAAAATC<br>ATGAAC | CATACACGCAAGCTA<br>GGCA    | 58.9                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30849743  | Ca2                                     | 30849743                      | ATT/ATTT                                                      | TCAACTTAGATATGCC<br>GTCCG  | TGGGTTGGTTTGAATC<br>ATCA   | 60.1                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30860005  | Ca2                                     | 30860005                      | CAAAAA/CAAAA                                                  | AGACAACATGTACCCC<br>GGAC   | TGAAGTGGCAAATTCG<br>CATA   | 59.7                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30860259  | Ca2                                     | 30860259                      | AG/A                                                          | TGAACAAAAAGTTGG<br>GTGA   | TGCTCAACTTTGACCC<br>ATTG | 59.0                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30860320  | Ca2                                     | 30860320                      | TAA/TAAA                                                      | TGAACAAAAAGTTGG<br>GTGA   | TGCTCAACTTTGACCC<br>ATTG | 59.0                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30860618  | Ca2                                     | 30860618                      | ATTTT/ATTTTTT                                                 | TGGGTCAAAGTTGAGC<br>ATGA  | CACCTTTGGAAAGAGC<br>TGGA | 60.2                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30860700  | Ca2                                     | 30860700                      | AC/A                                                          | TGGGTCAAAGTTGAGC<br>ATGA  | CACCTTTGGAAAGAGC<br>TGGA | 60.2                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30860764  | Ca2                                     | 30860764                      | T/TG                                                          | TGGGTCAAAGTTGAGC<br>ATGA  | CACCTTTGGAAAGAGC<br>TGGA | 60.2                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30861287  | Ca2                                     | 30861287                      | AA/AATA                                                       | CCAAAGGTGGGTGAAG<br>AAGA  | CAGGCCCAATTCACAA<br>AGTT | 60.1                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30861518  | Ca2                                     | 30861518                      | GAAA/GAAAA                                                    | CCAAAGGTGGGTGAAG<br>AAGA  | CAGGCCCAATTCACAA<br>AGTT | 60.1                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30865173  | Ca2                                     | 30865173                      | GAAAAAAA/GAAAAAA                                              | GCTGAGGGATTTCGAA<br>AGTAA | ATAATACCCCTCAGGG<br>TGCC | 58.5                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30887613  | Ca2                                     | 30887613                      | AT/A                                                          | TCAAGGGAGGATTACA<br>TGGG  | AAAGGGAAAGTTGCAT<br>CACG | 59.7                             | 826                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30887676  | Ca2                                     | 30887676                      | AA/AAGTA                                                      | TCAAGGGAGGATTACA<br>TGGG  | AAAGGGAAAGTTGCAT<br>CACG | 59.7                             | 826                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30890128  | Ca2                                     | 30890128                      | AAAATAAATAAATAAA/AAAATA<br>AATAAATAAA                         | GATGATGTAAATGGGA<br>GCCAA | CATTTGTGAATGTTGC<br>CCA   | 59.8                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30890182  | Ca2                                     | 30890182                      | AAA/AAAGAA                                                    | GATGATGTAAATGGGA<br>GCCAA | GGAATTGATCCACAAC<br>TCGG  | 59.8                             | 958                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30890210  | Ca2                                     | 30890210                      | TG/T                                                          | GATGATGTAAATGGGA<br>GCCAA | GGAATTGATCCACAAC<br>TCGG  | 59.8                             | 958                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30897629  | Ca2                                     | 30897629                      | TAAAAAAA/TAAAAAAA                                             | CCAACAGATCAAGGGG<br>AATG  | ATCGAGATCTCACCGT<br>GGAA  | 60.3                             | 548                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30897792  | Ca2                                     | 30897792                      | AAT/AATATAT                                                   | CCAACAGATCAAGGGG<br>AATG  | ATTGGGGTTTGGTGAA<br>ATGA  | 60.3                             | 708                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30933751  | Ca2                                     | 30933751                      | TC/T                                                          | TCGAAACGTGTGGTGA<br>TGAT  | ACAATTCCACGCAATGT<br>GAG  | 60.0                             | 895                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30936877  | Ca2                                     | 30936877                      | TAAAAAAA/TAAAAAAA                                             | TTGCACACAAGCGTTA<br>GAGC  | ATCAACCGCACACAATT<br>CAA  | 60.2                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30936957  | Ca2                                     | 30936957                      | ATTTTTTTTT/ATTTTTTTTTTT                                       | TTGCACACAAGCGTTA<br>GAGC  | ATCAACCGCACACAATT<br>CAA  | 60.2                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30937234  | Ca2                                     | 30937234                      | CTTTTT/CTTTTTTT                                               | TTGAATTGTGTGCGGT<br>TGAT  | CGTTGATGTGTACAC<br>GTTTC  | 60.0                             | 467                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30937778  | Ca2                                     | 30937778                      | TAAAAAAA/TAAAAAAA                                             | TGTGAAACGTGTGACA<br>CATCA | CCTCCATTCTATTTTGC<br>ATCA | 59.6                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30937965  | Ca2                                     | 30937965                      | CAAAAAAAAA/CAAAAAAAAA                                         | TGTGAAACGTGTGACA<br>CATCA | CATTGGTCCATCCCG<br>ATA    | 59.6                             | 961                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30939209  | Ca2                                     | 30939209                      | ATTTTTTTTT/ATTTTTTTTT                                         | TACTAGGGCCTTGCA<br>GGTT   | CCATCTAGGTGTTGGA<br>AGCAA | 59.6                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30940510  | Ca2                                     | 30940510                      | ATTTTTTTTT/ATTTTTTTTT                                         | CATAAGTGGGTATCCA<br>ACCGA | CATTGCAAGCAAATT<br>GACA   | 59.7                             | 620                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30963597  | Ca2                                     | 30963597                      | GTTT/GTT                                                      | CGATGGGTAGGCAAT<br>TGTG   | CACTTTGTGTTGCTAA<br>GGCA  | 60.0                             | 110                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30963897  | Ca2                                     | 30963897                      | TCAG/T                                                        | CGATGGGTAGGCAAT<br>TGTG   | TGGAGTGTGAAATATG<br>GGTGA | 60.0                             | 380                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30968038  | Ca2                                     | 30968038                      | CAAA/CAA                                                      | GTGTGCGAAAGGTTGG<br>TTTT  | CGAACCTACCCGATCA<br>AGAA  | 60.0                             | 168                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30968401  | Ca2                                     | 30968401                      | CAAAAAAAAA/CAAAAAAAAA                                         | TTCTTGATCGGGTAGG<br>TTCG  | ATTTGCTCCCGTCTCC<br>TTT   | 60.1                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30968434  | Ca2                                     | 30968434                      | ATT/ATTT                                                      | TTCTTGATCGGGTAGG<br>TTCG  | ATTTGCTCCCGTCTCC<br>TTT   | 60.1                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30968501  | Ca2                                     | 30968501                      | A/AT                                                          | TTCTTGATCGGGTAGG<br>TTCG  | ATTTGCTCCCGTCTCC<br>TTT   | 60.1                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30983014  | Ca2                                     | 30983014                      | AGTGT/AGT                                                     | ACAAATGGGATGGAT<br>GGAA   | TAATCCCAAGGCGATG<br>CTAC  | 60.0                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30983172  | Ca2                                     | 30983172                      | GAAAA/GAAA                                                    | GTAGCATCGCCTTGGG<br>ATTA     | TCGACATTCCCATTTTA<br>TTGC    | 60.1                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30983322  | Ca2                                     | 30983322                      | GTTTT/GTTTT                                                   | GTAGCATCGCCTTGGG<br>ATTA     | TGTCCACCCATAAGTAA<br>TCATTTG | 60.1                             | 744                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30983649  | Ca2                                     | 30983649                      | CTAT/CTATAT                                                   | GCAATAAAATGGAAT<br>GTCG      | TCGTTTTGGTGCAATAT<br>TTGTT   | 58.0                             | 802                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30983718  | Ca2                                     | 30983718                      | GAAAA/GAAA                                                    | GCAATAAAATGGAAT<br>GTCG      | ATTTCTTCGTCTGAGTG<br>CGG     | 58.0                             | 872                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30993636  | Ca2                                     | 30993636                      | TAAAAAA/TAAAAAA                                               | TCATTTCCATTGTTGT<br>CTCCTT   | GCTTGCCAAAATAACC<br>AACG     | 59.9                             | 369                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30999439  | Ca2                                     | 30999439                      | T/TC                                                          | CCCAAACCTTTTGGG<br>GTTG      | TAGCTTGAGCGTGGTT<br>TCCT     | 59.4                             | 625                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_30999481  | Ca2                                     | 30999481                      | GTT/GT                                                        | CCCAAACCTTTTGGG<br>GTTG      | TAGCTTGAGCGTGGTT<br>TCCT     | 59.4                             | 625                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31003095  | Ca2                                     | 31003095                      | CTCATCA/CTCATCATCA                                            | CGACATATTATTTGGG<br>ACAAACAT | GCAATACTTCCTCTTTG<br>GCG     | 59.1                             | 368                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31012061  | Ca2                                     | 31012061                      | ATTTTTTTTTTT/ATTTTTTTTTTT<br>T                                | GAGTCGGGTCAACCAG<br>GATA     | GCGAACTTTCGAGGTT<br>GTTG     | 59.9                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31130636  | Ca2                                     | 31130636                      | TAAAAAA/TAAAAAA                                               | TCCGTGTTTCCTCAAC<br>ATCA     | AAATGATAAAAGCCCA<br>GCC      | 60.1                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                          | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                        |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_31149462  | Ca2                                     | 31149462                      | CTTTTT/CTTTTTTT                                                                        | CCTCATTTTCCTCCTT<br>CCC    | GCTGTACAACTCGTG<br>CCCA     | 59.9                             | 877                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31149520  | Ca2                                     | 31149520                      | TAAAA/TAAAAA                                                                           | ATGGGTAAGGAAGGAG<br>GTGG   | GCTGTACAACTCGTG<br>CCCA     | 60.2                             | 802                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31240228  | Ca2                                     | 31240228                      | TCAA/T                                                                                 | CTGCCCCACTATTT<br>TCAA     | GAAACACTTGGCATGT<br>TAAGGA  | 60.1                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31271510  | Ca2                                     | 31271510                      | TAAAAAAAAA/TAAAAAAAAA<br>AAA                                                           | TGGGTGGGAGTAATTT<br>TTCG   | TTAAAGAGATTCGCAG<br>CGGT    | 59.8                             | 329                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31323113  | Ca2                                     | 31323113                      | GATATATATATATATATA/GATATA<br>TATATATATATATA                                            | TGTTCAACCAAACT<br>GGAA     | TTCATTTTAAAGGCATC<br>GTGA   | 60.0                             | 901                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31329635  | Ca2                                     | 31329635                      | TATAATAATAATAATAATAATAA<br>TAATAATAATAAT/TATAATAATAA<br>ATAATAATAATAATAATAATAAT<br>AAT | CGTACCGCTTGGTGGT<br>TTTA   | CACCACCACCACCATT<br>AAACT   | 60.9                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31450111  | Ca2                                     | 31450111                      | TCC/TC                                                                                 | TTCCCAATCGATCCTA<br>CGAG   | ATTGTGGAGAATCTGC<br>AGGG    | 60.0                             | 313                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31545785  | Ca2                                     | 31545785                      | TGG/TG                                                                                 | TGTGGCATGAATATTA<br>GGTTGG | CCTAAAGTTGAGTGAA<br>GCGAAA  | 59.7                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31648369  | Ca2                                     | 31648369                      | AATAT/AATATCTCATATAT                                                                   | TTACGTTGGAACCTG<br>CTTG    | ACCCGTTGGAAGATGA<br>AATG    | 59.9                             | 897                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31745963  | Ca2                                     | 31745963                      | AATATATATATATATATAT/AATAT<br>ATATATATATATAT                                            | TCCATAGAGCCATGGA<br>AAGG   | ATAATGTCAGCATGTAT<br>GCAAAA | 60.0                             | 448                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                   |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_31758836  | Ca2                                     | 31758836                      | TTAATAATAATAATAATAATAAT<br>AATAATAATAA/TTAATAATAATAA<br>ATAATAATAATAATAATAATAA    | CGACGTTTAATTAATTC<br>ATCCCA | GGAGTCATGCCCTTA<br>TCAA    | 60.1                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31841304  | Ca2                                     | 31841304                      | GATATATATATATATATATAT/GATAT<br>ATATATATATATATATAT                                 | GGAGAACTCAAGTTCA<br>TACCGTG | AGGTCAGTAGTTTGGC<br>GTGT   | 60.0                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31846061  | Ca2                                     | 31846061                      | TTTATTATTATTATTATTATTATT<br>ATTATTATT/TTTATTATTATTATTAT<br>TATTATTATTATTATTATTATT | GATTGGAGCACCATCC<br>TCTC    | TTGAGACAAAACGTT<br>CAACC   | 59.6                             | 805                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31854667  | Ca2                                     | 31854667                      | T/TTC                                                                             | GTGTTCCGCCTGATTT<br>CATT    | TCAAGGAGAAAACACA<br>ACCAAA | 59.9                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31856079  | Ca2                                     | 31856079                      | ATTT/AT                                                                           | TCTATCGAGAAGCAAA<br>ATGATGA | ACAAGGCTTTCAATTGT<br>GGG   | 59.0                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31858178  | Ca2                                     | 31858178                      | TTTAATATT/TTT                                                                     | TGTGTTTCAGAGCTGC<br>TAGTTGA | ATGAAAGGCATCCCA<br>AACA    | 60.2                             | 368                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31858424  | Ca2                                     | 31858424                      | AATTA/AA                                                                          | TGTTTTGGGATGCCTT<br>TCAT    | TGTTTTTCAAATTTGGG<br>AGGA  | 60.3                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31858882  | Ca2                                     | 31858882                      | CAA/CAAA                                                                          | TCCTCCCAAATTTGAAA<br>AACA   | TTTTCTTATAACGGGGC<br>AAAAA | 59.4                             | 246                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31860805  | Ca2                                     | 31860805                      | AC/ACC                                                                            | TCTCATTCACAAATTGG<br>CCTC   | TGTGCGACATACGACA<br>TACG   | 60.1                             | 241                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31864253  | Ca2                                     | 31864253                      | TCA/TCAACA                                                                        | GCAATCAAACAGGCC<br>CTAA     | TGACGTTTTGTTTATG<br>CCG    | 60.1                             | 763                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_31864424  | Ca2                                     | 31864424                      | T/TA                                                          | TGGCAACAAGAAGTTA<br>GGCA     | TGACGTTTTGTTTTATG<br>CCG      | 59.5                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31898826  | Ca2                                     | 31898826                      | ATTTTTTTTTTT/ATTTTTTTTTT                                      | TTTCCATGTCTACCCCT<br>TGG     | CAATTGACAAAAAGGT<br>GGTTCA    | 59.8                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3190348   | Ca2                                     | 3190348                       | CTTT/CT                                                       | CCGATCGGGTCTATTT<br>GTGA     | TGGTTGTCATACAATG<br>CGTG      | 60.9                             | 773                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31929843  | Ca2                                     | 31929843                      | ACC/AC                                                        | ACGTTTTGCAGCATTG<br>TTTT     | AAAAATCCTTTGGGAG<br>GTCG      | 60.5                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31931093  | Ca2                                     | 31931093                      | TT/TTAT                                                       | TCGTAACGCAAATTTTC<br>CAA     | TCCATCTCCAATTTTGT<br>TTTCA    | 59.2                             | 377                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31931439  | Ca2                                     | 31931439                      | TGAGAGAGA/TGAGAGAGAGA                                         | TCGTAACGCAAATTTTC<br>CAA     | TTTTTCACTTCTTTCAT<br>CTCTCG   | 59.2                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31933761  | Ca2                                     | 31933761                      | AATATATA/AATA                                                 | CTTTAGCCATGCCAATT<br>CGT     | TGGTTGTTTCCTTGCTT<br>TTT      | 60.1                             | 751                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31935770  | Ca2                                     | 31935770                      | GTTTTTTT/GTTTTTTTTT                                           | CACCAATGGTCTTTAAT<br>TTTTCTG | TTTTGGGACGTAGACC<br>TGTTG     | 59.0                             | 370                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31937114  | Ca2                                     | 31937114                      | ATTTTTTTTT/ATTTTTTTTT                                         | TTGAACCCAAGACTTT<br>GTAATGAA | GGTTAAAGACGTAACA<br>AGAAAAACG | 59.9                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31937481  | Ca2                                     | 31937481                      | TTTC/T                                                        | AATGCCATATTGGATT<br>TGTTAC   | TCCGATCGTTCAAATT<br>TCC       | 57.1                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_31945715  | Ca2                                     | 31945715                      | GAAAAAAAA/GAAAAAAAAA                                          | CACATGGAAGGCTAAAGGAA        | TTGAGTACCAAGGCAT<br>TGACC | 57.8                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31945753  | Ca2                                     | 31945753                      | TAT/TATTTAAT                                                  | CACATGGAAGGCTAAAGGAA        | TTGAGTACCAAGGCAT<br>TGACC | 57.8                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31950818  | Ca2                                     | 31950818                      | GTTATAC/GTTATACGAAATAAATT<br>ATAC                             | CCAATTAATAAGTTAGC<br>GGGTGA | TGTGTGAGGAGGACAA<br>CAAAA | 59.4                             | 870                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31950929  | Ca2                                     | 31950929                      | GAAAAAAAA/GAAAAAAAAAAAA                                       | GCACGCTAGTGCCGT<br>CTTT     | TGTGTGAGGAGGACAA<br>CAAAA | 60.5                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31953699  | Ca2                                     | 31953699                      | ATATA/ATATAGTATA                                              | TTCGTTTGATGAACAA<br>GTGACA  | GTGGATTGTGGGAACC<br>TCAT  | 59.2                             | 838                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31955680  | Ca2                                     | 31955680                      | TAAAA/TAAA                                                    | GGTTTTAAACTTGTGA<br>GGACCG  | TGTCGTTGTTGCATTG<br>TGA   | 59.9                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31955771  | Ca2                                     | 31955771                      | CTTTTT/CTTTTT                                                 | TCACAATGCAACAAC<br>GACA     | AAAAGCGGTGGCAAAT<br>GTTA  | 59.7                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31963928  | Ca2                                     | 31963928                      | GTACTT/GTACTTACTT                                             | CCTCGAGAAACCCAGC<br>TAGA    | GCATTCATGAGTTGTC<br>CCTT  | 59.6                             | 187                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31964191  | Ca2                                     | 31964191                      | AT/ATT                                                        | AAGGGCAAACATCATGA<br>ATGC   | CAAGGAAGGAGGAAAA<br>GGAGA | 60.1                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31964265  | Ca2                                     | 31964265                      | TG/T                                                          | AAGGGCAAACATCATGA<br>ATGC   | GGTGTGACAAAGGAAA<br>CGTG  | 60.1                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_31981326  | Ca2                                     | 31981326                      | AT/ATTT                                                       | ACGTTGTGTGGACAAT<br>GAGG | TCCGGAGGGTTTTCT<br>ACCT     | 59.4                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31983759  | Ca2                                     | 31983759                      | ATTTTTTTTT/ATTTTTTTTTTT                                       | GACACTTGTGCGTAT<br>GGGA  | CAATGGAGATTCCAAC<br>CTGT    | 59.6                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_31991643  | Ca2                                     | 31991643                      | ATTTTTTTTTTT/ATTTTTTTTTTTTTT                                  | TGGTCAATGAAATTC<br>GGT   | GGTTGTGTGTTTCCAT<br>CCC     | 60.2                             | 230                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32003491  | Ca2                                     | 32003491                      | TT/TTCCT                                                      | TCCAAATAGTAAGGT<br>TGGCA | CCATCTATCACTTGCA<br>GCAGTC  | 59.5                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32007729  | Ca2                                     | 32007729                      | AT/A                                                          | CTCTGCCGCAGTTTGA<br>TACA | AAAGTTCCGGAGAAAC<br>TTCG    | 60.0                             | 337                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32009592  | Ca2                                     | 32009592                      | GTTTTTTT/GTTTTTTTTT                                           | TTGGCATTCTCTAGCA<br>CACG | CGAGTAGTTTCAACCG<br>CCAT    | 60.0                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32012870  | Ca2                                     | 32012870                      | A/AG                                                          | AGGGCTTTACTCCTTTT<br>GGG | TTGACAAATGAAAGGA<br>GGTGG   | 59.6                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32013591  | Ca2                                     | 32013591                      | TCCC/TCC                                                      | TCTCCCTCCAAACACC<br>AAAC | ATGATTGAACGAAGGC<br>CAAG    | 59.9                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32022318  | Ca2                                     | 32022318                      | CTTT/CTT                                                      | CATGTGTTTGAGCAT<br>CCAG  | TGCAAAATTCATTGGAA<br>GCA    | 60.1                             | 443                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32032083  | Ca2                                     | 32032083                      | ATATTTTATTTTT/ATATTTTATTTT<br>TATTTTT                         | TGACAACGCATACGTG<br>GATT | AAATAACACGAAATTCT<br>AGCCCA | 60.0                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_32070956  | Ca2                                     | 32070956                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA<br>AA                           | TTTTTCCGACTTGGTC<br>CTTT   | GGAGCTGAAACTAACG<br>CAGC  | 58.7                             | 814                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32076569  | Ca2                                     | 32076569                      | TTAAGT/TT                                                     | GGGGAAGTAATTTTGT<br>GAATCC | GGCTTCATCTAGCAAT<br>GGTTG | 58.7                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32080788  | Ca2                                     | 32080788                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                 | TGTGCATTAAAGATGC<br>TCTTGG | AAGCGTTGAAACCACT<br>GTGA  | 60.3                             | 441                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32080846  | Ca2                                     | 32080846                      | TAAAAAAA/TAAAAAAA                                             | TGTGCATTAAAGATGC<br>TCTTGG | AAGCGTTGAAACCACT<br>GTGA  | 60.3                             | 441                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32098174  | Ca2                                     | 32098174                      | C/CAATATCT                                                    | TTAGCGCAAATGATTG<br>GTTG   | TGATGTGAAGCCAAAT<br>TCCA  | 59.7                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32102387  | Ca2                                     | 32102387                      | TAAA/TAAAAAAA                                                 | TTCCAAACGGAATCCA<br>TCAT   | TGTGGTCTTCCTTTGG<br>CACT  | 60.1                             | 308                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32110176  | Ca2                                     | 32110176                      | AAAACAAA/AAAA                                                 | GCACCCCTTCAAGAAGC<br>AAAC  | TTGGTCCATCGAATCA<br>CTTG  | 59.9                             | 221                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32112721  | Ca2                                     | 32112721                      | T/TAAA                                                        | TTGTCTTTCCTATGCCA<br>CCC   | TAAAGGACATGTGCAA<br>ACGC  | 59.9                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32116015  | Ca2                                     | 32116015                      | CTTTTTTTTT/CTTTTTTTTTTT                                       | CCCAAAGGCCCAAATT<br>TTAT   | TGGTCCTCCAACACCA<br>ATTT  | 60.0                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32116482  | Ca2                                     | 32116482                      | CTAT/CTATAT                                                   | CAAATTGGTGTGGAG<br>GACC    | ATAGGAAAAGCGCAAA<br>AGCC  | 60.2                             | 153                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_32117375  | Ca2                                     | 32117375                      | C/CTGAGGAA                                                    | GGACGTGGGTAAACATA<br>AACCAT | TTCTAGAGGCGAGTAA<br>TGTAGAAAAA | 59.9                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32122608  | Ca2                                     | 32122608                      | GAC/GACAC                                                     | TTTTGTGGGAATGTGG<br>GTTT    | CACACGTTTCATCCCATT<br>CAC      | 60.1                             | 324                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32152012  | Ca2                                     | 32152012                      | TAAAAAAAA/TAAAAAAAAA                                          | CCAACTCACCACACAT<br>CACC    | CCGCTACCGATTGTTTT<br>TGT       | 59.8                             | 163                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32152633  | Ca2                                     | 32152633                      | T/TA                                                          | GAGTTGGGTAGGGTAG<br>GGGA    | TTTCCCTTTTGCTTGT<br>CAT        | 60.2                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32160769  | Ca2                                     | 32160769                      | TCTTCACT/TCT                                                  | ACATCAATGAGATGAA<br>GCCG    | GGCCGAACACGAAAA<br>TAAA        | 58.7                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32167519  | Ca2                                     | 32167519                      | TGG/TG                                                        | AGAAATGGGAGCTTGT<br>TCCA    | GAGGATGGGTGAAAA<br>GCAA        | 59.7                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32168741  | Ca2                                     | 32168741                      | ATA/ATAGTAAATTA                                               | CCTGGCCATTGTCCT<br>TAGA     | AAATGAGTAGATGGTG<br>CAACGA     | 60.1                             | 687                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32209131  | Ca2                                     | 32209131                      | T/TG                                                          | GCAAAGATAGACACCA<br>CCCC    | AACCATCCCATGGAA<br>CAAA        | 59.4                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32209334  | Ca2                                     | 32209334                      | CTATATATA/CTATA                                               | TCCATGGGAATGGTTT<br>TGAT    | TTGAAGAGGAAGTTTT<br>GGCA       | 60.0                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32209671  | Ca2                                     | 32209671                      | TC/TCC                                                        | TCCATGGGAATGGTTT<br>TGAT    | TTTTAGTGTGCACCAAT<br>GTCAA     | 60.0                             | 899                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_32210099  | Ca2                                     | 32210099                      | CA/CAAATA                                                     | TCAGCTTCAATTATCTC<br>CAACAA | TCGGCGACAAAAATCA<br>CATA   | 58.9                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32213171  | Ca2                                     | 32213171                      | GTGAT/GTGATGAT                                                | CAACATGACAAGGACT<br>TTCCAA  | TTACCGGTATCGCAAG<br>GAAC   | 60.0                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32213424  | Ca2                                     | 32213424                      | CAAA/CAAAA                                                    | AGGGATAGATAACGGC<br>ACGA    | AAGGCCCTGCTAGAAT<br>GATG   | 59.6                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32218161  | Ca2                                     | 32218161                      | GTTTTTTTTTTT/GTTTTTTTTTTT                                     | ATTGTGCCGGAGCAAC<br>TACT    | TGTTACGGCTGTGAAT<br>CTGG   | 59.8                             | 138                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32220236  | Ca2                                     | 32220236                      | TAAAAAAAAA/TAAAAAAAAA                                         | GGTGACGGTACAAAC<br>CTCT     | TCAAGTGAGCAAAATGA<br>GCAAA | 60.0                             | 305                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32223160  | Ca2                                     | 32223160                      | GTT/GT                                                        | AATGGACGTACCATGC<br>ATCA    | GGGTTGAATCGCAGAC<br>TAGG   | 59.8                             | 438                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32245950  | Ca2                                     | 32245950                      | TA/TAGA                                                       | AACCGACAAAAGATTG<br>CATGT   | GCAGTTGCACAAGGTG<br>GTAA   | 59.5                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32253447  | Ca2                                     | 32253447                      | ACAC/A                                                        | GCTGTATGTACGCACC<br>CCTT    | TGAAATTTGCCTGTGTT<br>GCT   | 60.0                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32260990  | Ca2                                     | 32260990                      | GAGAA/GA                                                      | TGTTGTTTCTCCAAC<br>CCT      | TTTACCTTCTTTCCG<br>GGG     | 59.4                             | 157                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32261025  | Ca2                                     | 32261025                      | AAAGAGAAGAGA/AAAGAGAAGAGA<br>AGAGA                            | CCCCGGAAGAAGGT<br>AAAA      | CCTCTGTCTCCACC<br>TGCT     | 60.3                             | 126                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_32263139  | Ca2                                     | 32263139                      | A/AAAAATGG                                                    | GAAACAAAATGTCAC<br>CGGC  | ATTGCCAACACAC<br>CAAA      | 60.4                             | 282                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32263680  | Ca2                                     | 32263680                      | CAATA/CAATAAAAAATA                                            | TGCAACACCAAGTCAC<br>CATT | GTCAATGATTCGCGTA<br>GGGT   | 60.0                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32289345  | Ca2                                     | 32289345                      | AT/ATGT                                                       | CCTCCTAGTTGCATGG<br>CATT | AGGCATGGTCATCGAT<br>CAGT   | 60.1                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32289886  | Ca2                                     | 32289886                      | GTTTTTTTT/GTTTTTTTTTTTTT                                      | ACTGATCGATGACCAT<br>GCCT | GCAAAGTACATGCCT<br>CACA    | 60.5                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32291117  | Ca2                                     | 32291117                      | CA/C                                                          | TGTGCCAATAATTGG<br>TTGC  | AAAGCTTTGGAGGCAT<br>GCTA   | 59.4                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32293632  | Ca2                                     | 32293632                      | AAGAAATTCAGAAATTCA/AAGAAAT<br>TCAGAAATTCAGAAATTCA             | AAACCCTACGAAGTTT<br>GGCA | TTGTCAACCGTCCAAA<br>TACA   | 59.6                             | 237                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32293814  | Ca2                                     | 32293814                      | CT/CTTTGT                                                     | TGTATTTGGACGGGTG<br>ACAA | TACACCCACGAAACGT<br>GAAA   | 59.8                             | 571                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32300236  | Ca2                                     | 32300236                      | AA/AAATA                                                      | CCCATTAAATGAAGCT<br>CGGA | CGCATTTAGTCTTTCCC<br>TTTTG | 60.0                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32325491  | Ca2                                     | 32325491                      | T/TA                                                          | TCGTGTTTCGCGTGGT<br>AATA | CGTATCCAGTGTCCTAA<br>CACG  | 60.1                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32332565  | Ca2                                     | 32332565                      | AAAATAAATAAATAAATA/AAAATAAA<br>TAAATAAATAAATA                 | CGCCAAAGTCATTGAT<br>TGAA | CATCTTGTACGCCATA<br>GCCA   | 59.7                             | 338                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_3233452   | Ca2                                     | 3233452                       | A/AT                                                          | ACCCTTTAACCCCAAT<br>TGC      | TGCAAAATTGCAACAA<br>CCT    | 60.1                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32346783  | Ca2                                     | 32346783                      | CAAAAAACA/CAAAAAACATAAAAA<br>CA                               | TCCACACCAGAAGCAT<br>TCAA     | GTTCTGGAGGGAACAG<br>CTTG   | 60.2                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32356323  | Ca2                                     | 32356323                      | CAAA/CAAAA                                                    | GCTAGTTGCTGTGAAT<br>GGCA     | ACGTGTGGATGATTGG<br>ATGA   | 60.0                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32356462  | Ca2                                     | 32356462                      | T/TG                                                          | GCTAGTTGCTGTGAAT<br>GGCA     | ACGTGTGGATGATTGG<br>ATGA   | 60.0                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32356770  | Ca2                                     | 32356770                      | CCACAC/CCAC                                                   | AGCCTCACCTCATACG<br>GAAA     | GAATTGTTGAAGGATG<br>AGAGCA | 59.7                             | 345                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32358785  | Ca2                                     | 32358785                      | AAT/AATATAT                                                   | AACAACCTCTCATCCTC<br>GCAA    | ATGTATGGGCTGCTTT<br>GCTT   | 59.9                             | 700                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32359679  | Ca2                                     | 32359679                      | GACACA/GACACACA                                               | TTGATGAGTTCGGTCA<br>TGGAA    | AGCCGCTTAATTGATC<br>GTTG   | 60.0                             | 195                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32360594  | Ca2                                     | 32360594                      | CTTT/CTT                                                      | TTGGATCCACCTCATT<br>TCCA     | CATGATCTCATCGGCT<br>GCT    | 60.1                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32361822  | Ca2                                     | 32361822                      | ATTT/ATT                                                      | ACGTTGTATTCGCAAG<br>AGGG     | TCACCTTTTCATCAATG<br>CTCA  | 60.1                             | 263                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32365433  | Ca2                                     | 32365433                      | TA/T                                                          | TCATTTTATCATCCATC<br>TTTGTGG | GAAATGATGGACAAAG<br>TCACGA | 60.1                             | 747                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)  | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                |                             |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_32366421  | Ca2                                     | 32366421                      | ATCAAAATTC AAAATT/ATCAAAATT                                    | TCGTGACTTTGTCCAT<br>CATTTTC | GCTTGGCAACATTCTT<br>CACA      | 60.0                             | 739                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32369105  | Ca2                                     | 32369105                      | GAAAAAAAA/GAAAAAAAA                                            | ACGTCCCTCCACGGTA<br>ATTT    | GCCACTTTCTTTGGATC<br>GAG      | 60.6                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32370223  | Ca2                                     | 32370223                      | AAAAAATTAATGAAAAATTAATGAAA<br>AATTAA/AAAAAATTAATGAAAAATTA<br>A | TCAAGCAAGTCACAAC<br>ATTTC A | TGCTATTTTAATTGTGA<br>GCATGAGA | 59.4                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32378287  | Ca2                                     | 32378287                      | GAAAAAAAA/GAAAAAAAA                                            | AGCCTCTCCAGAATG<br>CAAA     | TAAGACCACCGACCTT<br>CCAC      | 60.0                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32378634  | Ca2                                     | 32378634                      | GTTTT/GTTTT                                                    | GTGGAAGGTCGGTGG<br>TCTTA    | ACCACACCAATCCTTT<br>CAA       | 60.0                             | 144                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32379021  | Ca2                                     | 32379021                      | CATTATTATCATTGATT/CATT                                         | TGGAAGGTCGGTGGTC<br>TTAG    | TACCGCAATAAACTCG<br>CACA      | 60.1                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32379585  | Ca2                                     | 32379585                      | AATTAATTTT/AATTAATTTTGATTAA<br>TTTT                            | TGTGCGAGTTTATTGC<br>GGTA    | CATTGGTTCAAATGT<br>CATGG      | 60.3                             | 624                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32379797  | Ca2                                     | 32379797                      | AGC/A                                                          | GAAACAGAAAATTGGA<br>GCTTCA  | TGGGCTGCGAAAAGTT<br>AGTT      | 59.8                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32392527  | Ca2                                     | 32392527                      | GTTT/GTTTTT                                                    | CTGAAGGCTAGGCAGG<br>TTTG    | TCGAGCCACCATCAAC<br>ATTA      | 60.0                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32393084  | Ca2                                     | 32393084                      | T/TA                                                           | TGCCCATCCTTATGCT<br>CTTC    | ATCACGTGCAACCACA<br>AGTC      | 60.2                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_32393117  | Ca2                                     | 32393117                      | T/TC                                                          | TGCCCATCCTTATGCT<br>CTTC | ATCACGTGCAACCACA<br>AGTC   | 60.2                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32393187  | Ca2                                     | 32393187                      | AATAT/A                                                       | TGCCCATCCTTATGCT<br>CTTC | ATCACGTGCAACCACA<br>AGTC   | 60.2                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32393441  | Ca2                                     | 32393441                      | TGG/TGTGGG                                                    | TCGCACTTTTTCGTGA<br>GGA  | GGGCTTGTTTGACGCA<br>TTAT   | 59.5                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32393633  | Ca2                                     | 32393633                      | TAACATAATAA/TA                                                | GACTTGTGGTTGCACG<br>TGAT | GGGCTTGTTTGACGCA<br>TTAT   | 59.6                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32395584  | Ca2                                     | 32395584                      | AT/ATCACT                                                     | AGTGACTAGGGGCAAT<br>GGTG | AGGAAGAATATGGGT<br>GGGG    | 60.0                             | 724                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32396302  | Ca2                                     | 32396302                      | GTTTTTTTTTTTT/GTTTTTATTTTT<br>TTTTTT                          | CCCCAACCCATATTCTT<br>CCT | TTTTTGGTGGCAAAATC<br>CAT   | 60.0                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32399316  | Ca2                                     | 32399316                      | CTTTTTTTT/CTTTTTTTTTTTT                                       | TGGGGCACTCTTCAAA<br>TAGG | GCCTCTTCAAAAGTCG<br>GTCA   | 60.1                             | 215                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32406998  | Ca2                                     | 32406998                      | GTATATATATATATATATATATAT<br>AT/GTATATATATATAT                 | CAGACCCTTTCCAAGC<br>TGAC | CGATCAAGCTTTGGTTT<br>TGG   | 59.8                             | 406                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32424283  | Ca2                                     | 32424283                      | TAAAAAAAAA/TAAAAAAAAA                                         | GCGTGATTGATGACAA<br>CACA | TTCTCCAATCAAATGAA<br>GTCCA | 59.1                             | 866                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32453109  | Ca2                                     | 32453109                      | ATTTTTTT/ATTTTTTTTTT                                          | TCTTCACACAATCCCA<br>CCAA | CTCAAGTCGACAAGCC<br>TTCC   | 59.9                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_3245422   | Ca2                                     | 3245422                       | GATATATATATATATATATATA/GA<br>TATATATATATATATA                 | TTTCAACGGAACAC<br>AACA   | CATGTCAGGCAGTTAC<br>CCCT     | 60.0                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32478862  | Ca2                                     | 32478862                      | TAAAAAAAA/TAAAAAAAA                                           | AAATTGGTAATCGGAC<br>GCTG | TGTCCACATGGGAAGT<br>TTGA     | 60.0                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32478897  | Ca2                                     | 32478897                      | CTT/CTTT                                                      | AAATTGGTAATCGGAC<br>GCTG | TGTCCACATGGGAAGT<br>TTGA     | 60.0                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32479454  | Ca2                                     | 32479454                      | AG/A                                                          | CAAACCTCCCATGTGG<br>ACAA | TCCTATACCACATTTAA<br>AGCAAAA | 59.4                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32520939  | Ca2                                     | 32520939                      | ATTTTTT/ATTTTTT                                               | AACATGGAAGATCGGT<br>TGGA | GATCAATGCGAGTTTG<br>TTGG     | 60.3                             | 318                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32713699  | Ca2                                     | 32713699                      | C/CG                                                          | AACGCATCGGTAAACA<br>CTCC | GAGGTACTACAGCTTG<br>CCCC     | 60.0                             | 234                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32713890  | Ca2                                     | 32713890                      | AAAAACAAA/AAAAACAAACAAA                                       | AACGCATCGGTAAACA<br>CTCC | TGTTTTGCAGCAAGAT<br>GTCC     | 60.0                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_32998084  | Ca2                                     | 32998084                      | AC/A                                                          | TCAATCCCCATCAATCA<br>TCA | ACCAACACCCCAATT<br>GTTA      | 59.7                             | 705                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_33023522  | Ca2                                     | 33023522                      | GATATATATATATATATA/GATATA<br>TATATATATATATA                   | TTCAAGTGGTCGTGAC<br>CGTA | CATCAAAATTTTCAAAC<br>AAAACCA | 60.2                             | 885                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3312282   | Ca2                                     | 3312282                       | TGAAGAAGAAGAAGAAGAAGA<br>A/TGAAGAAGAAGAAGAAGAAG<br>AAGAA      | AATTGAGCCTTTTGCC<br>ATTG | TCCCTCCCTTCACTCTC<br>CTT     | 60.1                             | 215                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_33253608  | Ca2                                     | 33253608                      | GATTAATAAATAATTAATAA/GATTA<br>ATAAATAATTAATAAATAATTAATA<br>A  | TGATTATGGTTTCACG<br>TTTCTG   | TGTCAGCCACTCAAGA<br>ATCG   | 59.4                             | 383                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_33257195  | Ca2                                     | 33257195                      | ATTTTTTTTT/ATTTTTTTTT                                         | ATCGCATTTGCCTTTG<br>TTT      | GCTGTCGTTTGACGCA<br>TAAA   | 59.6                             | 801                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_33278516  | Ca2                                     | 33278516                      | ATGTTGTTGTTGTTGTT/ATGTTGTT<br>GTTGTTGTTGTT                    | AGGGGTCACATGGTTT<br>TGAA     | AGGTGGTTGCTGATAG<br>GTGG   | 60.2                             | 335                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_33379763  | Ca2                                     | 33379763                      | T/TA                                                          | GGGGAGGTTGTTTCAA<br>AGGT     | CTCTTCGGCCATAT<br>CAGC     | 60.2                             | 284                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_33389624  | Ca2                                     | 33389624                      | TTATATATATATATATA/TTATATA<br>TATATATATATATA                   | CGGGACTTACAACCCA<br>GAAA     | GCGCAAAGCTTTTGAT<br>TCTT   | 60.0                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_33405227  | Ca2                                     | 33405227                      | AATATATATATA/AATATATATA                                       | AAAGAGACATGACTTT<br>GTCCATCA | TTTCGCTACCCATCATA<br>CCC   | 60.0                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_33463714  | Ca2                                     | 33463714                      | TAAAA/TAAAA                                                   | TCGTTCCATATTCGGT<br>AGCC     | ACAACCGTCCCTCTG<br>TGAC    | 59.9                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_33553516  | Ca2                                     | 33553516                      | TAAAAAAAA/TAAAAAAAA                                           | ATTATCGGTTCAACGG<br>TCCA     | GATGTTAATGGAGTGT<br>CCGAGA | 60.2                             | 752                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_33610275  | Ca2                                     | 33610275                      | GATATATATATATATATAT/GATAT<br>ATATATATATATATAT                 | CTAACCTTTGCTGGT<br>CCAC      | ACTCCCTCCCGTCAAT<br>TTTT   | 59.6                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_33642680  | Ca2                                     | 33642680                      | TATAATAATAATA/TATAATAATAAT<br>AATAA                           | TGGATAGCCAGTGACA<br>GGAA     | TTTTTGCCGATAATGG<br>GAAC   | 59.2                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                     |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_33984310  | Ca2                                     | 33984310                      | CTATATATATATATATATATATAT<br>A/CCATATATATATATATATATATA<br>TATATA     | TGGCTATGATCACAATT<br>GGC    | CCCTTTGCAAGAGACT<br>CCAA    | 59.5                             | 869                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_33984629  | Ca2                                     | 33984629                      | CAAAA/CAAA                                                          | AACAAAGCAGAAATAT<br>CCTGTCG | AGCATAGCCAAAACCC<br>CTTT    | 59.7                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_33986085  | Ca2                                     | 33986085                      | TAC/TTTTTCCAAAATTGAC                                                | CGAGACAAGTTTTCCA<br>AGCA    | ACTCCAAGATCATCATC<br>GGC    | 59.0                             | 818                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_33986265  | Ca2                                     | 33986265                      | TT/TTATAT                                                           | AACTTTGGATCTACAC<br>GCGA    | ACTCCAAGATCATCATC<br>GGC    | 58.4                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3400176   | Ca2                                     | 3400176                       | TA/TAAA                                                             | TCATCCACCATGAAAG<br>CAAA    | TGTCTCGTCTCAATCAC<br>TTTCAG | 60.0                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34028835  | Ca2                                     | 34028835                      | AC/A                                                                | AAAGGGGTTTTGGCTA<br>TGCT    | CATGATCATAATTGCAT<br>GGAAAA | 60.0                             | 229                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34054996  | Ca2                                     | 34054996                      | GTT/GTTT                                                            | GGTAAGGGCTCCTTCC<br>AAAC    | ATCACGCAACATAACAC<br>CCA    | 59.9                             | 207                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34073061  | Ca2                                     | 34073061                      | TTATATATATATATATATATATATA<br>TAT/TTATATATATATATATATATA<br>TATATATAT | TGAATGTTTTCGATGAT<br>GTGC   | GATAAGTCCATTGGTC<br>CCCTT   | 59.5                             | 758                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34087701  | Ca2                                     | 34087701                      | CATATATATATATATAT/CATATAT<br>ATATATATATATATAT                       | ATGGTGGTGAGCAACT<br>TTCC    | AACAAACAGCCATTCCA<br>AGG    | 60.0                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34327217  | Ca2                                     | 34327217                      | GA/GAGAA                                                            | TATGCAAGCAGCACCA<br>TAGC    | GGTGGTGTTTCCAAGA<br>AGGA    | 60.0                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                           |                         |                         |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_34353539  | Ca2                                     | 34353539                      | CATATATATATATATATATATATATATATATATAT/CATATATATATATATATATATATATATAT         | CATGAGCTTGAGTCGCAAAA    | TAGGAGGCATATGTGAGGGG    | 60.1                             | 760                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34353805  | Ca2                                     | 34353805                      | GTTTTTTTT/GTTTTTTTT                                                       | AGTTGAAGGAGTGCATGAGGA   | TAGGAGGCATATGTGAGGGG    | 59.9                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34355206  | Ca2                                     | 34355206                      | CTTGGGCT/CTTGGGCTTTGTTGGGCT                                               | TCTTTGATGCAATGCCAGAG    | ATCATTCGAGGTGCCATCAT    | 59.9                             | 975                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34355457  | Ca2                                     | 34355457                      | TAAAAAA/TAAAAAA                                                           | ATTCTTGGGCTGTGTTTGG     | GGGTGATGAGGACTGGTTGT    | 60.0                             | 725                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34355554  | Ca2                                     | 34355554                      | CAAAAAAAAA/CAAAAAAAAA                                                     | ATTCTTGGGCTGTGTTTGG     | GGGTGATGAGGACTGGTTGT    | 60.0                             | 725                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34357732  | Ca2                                     | 34357732                      | CATATATATATATATATATATATATATATATATAT/CATATATATATATATATATATATATATATATATATAT | CATGAGCTTGAGTCGCAAAA    | GCAACAAGATGGGGACAAGT    | 60.1                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34450150  | Ca2                                     | 34450150                      | TTATATATATATATATATATATATATATATATATAT/TTATATATATATATATATATATATAT           | AGCTAGCTCAGAATGCAGCC    | CCCACAAAATTGCTTCGTT     | 59.9                             | 324                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34562775  | Ca2                                     | 34562775                      | TCTTTA/TCTTTACTTTA                                                        | ATAGCGTGCAACGATCTCT     | CATAGCGCCCATAAAAAGAA    | 59.9                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34576817  | Ca2                                     | 34576817                      | TTATATATATATATATATATATA/TTATATATATATATATATATA                             | CCTCTGTCATGAATCTCT      | TGAGTGAAGATTGAATGATGACG | 58.5                             | 242                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34584559  | Ca2                                     | 34584559                      | TAAAAAA/TAAAAAA                                                           | TGGCGATTTCATTTGTGTT     | CCACGAAATTATTTTGTAGGC   | 59.0                             | 160                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                 | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_34683764  | Ca2                                     | 34683764                      | TC/TCC                                                                                        | GTTTTTCGCAACCACCTTC       | CGCTTTTGCACCTAACC<br>TCC  | 59.6                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34684386  | Ca2                                     | 34684386                      | CAACGTTAAC/CAAC                                                                               | ACAATACTGCGGCCTG<br>TTTC  | GATTCCGATCGTTTTTC<br>ACG  | 60.1                             | 830                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34684591  | Ca2                                     | 34684591                      | TTATATATATATATATATATATATA<br>TA/TTATATATATATATATATATATA<br>ATA                                | TGGAGTTTTGTGTGAT<br>GGACA | GATTCCGATCGTTTTTC<br>ACG  | 60.0                             | 758                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34684688  | Ca2                                     | 34684688                      | CATCTT/C                                                                                      | CGTACGTAGCAATGCAACAA      | ATTCCGATCGTTTTTC<br>CGA   | 59.8                             | 229                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34684923  | Ca2                                     | 34684923                      | ATTTTTTT/ATTTTTTTT                                                                            | TCGTGAAAAACGATCG<br>GAAT  | TGCTTGATTTTAATGGA<br>TGCC | 60.4                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34685252  | Ca2                                     | 34685252                      | CATAAATAAATAAATAA/CATAAATA<br>AA                                                              | TCGTGAAAAACGATCG<br>GAAT  | TGGAGAGAAACAAAT<br>GGGG   | 60.4                             | 816                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34685695  | Ca2                                     | 34685695                      | ATTTTTTT/ATTTTTTTT                                                                            | CCCCATTTTGTCTCTCT<br>CCA  | TTGTTTCTCCCAGTTT<br>TGG   | 59.9                             | 234                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34775299  | Ca2                                     | 34775299                      | AATATATATATATATATATA/AATA<br>TATATATATATATATA                                                 | CCCAAGTGGTGGTTCT<br>GAGT  | CATGCTTCACTCTTAG<br>GGCA  | 60.0                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34854539  | Ca2                                     | 34854539                      | ANNNNNNNNN/ANNNNNNNNN                                                                         | GTTCTTTTGCCCGTCA<br>TCAT  | TCAAATTGAATGCGGG<br>TTTT  | 59.9                             | 387                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_34983521  | Ca2                                     | 34983521                      | AATATATATATATATATATATATAT<br>ATATATATATATA/AATATATATAT<br>ATATATATATATATATATATATATA<br>TATATA | CAATGCATGCTCCCC<br>TAAT   | CTAAAAGCCCAAAGCT<br>GCAC  | 59.9                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                               | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                             |                               |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_35125192  | Ca2                                     | 35125192                      | CT/CTTT                                                                                                                                     | GATGGCTTTGAGGCAG<br>AGAG      | AAGAAGCAAGCAGTGG<br>AAGC   | 60.1                             | 138                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35149862  | Ca2                                     | 35149862                      | TTATATATATATATATAT/TTATAT<br>ATATATATATATATATAT                                                                                             | ACTCATCATCGTGCCC<br>TTTC      | AACCACACACCACCCT<br>TCTC   | 60.1                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35227098  | Ca2                                     | 35227098                      | AAATAATAATAATAATAATAATA<br>ATAATAA/AAATAATAATAATAAT<br>AATAATAATAATAATAA                                                                    | AGAAAATGACCCGCAT<br>CTTG      | TCATTTCTTCGGTCGG<br>TTTC   | 60.1                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35228308  | Ca2                                     | 35228308                      | TTTATTATTATTATTATTATTATC<br>ATTATTATTATTATTATTATTATT<br>ATTATTA/TTTATTATTATTATTATTA<br>TTATTATTATTATCATTATTATTATTA<br>TTATTATTATTATTATTATTA | TTATTTACCGTCGTGT<br>CCA       | GGAAAAGGAGTCACCA<br>CCAA   | 60.0                             | 624                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35258590  | Ca2                                     | 35258590                      | A/ATT                                                                                                                                       | AAAAAGTTTTAACACG<br>GAGGTTTTT | TGTTGTTGGATTGGAC<br>ATGG   | 59.8                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35258736  | Ca2                                     | 35258736                      | ATTTTT/ATTTTT                                                                                                                               | AAAAAGTTTTAACACG<br>GAGGTTTTT | TGTTGTTGGATTGGAC<br>ATGG   | 59.8                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35259201  | Ca2                                     | 35259201                      | ATTTTT/ATTTTTTTTTT                                                                                                                          | CCATGTCCAATCCAAC<br>AACA      | GTTGCGAAAAAGTTCA<br>TCCG   | 60.2                             | 744                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35288109  | Ca2                                     | 35288109                      | ATTTTT/ATTTTTTT                                                                                                                             | TGCTTTATAGTGCTATT<br>ATGTGCCA | CGTCATTAAAGGGAA<br>ACCAA   | 60.1                             | 757                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35288455  | Ca2                                     | 35288455                      | TT/TTAT                                                                                                                                     | TTCGATGGTATGCAGT<br>AATTGG    | TTCCCATGAAAGAGAG<br>GTGG   | 59.9                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35291896  | Ca2                                     | 35291896                      | GTTTT/GTTTTT                                                                                                                                | AAAAAGTTCGAAGCG<br>TATTC      | TTCATTAAATTGCACA<br>AACCAA | 57.6                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                   |                             |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_35297760  | Ca2                                     | 35297760                      | AACTGAACTG/AACTGAACTGTACT<br>GAACTG                               | ACCAGGAAAAGAAGAA<br>GGGC    | TTTGGGTTGGGATGA<br>CATT       | 59.7                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35297846  | Ca2                                     | 35297846                      | TTGA/TTGATTCAACTGAACTGA                                           | ACCAGGAAAAGAAGAA<br>GGGC    | TTTGGGTTGGGATGA<br>CATT       | 59.7                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35298057  | Ca2                                     | 35298057                      | AT/AATAGCGCTT                                                     | AATGTCATCCCAACCC<br>AAAA    | TCGCAATAAAAAACATAT<br>AAAACCA | 60.0                             | 190                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35303488  | Ca2                                     | 35303488                      | ATTTTTT/ATTTTTTT                                                  | TTCCGAATAAGGATTTT<br>TTGG   | ATGGTTTGGGAAAAG<br>AACC       | 58.2                             | 137                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35304698  | Ca2                                     | 35304698                      | C/CG                                                              | GCTTGGAACAGCCTC<br>AGAC     | CAGGGTGGTACTGCAA<br>TGTG      | 60.0                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35329169  | Ca2                                     | 35329169                      | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATAT             | CAATTTTGAAGACGA<br>TTTTGA   | TGCCCCGAAAAAGTTC<br>ATCC      | 59.1                             | 330                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35359085  | Ca2                                     | 35359085                      | TTATATATATATATATATATATATA<br>TATAT/TTATATATATATATATATA<br>TATATAT | CGTCGAATCCTAGAGC<br>GAAT    | TGGTGTGGAGTCATA<br>CTTTTCA    | 59.4                             | 306                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_354010    | Ca2                                     | 354010                        | TTCTCTCTCTCTCTCTCTCTCTCT<br>CTC/TTCTCTCTCTCTCTCTCTCT<br>CTCTC     | GAGGAATTGGAACGCG<br>TAAA    | TGATTCAGGGCTTTTG<br>ATCC      | 60.1                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35425064  | Ca2                                     | 35425064                      | GAAAAAAAAA/GAAAAAAAAA                                             | TGTCGAAATGATTAGC<br>AAAAGAA | ACATTTTCCCTCCCTTG<br>GTC      | 58.9                             | 257                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35524033  | Ca2                                     | 35524033                      | CTTTTTTTTT/CTTTTTTTTTT                                            | TGTCGACCACTAAAAT<br>TCAAAAA | ACAAAAATCCATACCTG<br>CGG      | 59.9                             | 647                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_35559534  | Ca2                                     | 35559534                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                     | CCAAATATCCACGT<br>GTTT      | TTCTGGACGAAAATG<br>AACC   | 57.3                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35581740  | Ca2                                     | 35581740                      | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATATA       | TTGCCACTTGATACAG<br>CAAAA   | TTGAAAGGATAACATG<br>GCCG  | 59.4                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35648294  | Ca2                                     | 35648294                      | GC/G                                                          | TGATACACGGTCCACA<br>CTTCA   | TCGCTTCCACCAAATT<br>TTC   | 60.0                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35656426  | Ca2                                     | 35656426                      | AATATATATATATATATATATATA/<br>AATATATATATATATATATATA           | TGGTGTTGGAGTCATA<br>TTTTTCA | AACTAGTGGAACCCG<br>TGCG   | 59.4                             | 231                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35657396  | Ca2                                     | 35657396                      | AAGAGAGAGA/AAGAGAGAGAGA                                       | GCCGTGATTTGGTGGT<br>AAAT    | CCTCCAACAAAAGGA<br>ACCA   | 59.7                             | 295                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35737843  | Ca2                                     | 35737843                      | TG/T                                                          | TACCGGAAATTTCAAC<br>GAGG    | TTTATGGTTGGGCAAC<br>TTTTT | 59.9                             | 821                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35789864  | Ca2                                     | 35789864                      | AATTTGATTT/AATTTGATTTGATTT                                    | TGCCTGCGAGATCTTA<br>ATCA    | CCAAATCGAACCCAAAT<br>CAC  | 59.5                             | 365                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35815027  | Ca2                                     | 35815027                      | ATTTTTTTTT/ATTTTTTTT                                          | TAAGACCATGCATCTC<br>ACGC    | CGTGCATGGATCAAAC<br>TAGG  | 59.8                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35822980  | Ca2                                     | 35822980                      | AATATATATATATATATA/AATATA<br>TATATATATATATATA                 | TTAATCGCAGCGTGCA<br>ATAG    | GAAATTAGATTGCCG<br>GAAGAA | 60.0                             | 261                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35853696  | Ca2                                     | 35853696                      | AAATAA/AAA                                                    | GTTGCCAGCTTGTTT<br>TTTC     | GGGAGAGTGGGTGTTT<br>ATGC  | 59.9                             | 404                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_35854793  | Ca2                                     | 35854793                      | TTTAAAGTATGTAAGAA/T                                           | CAAAGGTAGATGATG<br>CCGAA  | CCAATGCATTTTAGTTG<br>TGGTG | 60.1                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35855144  | Ca2                                     | 35855144                      | AAACTAAATCACCACAATAAAT/<br>AAACTAAAT                          | CAAAGGTAGATGATG<br>CCGAA  | AGCCTCTGAAGCAAAA<br>ACCA   | 60.1                             | 962                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35855722  | Ca2                                     | 35855722                      | C/CG                                                          | TGGTTTTGCTTCAGAG<br>GGCT  | CTCAACATGTCCACCA<br>GCAC   | 60.0                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35855864  | Ca2                                     | 35855864                      | ACAAT/A                                                       | TGGTTTTGCTTCAGAG<br>GGCT  | CTCAACATGTCCACCA<br>GCAC   | 60.0                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35866504  | Ca2                                     | 35866504                      | CTATTATTATTATTA/CTATTATT<br>ATTATTATTATTA                     | GAAGAGGAGGGTAATT<br>TGGGA | AGACTTTCATGCATGC<br>CCTT   | 59.4                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35871808  | Ca2                                     | 35871808                      | AACTC/A                                                       | GATGAAATCCAATCCA<br>TGCC  | TTTCATTCCATGGGAA<br>AAA    | 60.1                             | 871                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35872708  | Ca2                                     | 35872708                      | T/TC                                                          | CCCTGACCTTGAAATA<br>TGCC  | TTGTTTGCAAATCATT<br>CACG   | 59.4                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35883864  | Ca2                                     | 35883864                      | TCCCCC/TCCCCC                                                 | ATGCCACAGCCAAATT<br>CATA  | TTGTTCACCAATTCCC<br>AGT    | 59.0                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35885474  | Ca2                                     | 35885474                      | TACAC/TAC                                                     | TGGTCAAACATGAC<br>CAAA    | ACATGAGGAAGGAGAC<br>CACG   | 58.4                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35892205  | Ca2                                     | 35892205                      | AAAAATAAAT/AAAAATAAATAAAA<br>T                                | CAACGACGAGTTTCAA<br>GCAA  | CATGTGTTTGCTTGG<br>TTTG    | 60.0                             | 878                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_35892945  | Ca2                                     | 35892945                      | CAAA/CAA                                                      | CTCCAAATGGCAACCA<br>AAAT | TTTAGGGGTGGACAAA<br>ATTCA    | 59.8                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35893811  | Ca2                                     | 35893811                      | ATTTTTTT/ATTTTTTTT                                            | GGTTAGCTTGGCCCAA<br>AAGT | GGGTAGAGTGGAGGAA<br>AGGG     | 60.5                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35924188  | Ca2                                     | 35924188                      | TTAATGTAATGTAA/TTAATGTAA                                      | TCCAACCTCAATCACC<br>AATG | ACAACATCAGCCATGT<br>CCAA     | 59.3                             | 907                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35925409  | Ca2                                     | 35925409                      | CCTGT/CCTGTGGCTGT                                             | TTGTTCAGTGACCTGC<br>AAGC | TGGTGGGTTATCCCAA<br>TAAA     | 60.0                             | 750                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35926054  | Ca2                                     | 35926054                      | AATATATA/AATATA                                               | ATTGGGATAACCCACC<br>AACA | GAGAAGATTGAAGGAG<br>GGGC     | 59.9                             | 624                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35926372  | Ca2                                     | 35926372                      | T/TA                                                          | ATTGGGATAACCCACC<br>AACA | ATGCGCAAAGAGCCTT<br>GTAT     | 59.9                             | 691                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35939441  | Ca2                                     | 35939441                      | TTTTGT/TTT                                                    | TCTCCGGTTTCTAAGG<br>CAAA | GGGCTCCACAAAATC<br>TCAA      | 59.8                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35940345  | Ca2                                     | 35940345                      | GTTT/G                                                        | GCCGCCAAAGATTAAA<br>ATTG | AAGGAGGATTAGGGAT<br>GCGT     | 59.6                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35957274  | Ca2                                     | 35957274                      | ATTTTTTTT/ATTTTTTTT                                           | TCACCTCATTTTGTG<br>GCA   | TTTATTATATCACGGAT<br>TCACGGA | 60.1                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35961541  | Ca2                                     | 35961541                      | ATTTTTTTT/ATTTTTTTT                                           | TCATCAAAGACATTCTG<br>GCC | TTCGACAATATGGCCA<br>ATGA     | 59.7                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_35961843  | Ca2                                     | 35961843                      | TAAA/TAA                                                      | TCATCAAAGACATTCTG<br>GCC  | TTCGACAATATGGCCA<br>ATGA    | 59.7                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35961921  | Ca2                                     | 35961921                      | TAAAA/TAAA                                                    | AGACGCTCATCACTCA<br>ATTCA | TTCGACAATATGGCCA<br>ATGA    | 59.9                             | 251                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35962691  | Ca2                                     | 35962691                      | ATTTTTTT/ATTTTTTTT                                            | TGAGTCATGAGATCGA<br>CGAAA | TTCAAATTTAACGGTTG<br>GATCA  | 59.4                             | 367                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35962726  | Ca2                                     | 35962726                      | GAAAA/GAAAAA                                                  | TGAGTCATGAGATCGA<br>CGAAA | TTCAAATTTAACGGTTG<br>GATCA  | 59.4                             | 367                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35971845  | Ca2                                     | 35971845                      | TAT/TATATCACAT                                                | GCGGAGCAGAACCCCTT<br>ATTA | TGACTTTTTATTTTTC<br>GCACTC  | 59.3                             | 955                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35995557  | Ca2                                     | 35995557                      | TAAAAAAAA/TAAAAAAAAAA                                         | CGTGTGAGTTTCGTCG<br>CTAA  | TGGTTTGGGTGGTTCA<br>TTTT    | 60.1                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35995631  | Ca2                                     | 35995631                      | TCAAAAAACAAAA/TCAAAAAAC<br>AAAAAACAAAA                        | CGTGTGAGTTTCGTCG<br>CTAA  | TGGTTTGGGTGGTTCA<br>TTTT    | 60.1                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_35996261  | Ca2                                     | 35996261                      | TTCTCT/TTCT                                                   | CCATTGTCACGGCA<br>TAAT    | AAATCAACGACGATG<br>AATAAGAA | 60.7                             | 330                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_36001001  | Ca2                                     | 36001001                      | AAA/AAATAAATAA                                                | CGCGTTGGTACTTTCA<br>TGTG  | TCCCAAGTTAGGGTA<br>AGGC     | 60.2                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_36001500  | Ca2                                     | 36001500                      | T/TC                                                          | GCCTTACCCCTAACTT<br>GGGA  | AAAAAGTCGTCGGGTC<br>AATG    | 60.3                             | 333                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_36146995  | Ca2                                     | 36146995                      | ACAACCCCA/ACA                                                 | AGGGAAACCCACCTCT<br>TGAT   | AAATCCAAAGTGCTTG<br>CGTT   | 59.8                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_36177749  | Ca2                                     | 36177749                      | ATTTTTT/ATTTTTTTT                                             | TAGTTGAAGGCCATGC<br>AAGA   | AGTACTCCAGACCCCC<br>AACA   | 59.4                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_36290906  | Ca2                                     | 36290906                      | ACCCCCCCCCC/ACCCCCCCCC                                        | TGCGATGTGCTGACAG<br>TGTA   | CGTGCCTCCACTGAAA<br>ATTA   | 60.1                             | 884                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_36463610  | Ca2                                     | 36463610                      | GTTTTTTTTT/GTTTTTTTTT                                         | GCCCTGATATACCAAC<br>CCCT   | TACACACCACACGCTT<br>CACA   | 60.0                             | 912                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_36464328  | Ca2                                     | 36464328                      | CTCGAGTT/CTCGAGTTCGAGTT                                       | TGTGAAGCGTGTGGTG<br>TGTA   | AGGACTAACGGGAATT<br>GGAG   | 59.8                             | 754                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_36493996  | Ca2                                     | 36493996                      | CATATATATATATATATATAT/CAT<br>ATATATATATATATATATATAT           | TCTTTCACCTCACTCCCC<br>TTTG | GAGAGATACGCGGATG<br>GAAA   | 59.3                             | 335                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_366324    | Ca2                                     | 366324                        | ATTTTTTTTTT/ATTTTTTTTTTT                                      | CAAGGGGCATTACCTT<br>ACCA   | CTCCTCTCTTGCTTTTG<br>GCA   | 59.8                             | 727                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3687741   | Ca2                                     | 3687741                       | AT/ATT                                                        | GGACAAAATGGCAAGG<br>AAGA   | TTCTACGCTTTTGAAA<br>CAATTT | 60.1                             | 223                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3726404   | Ca2                                     | 3726404                       | CTTTTTTTTTT/CTTTTTTTTTT                                       | TCTCCAGTTTGGTCC<br>TCCA    | AATCGCAAAAGTAATCC<br>CCC   | 60.6                             | 252                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_37373     | Ca2                                     | 37373                         | TTATATATATATATATATATAT/TT<br>ATATATATATATATATAT               | TCATGGTCTGGGTTTG<br>AACT   | TGAATCGCGAAATTAG<br>TCCC   | 58.0                             | 708                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)          | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                        |                               |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_3857450   | Ca2                                     | 3857450                       | TTTTATTTATTTATTTATTTATTT<br>T/TTTTATTTATTTATTTATTTAT<br>TTATTTATTTATTT | GGGAAATTGTGGTGTG<br>AGGT      | TTCGTGCAACGCTATA<br>ATTCC  | 59.7                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3937629   | Ca2                                     | 3937629                       | GATAAATAAATAAATAAATAA<br>TAAATAA/GATAAATAAATAAAT<br>AAATAAATAAATAAATAA | AAGTGTTTTGGTGTCTG<br>TCCC     | GACTTCTATTGCCCC<br>ACAA    | 60.0                             | 154                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3949908   | Ca2                                     | 3949908                       | TAAAAAAAAAAAAA/TAAAAAAAA<br>A                                          | TCAAAGAATAGAGGTA<br>TTGTCTCCG | CTAAAGCCTGCCCAT<br>TCTG    | 60.0                             | 795                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_3955516   | Ca2                                     | 3955516                       | TATAATAATAATAATAATAA/TAT<br>AATAATAATAATAATAATAATAA                    | TTTCCGATTTCGAGGT<br>GTTC      | TGAATAGTGAAACA<br>CAACAATG | 60.1                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4057856   | Ca2                                     | 4057856                       | AATATATATATATATATA/AATATATA<br>TATATATA                                | TGCAAAATGGAGATTT<br>GTGG      | TGATGGGAGCATGTGA<br>CACT   | 59.5                             | 712                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4060085   | Ca2                                     | 4060085                       | AATATATATATATATATATATATA<br>ATA/AATATATATATATATATATATA<br>ATA          | GACCTTGCATGGAGTG<br>TTGA      | GGCATAGCCATGAAGA<br>ACTTG  | 59.7                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_416248    | Ca2                                     | 416248                        | TTATATATATATATATATATATATA<br>TAT/TTATATATATATATATATATA<br>T            | ATAAATGAAGGGGTGG<br>GAGG      | GTTTCCCATAAACAGCA<br>CCC   | 60.0                             | 882                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_42172     | Ca2                                     | 42172                         | TTATATATATATATATATATATATA/T<br>TATATATATATATATATA                      | TGGCAGTCTGTTTCAC<br>GTTT      | CAAGGGACCAGATTCT<br>GCAT   | 59.3                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4266265   | Ca2                                     | 4266265                       | A/ATTAATCCGAAAG                                                        | TGGACGTTTAACGGTT<br>GACA      | CCCAGTAGAAAAGAAG<br>GGGC   | 60.0                             | 705                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_428237    | Ca2                                     | 428237                        | GAAAA/GAAAAA                                                           | GTGAAACCAACCCCA<br>AATG       | GACTCTTTGCCCTTCAA<br>TCG   | 60.1                             | 181                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                           |                              |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_4285697   | Ca2                                     | 4285697                       | TAAAA/TAA                                                                                 | CCAGTCCCAGAAATTA<br>ACGA     | ACTTGCGATAATCGATT<br>GGG | 59.9                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4383503   | Ca2                                     | 4383503                       | GTTTTTTTTT/GTTTTTTTTT                                                                     | GTTGGATTATGGTGG<br>CGAT      | CTTCAAAGCCTTGCT<br>GGC   | 59.7                             | 221                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4502043   | Ca2                                     | 4502043                       | ANNNNNNNNN/ANNNNNNN                                                                       | GCTTTGGGTGAACAAA<br>TGCT     | AGGCACCCTTCAACAA<br>AATG | 60.1                             | 258                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4527479   | Ca2                                     | 4527479                       | GAAGACAAAAAACATAAGACAAA<br>AAAAACAT/GAAGACAAAAAACAT<br>AAGACAAAAAACATAAGACAAA<br>AAAAACAT | GCAATTTACCTCTTCT<br>GCC      | TGACGAAGCCACAAT<br>AACA  | 59.8                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4557115   | Ca2                                     | 4557115                       | GTTTTT/GTTTTTT                                                                            | ACGGTTGAGAATTGAG<br>TGCC     | AAAAGCTCGCGAATGT<br>CAGT | 60.1                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4639205   | Ca2                                     | 4639205                       | TAAAAAAAAA/TAAAAAAAAA                                                                     | AACACTCGTACCTTTAT<br>TTCTGGG | ATGCAGCAATTTCCATC<br>CTC | 59.8                             | 950                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4655023   | Ca2                                     | 4655023                       | AATATATATATATATATATATAT<br>A/AATATATATATATATATATAT<br>A                                   | AATATGCGGAATTTGG<br>TCCT     | TTGTGTTCCGTAGCA<br>CGAG  | 58.4                             | 891                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4655248   | Ca2                                     | 4655248                       | CAAAAAAAAA/CAAAAAAAAA                                                                     | CAAAAGGACCACAAA<br>TTGG      | TTGTGTTCCGTAGCA<br>CGAG  | 58.0                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4655453   | Ca2                                     | 4655453                       | TTATATATATATATATATATATAT<br>TATATATATA/TTATATATATATAT<br>ATATATATATATATATATATATA          | TCGTGCTACGGAAACA<br>CAAC     | TCCTTTTCACGAGGTC<br>ATCC | 59.8                             | 370                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4793170   | Ca2                                     | 4793170                       | GATAATAATAATAATAATAATAA<br>T/GATAATAATAATAATAATAATA<br>ATAAT                              | GCCATGTGGAAGAACA<br>AGGT     | CCAAACTGGGGAGAA<br>ACAA  | 60.0                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                        | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                      |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_4850252   | Ca2                                     | 4850252                       | GTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATT/GTTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATT                 | AAATTCATCCTCGCTC<br>GCTA  | TTTCCCGACTTGGTCC<br>TTTA  | 59.9                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4891048   | Ca2                                     | 4891048                       | TTTTATTTATTTATTTATTTATTTAT<br>T/TTTTATTTATTTATTTATTTATTTAT<br>TTATTT                                                 | AACGGTGTGAAAGGGA<br>AATG  | TGAATTGAATTTGGAAG<br>GGG  | 59.8                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4891335   | Ca2                                     | 4891335                       | AAATTGAAG/A                                                                                                          | AACGGTGTGAAAGGGA<br>AATG  | TGAATTGAATTTGGAAG<br>GGG  | 59.8                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4892794   | Ca2                                     | 4892794                       | CATATATATATATATATATATATATA<br>TATATATAT/CATATATATATATATAT<br>ATATATATATATATATATATATATA<br>TATATAT                    | GCGGACATAAGGAAGA<br>TGTGA | AGGTCTGCGAAGATGG<br>AAAA  | 60.1                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4894086   | Ca2                                     | 4894086                       | TA/TAGACAACTCAA                                                                                                      | TTGAACTACAACCAGC<br>GCAC  | TTTTGTTCATTTCTTG<br>CTCCA | 59.9                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4894836   | Ca2                                     | 4894836                       | ATGATT/AT                                                                                                            | AAAGGGAAGAAATTTT<br>GGGA  | AACCGGACGATCATTT<br>GAAG  | 59.9                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4895677   | Ca2                                     | 4895677                       | AA/AATATGA                                                                                                           | CCAGGATAAAACAGCC<br>CAGA  | TGGATGCTTTCCCAAC<br>TTTC  | 60.1                             | 467                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4915954   | Ca2                                     | 4915954                       | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAA/A<br>AATCATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAA | TTATCGGACATTTTCCC<br>GAG  | CTAGGTCGCCCTTTCA<br>GGTT  | 59.9                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_4966099   | Ca2                                     | 4966099                       | A/ATGTTTTGCGCGGC                                                                                                     | GGATGACATGGCTTTC<br>AACA  | GATGTTTCTTCTTAGCG<br>GCG  | 59.5                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_5112695   | Ca2                                     | 5112695                       | CGAATGAAT/CGAAT                                                                                                      | TTGCTGTTTTCTGTTC<br>CTG   | GGACAAAGCCCAGATT<br>TTCA  | 60.0                             | 381                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)          | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                        |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_6505178   | Ca2                                     | 6505178                       | TA/TAA                                                                 | CGTAATAACGGCGAGG<br>AAAA | TGAGCAGGGGAAGA<br>GTAGA  | 60.1                             | 548                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_6513260   | Ca2                                     | 6513260                       | AAATAATAATAATAATAATAATA<br>ATAATAAT/AAATAATAATAATAATA<br>TAATAATAATAAT | ATGGTCCAAGGAAATT<br>GTGC | AGTCGTCGAGGCCAAA<br>TCTA | 59.8                             | 265                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_661366    | Ca2                                     | 661366                        | G/GGGGTAA                                                              | AAGCTCAACATGCAAA<br>ACCC | TCCCAACCCAAATAAAC<br>CAA | 60.1                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_6640316   | Ca2                                     | 6640316                       | TAAAAA/TAAAAAA                                                         | ATGGCCACGAATCTGA<br>AGAG | ACGGTTGTTTGGCAT<br>TGAT  | 60.2                             | 890                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_6640452   | Ca2                                     | 6640452                       | GAAAA/GAAAAA                                                           | AAAAAGGTCCTAGGT<br>GGGA  | ACGGTTGTTTGGCAT<br>TGAT  | 59.8                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_6641737   | Ca2                                     | 6641737                       | CATATAT/CATATATATAT                                                    | GTATTCAGGGGCGAAG<br>GAAT | AATGCAAACGACAAAG<br>GAGG | 60.3                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_6641916   | Ca2                                     | 6641916                       | TG/T                                                                   | GTTCTATGGGGACAGG<br>GTCA | TATCAACTACCAGAGC<br>GGGG | 59.8                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_6642487   | Ca2                                     | 6642487                       | ATTTT/ATTTTTTTTT                                                       | CCCCGCTCTGGTAGTT<br>GATA | ACCCACTTTGAGAAAC<br>GTGC | 60.1                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_6642515   | Ca2                                     | 6642515                       | TTATATATATATATATATATATAT<br>ATATATATATATATATATATA                      | CCCCGCTCTGGTAGTT<br>GATA | ACCCACTTTGAGAAAC<br>GTGC | 60.1                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_6643755   | Ca2                                     | 6643755                       | G/GGA                                                                  | ATGGAACAAGCAGCGA<br>AGTT | GTTGATACGAGGGGGT<br>TGAA | 59.9                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                            | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                          |                             |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_6643843   | Ca2                                     | 6643843                       | CTTTTTTTTT/CTTTTTTTT                                                                                                                     | ATGGAACAAGCAGCGA<br>AGTT    | GTTGATACGAGGGGT<br>TGAA       | 59.9                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_6648530   | Ca2                                     | 6648530                       | TAAAAA/TAAAAAAA                                                                                                                          | TTATCGATCGTCGGTG<br>TCAA    | TTCCATATGCACCTCC<br>CATT      | 60.1                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_6657720   | Ca2                                     | 6657720                       | AATG/AATGATG                                                                                                                             | AAGAATTGTTGTCCCC<br>CTCC    | GGAACCAAAACAAAAG<br>GCAA      | 60.2                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_6659290   | Ca2                                     | 6659290                       | GTTT/GTTTT                                                                                                                               | TGTTTGACAAATGTTAA<br>GTGCG  | GGTGTGACTGGCCGTA<br>TTTT      | 58.8                             | 621                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_66642     | Ca2                                     | 66642                         | TTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAA/TTAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATAA | TGAAAAATTTGGGGTG<br>TTACAA  | GGTGACTTAATTTTGAA<br>GAAGACGA | 59.2                             | 813                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_6692032   | Ca2                                     | 6692032                       | AAATAATAATAATAAT/AAATAATAAT<br>AAT                                                                                                       | GAACGAAAATGTGTTTT<br>ATGGG  | CTCTCAAGGTGTGACT<br>GCCA      | 58.4                             | 157                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_6753729   | Ca2                                     | 6753729                       | ATATAT/ATATATGTATAT                                                                                                                      | TGATGCCATGATATGA<br>ATGCT   | GGCCAAGAGAAGTTCTG<br>AGTG     | 59.0                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_6815005   | Ca2                                     | 6815005                       | ATTATTTATTTATTTATTTTAT/AT<br>TATTTATTTATTTATTTA                                                                                          | GAAATTTTAGGCGCAA<br>CAGC    | TCCAATCCCATTGTCCA<br>CTT      | 59.9                             | 703                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_6865791   | Ca2                                     | 6865791                       | ATTTTTTT/ATTTTTTT                                                                                                                        | ACCCACCCCATAAAAA<br>GAGG    | TTAAAAAGGAGATGTG<br>CGGG      | 60.0                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_700339    | Ca2                                     | 700339                        | ATTTTTTTTT/ATTTTTTTTT                                                                                                                    | AACTAGGTCAGAAAC<br>CGATAGAA | CCAACACAAACCTAAAC<br>CGA      | 57.7                             | 896                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_7041526   | Ca2                                     | 7041526                       | T/TC                                                          | GCCCTCAGATGAGAGT<br>CAGG  | CAGCGGAAAAGTTTCT<br>CCAA   | 59.9                             | 324                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7043443   | Ca2                                     | 7043443                       | AATATATATATATATATATATAT/ATATATATATATATATATATATATAT            | ATGGGTCGTGTTCGAT<br>TGTT  | AACCAACTATTGACCC<br>CAAAAA | 60.2                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7171869   | Ca2                                     | 7171869                       | TTAT/TT                                                       | CGGCCATTAAATTCT<br>GACA   | TTGCATTATGTTTCTGG<br>CAAA  | 58.6                             | 320                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7171912   | Ca2                                     | 7171912                       | TATTTAATTTAATTTAATT/TATTTAA<br>TTTAATT                        | CGGCCATTAAATTCT<br>GACA   | TCATTTCATAACGAGTG<br>ACCCA | 58.6                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7172121   | Ca2                                     | 7172121                       | CTATATATATATAT/CTATATATATAT                                   | TTTGCCAGAAACATAAT<br>GCAA | TCATTTCATAACGAGTG<br>ACCCA | 59.2                             | 285                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7172172   | Ca2                                     | 7172172                       | ATTTTTTTTT/ATTTTTTTTTT                                        | TTTGCCAGAAACATAAT<br>GCAA | TTTTGGAAAAATGAAG<br>GACCA  | 59.2                             | 774                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7173102   | Ca2                                     | 7173102                       | GAAAAA/GAAAAA                                                 | CTCAATCCAACACAC<br>GCTT   | AATGACCACCTCTTGT<br>GCC    | 58.8                             | 787                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7220242   | Ca2                                     | 7220242                       | TGA/T                                                         | GCCCTCAGATGAGAGT<br>CAGG  | TATTGTGCGACGTCTT<br>CTCG   | 59.9                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7276294   | Ca2                                     | 7276294                       | CAAAA/CAAAA                                                   | TCCACCACAATCGTTA<br>AGCA  | AGCGGAGATTTTACCG<br>GATT   | 60.1                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7295625   | Ca2                                     | 7295625                       | GA/GAA                                                        | GAGGCAAATTACGTGG<br>CAGT  | CTCAAATCATGCTCTTG<br>GCA   | 60.1                             | 355                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                   |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_7407914   | Ca2                                     | 7407914                       | TTCTAGTTTTGGGATCCTCTAGTTT<br>T/TTCTAGTTTTGGGATCCTCTAGTT<br>TTGGGATCCTCTAGTTTT     | TCCCTTTGGTTCAGGT<br>TGTC  | GGAAAAGCAAGGATGC<br>TGAA   | 59.9                             | 372                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7528105   | Ca2                                     | 7528105                       | CAAAAAAAAA/CAAAAAAAAA                                                             | AGAGGCCAACCTCTGT<br>CTCA  | TCGTCAGGAGGTTGAT<br>GATG   | 60.0                             | 313                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7557453   | Ca2                                     | 7557453                       | TTATATATATATATATAT/TTATATAT<br>ATATATATATAT                                       | CGCACACACGAATATT<br>CACC  | ACGACAACATGGTGGA<br>ACAC   | 60.0                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7565416   | Ca2                                     | 7565416                       | CATATATATATATATA/CATATATATA<br>TATATATA                                           | AACATATGCAAACTTC<br>GCCC  | ATCTCTCTCCGCCATT<br>TTT    | 60.0                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7586948   | Ca2                                     | 7586948                       | AAATAATAATAATAATAATAATA<br>ATAATAATAA/AAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA | GCGACCTGGTGATTT<br>GTTT   | CCGCGTAGATGTGAAA<br>CTGA   | 60.0                             | 348                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7587644   | Ca2                                     | 7587644                       | TTTATTATTATTATTATTATTATT<br>/TTTATTATTATTATTATTATTAT<br>TATT                      | GGCTAGACGAGTTCGA<br>CGAC  | AATAGATGGTCGCATC<br>CTGG   | 60.0                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7589173   | Ca2                                     | 7589173                       | GATGTAA/GA                                                                        | CAACACCTTGTGCAAT<br>CAGG  | AGGCCATGAGGTTGTT<br>TGAG   | 60.2                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7607086   | Ca2                                     | 7607086                       | TAAAAAAAAAAAAA/TAAAAAAAAAAAA<br>A                                                 | TGTCAAAGGAGCAACA<br>CAACT | ACCCCGACGTACACAC<br>TCTC   | 58.4                             | 855                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7617731   | Ca2                                     | 7617731                       | CTAAATAAAATAAA/CTAAATAAA<br>ATAAAATAAAATAAA                                       | CCAAGATCTCGTAGTG<br>CAACA | TGGGTTTAGTCCGTTTT<br>TCTTC | 58.9                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7635741   | Ca2                                     | 7635741                       | CAAAAAAAAA/CAAAAAAAAA                                                             | CCTCGATCTTGTCTG<br>GTTC   | TGTAGAAAAAGAGGC<br>CACG    | 59.7                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                         |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_7655513   | Ca2                                     | 7655513                       | GTTTTTTTTTTT/GTTTTTTTTT                                       | CCCACAATAGCACCATCTTGT    | TCAAGTTGAAGCATCATGGTC   | 60.6                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7657147   | Ca2                                     | 7657147                       | CTTTTT/CTTTTTT                                                | TTATGTGGGGGATTGTGATG     | TTCCACGTCCTTTTCATTC     | 60.4                             | 705                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7668484   | Ca2                                     | 7668484                       | CC/CCCAC                                                      | CCAACACAAGCACCAACATC     | GGAGGGGTAGAAGTGAAGG     | 60.0                             | 188                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7669241   | Ca2                                     | 7669241                       | TAA/TAAA                                                      | TGTTGCGCTCTTCATCAGTG     | TGTGTTTTGGGTTTCGACTAGG  | 60.0                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7669371   | Ca2                                     | 7669371                       | TAAAAAAAA/TAAAAAAAAA                                          | TGTTGCGCTCTTCATCAGTG     | TGTGTTTTGGGTTTCGACTAGG  | 60.0                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7669611   | Ca2                                     | 7669611                       | A/ACACTCATT                                                   | CCTAGTCGAACCCAAACACA     | TTGCTCACGAAGGAAATGACT   | 60.0                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7671677   | Ca2                                     | 7671677                       | ATGATT/A                                                      | TACACCCACCATGGGAATCT     | ACCCCATACCCCTCCATTA     | 60.1                             | 227                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7678380   | Ca2                                     | 7678380                       | AAA/AAATAA                                                    | GGTGAGGATGCATGAGATGA     | ACCAAGATGACCAGCAAGG     | 59.6                             | 949                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7678453   | Ca2                                     | 7678453                       | GAAAAAAAA/GAAAAAAAA                                           | TTTTCGATTGTGATTAGAGAGATT | ACCAAGATGACCAGCAAGG     | 58.5                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7696798   | Ca2                                     | 7696798                       | AAAA/AAAACAAA                                                 | TGTTTCCACGATTCAAGTTTC    | AAAGCCAATAATCTAATTGGGG  | 59.1                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_7705341   | Ca2                                     | 7705341                       | ATAGTA/ATA                                                    | CTGCGGTACAACCATC<br>TCCT    | CGCCGTCGTTACTGTT<br>CATA     | 60.1                             | 355                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7706402   | Ca2                                     | 7706402                       | ATTTTTTTTT/ATTTTTTTTT                                         | GACCCATTTCACAAA<br>CACC     | CATCCACTTTCTTGCCCT<br>GTATTT | 60.1                             | 956                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7708059   | Ca2                                     | 7708059                       | ATTTTTTTTT/ATTTTTTTTT                                         | GCCTTGGGACCTCCTA<br>AAAG    | AGAGGGAGAGAGGAA<br>GGCTG     | 60.1                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7714112   | Ca2                                     | 7714112                       | TG/TTGG                                                       | CTCACTCGATCGATGG<br>TTCA    | TGACAATGCTGGCTGT<br>TAGC     | 59.8                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7718955   | Ca2                                     | 7718955                       | TGAAA/T                                                       | GAGCTTCATTGAAATC<br>GGGA    | TCATATAGGAGGTCGC<br>ACCC     | 60.2                             | 821                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7722723   | Ca2                                     | 7722723                       | ATTTTTTTTT/ATTTTTTTTT                                         | AAAGCAGTGCCTTCG<br>GAGA     | TCCTACCCTTTTGGCTT<br>AAAAA   | 60.0                             | 408                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7723173   | Ca2                                     | 7723173                       | ATTTT/ATTTT                                                   | TTTTTAAGCCAAAAGG<br>GTAGGA  | AACCGCAATTTTATAA<br>GACACG   | 59.2                             | 321                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7723572   | Ca2                                     | 7723572                       | ATTTTTTTTT/ATTTTTTTTT                                         | CGTGTCTTATAAAAATT<br>GCGGTT | TTTGCAAGCCAAGCAC<br>ATAC     | 59.5                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7724864   | Ca2                                     | 7724864                       | TA/TAAAGAGATTGAGA                                             | ACCAGAGACTGCAG<br>CAAA      | AACAAGATTCTGAATG<br>CTCC     | 59.6                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7731377   | Ca2                                     | 7731377                       | GAAAAA/GAA                                                    | GTGGTTGTGATGTTGA<br>ACGC    | CTCCCGCTAACTCCTC<br>TTCC     | 60.0                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_7739105   | Ca2                                     | 7739105                       | ACTTTGT/A                                                     | GGTTCTACGGCAACGT<br>CAAT      | TTACGCGTGTCATTTTC<br>TCG    | 60.0                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7743405   | Ca2                                     | 7743405                       | CG/C                                                          | ATCCATCATGTTTCATGC<br>CCT     | ATCTCCACCCGTTCTCT<br>TGA    | 60.2                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7744794   | Ca2                                     | 7744794                       | CATGACATGAATGA/CATGA                                          | CATTTTGATTGGGAAT<br>GTGC      | CAACAACAGTCCAAAG<br>TAGGCA  | 58.8                             | 585                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7745257   | Ca2                                     | 7745257                       | CAAAA/CAAAAA                                                  | TGGCATGACATGAATG<br>AAGAA     | GAGCAATTTGTGTGGA<br>CCCT    | 60.1                             | 760                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7749962   | Ca2                                     | 7749962                       | TT/TTAT                                                       | GGAGCTGCAACCATCT<br>TCTC      | TGGATTGGGCTGAAT<br>TAGG     | 60.0                             | 321                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7756359   | Ca2                                     | 7756359                       | CAAA/CAAAA                                                    | AACCAGCATGTGTTGT<br>TGGA      | TGTGGTGGGGGAATTA<br>AAAA    | 60.0                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7771490   | Ca2                                     | 7771490                       | ATTTTTTTTT/ATTTTTTTTTTT                                       | ACCATTATTATTTTCG<br>TGTTAATGA | GGTACCATGGATGATA<br>TTTAGCC | 57.3                             | 188                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7772575   | Ca2                                     | 7772575                       | AGG/AGGG                                                      | TTAAGGGACACGGGT<br>GTTA       | TCCACCTCTCAATTTT<br>TCAA    | 60.2                             | 898                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7772843   | Ca2                                     | 7772843                       | C/CG                                                          | CAATTGGTGCCGTTA<br>TTTT       | GGGGTTGTAAAATGTG<br>TGTGG   | 59.7                             | 811                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7772892   | Ca2                                     | 7772892                       | ATTTT/ATTT                                                    | CAATTGGTGCCGTTA<br>TTTT       | TTGGGGGAAGAAAATT<br>GAGA    | 59.7                             | 958                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_7773617   | Ca2                                     | 7773617                       | TTAAATAAAAT/TTAAATAAAATAAAT<br>AAAAT                          | GCTGAGCCCAACAAG<br>CTAA      | CCACTGTGGAAGGTA<br>AATGC   | 60.5                             | 845                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7774634   | Ca2                                     | 7774634                       | AA/AAGA                                                       | TTCGATGCTACCCATA<br>ACACA    | TCCTTACGTTCCACGG<br>TAATTT | 59.1                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7774796   | Ca2                                     | 7774796                       | TAAAAAAAAA/TAAAAAAAAA                                         | TTGGATCATTTTGAGTT<br>TGAGG   | TCCTTACGTTCCACGG<br>TAATTT | 59.1                             | 358                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7774902   | Ca2                                     | 7774902                       | ATTAATATAATTTTTTT/ATT                                         | AAATTACCGTGGAACG<br>TAAGGA   | TGCTTTGTGTAATCG<br>TGGT    | 59.8                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7780730   | Ca2                                     | 7780730                       | ATTTTTTTTTTT/ATTTTTTTTTT                                      | TTGTCTCCATCTCCAG<br>CCTT     | TGTTGTTGAGTTGGG<br>ACACA   | 59.8                             | 995                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7792210   | Ca2                                     | 7792210                       | CAAAA/CAAA                                                    | GCGAAAACCTAAAGGA<br>CTAAACCA | CAACCCGAAGTTGCTC<br>ATTT   | 60.1                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7792884   | Ca2                                     | 7792884                       | TTC/T                                                         | ATGAGCAACTTCGGGT<br>TGAC     | CTAGTTCCTCGTTGGA<br>GGGG   | 60.1                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7793328   | Ca2                                     | 7793328                       | GAAAAA/GAAAA                                                  | ATATCCCTCCAACGA<br>GGAA      | TTTATTGCGGTTTCCT<br>TCA    | 60.7                             | 877                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7795279   | Ca2                                     | 7795279                       | CAT/C                                                         | AAAAGAAACCCGAGAG<br>ACAA     | AGCAAGCACAAACCGT<br>TCTT   | 59.7                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7810805   | Ca2                                     | 7810805                       | GAAA/GAAAA                                                    | GCTCTTTGAGAAGAGG<br>GGGT     | TGGTATCCTTCCTTCC<br>GTTC   | 59.8                             | 782                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_7811963   | Ca2                                     | 7811963                       | CAAAAAAAAA/CAAAAAAAAA                                         | ACTAACTCGGTGGGGA<br>ACAA | TCCCTTGTTCTTGCTGT<br>GAA   | 59.4                             | 330                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7815016   | Ca2                                     | 7815016                       | TAATAACAAATAACAAA/TAATAACA<br>AATAACAAATAACAAA                | TTTTACCAACACCGT<br>CAAA  | AAATAATCGTGGCCTT<br>GCAC   | 60.0                             | 901                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7893331   | Ca2                                     | 7893331                       | CAG/CAGAG                                                     | AAACAAATTCGCGGTG<br>CTAC | TGATGAAACCACCCAG<br>TTGA   | 60.1                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7894501   | Ca2                                     | 7894501                       | ATT/AT                                                        | GGCTCTGGCTTTGAGT<br>TGAG | GGGGATGCTACAACCA<br>TGAC   | 60.1                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7894638   | Ca2                                     | 7894638                       | ATTTTT/ATTTTTT                                                | GTCATGGTTGTAGCAT<br>CCCC | GCCAAATGAGGTTAAT<br>GAAGGA | 60.2                             | 278                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7894801   | Ca2                                     | 7894801                       | TTTGCAATTGCA/TTTGCA                                           | GTCATGGTTGTAGCAT<br>CCCC | GATGGGGATGGAAGAT<br>GAAA   | 60.2                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7899077   | Ca2                                     | 7899077                       | TAAA/TAAATAAAA                                                | TCAGGCTCAACAACAT<br>CAGC | AGGTTTGGAAGTTTGG<br>CCTT   | 60.0                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7899449   | Ca2                                     | 7899449                       | GAAAAA/GAAAAA                                                 | AAGGCCAACTTCCAA<br>ACCT  | TGGATTGTGGGTTTGA<br>CTCC   | 60.0                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7925215   | Ca2                                     | 7925215                       | TTTTTTA/T                                                     | TTTTATGCCGCAAGA<br>ATTG  | ATACGGCCTTTGATGT<br>CGAG   | 58.8                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_792603    | Ca2                                     | 792603                        | ATTTTTTTTT/ATTTTTTTTTT                                        | TCAATGATTGCACGG<br>AGAA  | AACCAACTTCCATG<br>CCTC     | 60.2                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                  |                            |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_7932313   | Ca2                                     | 7932313                       | ATTTTTTTT/ATTTTTTT                                               | ATTTTCTTTGACGGAC<br>GGAA   | GGAGAAATTTGCCAAA<br>GGAA      | 59.5                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7933051   | Ca2                                     | 7933051                       | AC/A                                                             | CCCCAAAAAGTGCTTC<br>AAAA   | TGACAAGCACGCTTAA<br>GGAA      | 60.1                             | 694                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7933075   | Ca2                                     | 7933075                       | ATTTTATTTTTTAT/ATTTTAT                                           | CCCCAAAAAGTGCTTC<br>AAAA   | TGACAAGCACGCTTAA<br>GGAA      | 60.1                             | 694                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7940035   | Ca2                                     | 7940035                       | TA/TAA                                                           | CAACATTGACAACGGA<br>ATCG   | AAAATGGACAAAATTG<br>GAGCA     | 60.0                             | 927                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7940111   | Ca2                                     | 7940111                       | ATTTTTTT/ATTTTTTT                                                | TCTTGACCGTTAGATT<br>GAACCA | CAAAATGGACAAAATTG<br>GAGC     | 59.6                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7940136   | Ca2                                     | 7940136                       | ATTTTTTT/ATTTTTTTT                                               | TCTTGACCGTTAGATT<br>GAACCA | CAAAATGGACAAAATTG<br>GAGC     | 59.6                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7940384   | Ca2                                     | 7940384                       | CTTAATTTAAATATT/C                                                | TGACCAAAATCTTCTCT<br>TTCCA | GTGCCTCAACCATGAC<br>ACTG      | 58.8                             | 818                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7940860   | Ca2                                     | 7940860                       | ATTTTTTT/ATTTTTTTT                                               | CAGTGTCATGGTTGAG<br>GCAC   | GAAGTTGGAACGACGG<br>TGAT      | 60.2                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7949331   | Ca2                                     | 7949331                       | CAAAATAAAATAAAATAAAATA<br>AAATAA/CAAATAAAATAAAATAAAAT<br>AAAATAA | TTGCTAACTCTGTTGG<br>CCCT   | ACGAGGATCACCCAGT<br>TCAC      | 59.9                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_7966683   | Ca2                                     | 7966683                       | ATTTTTTTTTTT/ATTTTTTTTTTTT                                       | GATGTCACTCCCTGGC<br>TCAT   | TTTTCACATTTTCATGT<br>CAAATACA | 60.1                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)  | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_8029116   | Ca2                                     | 8029116                       | ATTTTTTTTT/ATTTTTTTTT                                          | AATGTATCGGGACCTC<br>ACAA  | TTTTCTTGGTGCGCTT<br>TTT     | 57.9                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_8062546   | Ca2                                     | 8062546                       | CATATATATATATATATATAT/CAT<br>ATATATATATATATAT                  | ACGGGTGCGAATTTTC<br>TATG  | CACCTCTTCTACTCCC<br>GCAC    | 60.0                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_8166930   | Ca2                                     | 8166930                       | AAATAATAATAATAATAATAATA<br>AT/AAATAATAATAATAATAATAA<br>TAATAAT | CCTAGGGATGCGACCA<br>TCTA  | TCCTCTCTTTTGGCAC<br>ATT     | 60.1                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_8308316   | Ca2                                     | 8308316                       | TAAAAAAA/TAAAAAAA                                              | AATTGGGACCATTGTA<br>TAGGC | GCCTCTACCATCTTGA<br>CAGC    | 60.0                             | 171                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_8374636   | Ca2                                     | 8374636                       | AATATATATATATATATATAT/AAT<br>ATATATATATATATATAT                | AAAGGGACAATGAAGG<br>CAAG  | TTGAAAATGTGATGTTT<br>CTTCCA | 59.2                             | 636                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_8420149   | Ca2                                     | 8420149                       | AATATATATATATATATATATATA/<br>AATATATATATATATATATATAT<br>ATA    | CACCCTTACAAGTCGC<br>CATT  | AATCGGCATTTCAACT<br>TGG     | 60.0                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_8420270   | Ca2                                     | 8420270                       | AACA/AACACA                                                    | CCAAGTTTGAAATGCC<br>GATT  | GCTGCATGATCTTATG<br>CTCG    | 59.9                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_8478800   | Ca2                                     | 8478800                       | AATTT/A                                                        | CCCGTATGAATGAACG<br>GAAC  | CTACCCCCACATTTCAA<br>TCG    | 60.2                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_8478910   | Ca2                                     | 8478910                       | ACT/A                                                          | CCCGTATGAATGAACG<br>GAAC  | CTACCCCCACATTTCAA<br>TCG    | 60.2                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_854136    | Ca2                                     | 854136                        | TAAAAAAAAA/TAAAAAAAAA                                          | CAAGTGGAACCCACCA<br>ATT   | CTTGCTGTGTGCGAAG<br>ATGA    | 59.7                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_8541841   | Ca2                                     | 8541841                       | TAAAAAAAAA/TAAAAAAAAA                                         | TTCATATCATTCAAATG<br>CCCA | ACACCTAGTTCACCCC<br>CTCC     | 58.8                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_8708914   | Ca2                                     | 8708914                       | ATTTTTTTT/ATTTTTTTT                                           | GCCCACACCGAAGAAA<br>TAAA  | TTCATTTTGCTCCATCA<br>CTTTC   | 59.9                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_8714762   | Ca2                                     | 8714762                       | TAAAAAAAAA/TAAAAAAAAA                                         | AGGATGCGCTCTTCCA<br>ACTA  | TTGAACCATGTGCGAC<br>CTAA     | 60.0                             | 222                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_8820736   | Ca2                                     | 8820736                       | ATTTTTTTTTT/ATTTTTTTTT                                        | TTACCATGATGTCGGT<br>GGTG  | GTGAGCAAATGTTTCG<br>GGAT     | 60.2                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_9233338   | Ca2                                     | 9233338                       | TAGAGAGAGAGAGAGAGAGAGA<br>GA/TAGAGAGAGAGAGAGAGAG<br>AGA       | TCGACCGAATCGTAGG<br>AAAC  | TCATTCCATCTTTCATG<br>GCA     | 60.1                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_9281281   | Ca2                                     | 9281281                       | TTATATATATATATATATATA/TTA<br>TATATATATATATATATATATATA<br>A    | CAAATTGAGGCCAAC<br>AACT   | CGAATCTTTTTGGGG<br>GATT      | 60.0                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_9408358   | Ca2                                     | 9408358                       | CTT/CTTTCTATT                                                 | CATCAAAACAGCAGC<br>GAAA   | TCGTGTCTTCTTTCCAT<br>CCA     | 60.0                             | 934                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_9427423   | Ca2                                     | 9427423                       | TAAAAAAAAA/TAAAAAAAAA                                         | AATATTGCGACAACGC<br>ATGT  | TGAAATGTTTAATTGTA<br>GGTTCGG | 59.1                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_9494071   | Ca2                                     | 9494071                       | T/TA                                                          | GAAGTGAACAACAAC<br>GACAA  | GGTCTCGAAATCCCTG<br>ATGA     | 59.8                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca2_P4_9494155   | Ca2                                     | 9494155                       | CAAA/CAAAA                                                    | GAAGTGAACAACAAC<br>GACAA  | GGTCTCGAAATCCCTG<br>ATGA     | 59.8                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                              | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                            |                           |                             |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_9500229   | Ca2                                     | 9500229                       | CGTATGCTAGACCTGG/CGTATGCT<br>AGACCTGGGTATGCTAGACCTGG                                       | AGAGTTGGGGGAGA<br>AGAAA   | GCAACAACAGCAGAGA<br>CAATG   | 60.0                             | 213                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_9594399   | Ca2                                     | 9594399                       | GTTTTTTTTTTTT/GTTTTTTTTTTTT<br>T                                                           | CAACTCAGGAATGCGT<br>GAAA  | TTCACGCCAACATTAA<br>ACG     | 59.8                             | 726                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_9690407   | Ca2                                     | 9690407                       | TAAAAAAAAAAAAA/TAAAAAAAAAAAA<br>A                                                          | TGATGCAAATATCTACC<br>GCAA | TTCAAGGGACGTAAAT<br>GCAA    | 59.2                             | 558                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_9694226   | Ca2                                     | 9694226                       | TTATATATATATATATATATATA/TTA<br>TATATATATATATATATA                                          | TGTGCGTTGTAAAGGA<br>GTGC  | CGTCGGAATCCAAAG<br>TCAT     | 59.9                             | 504                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_9709233   | Ca2                                     | 9709233                       | ATTTTTTTTTT/ATTTTTTTTTTTTT                                                                 | TTCAATGCACTTCTGAA<br>CCG  | TGTGAACACAAGAGCA<br>AGGG    | 59.8                             | 644                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_981417    | Ca2                                     | 981417                        | ACTCTCTCTCTCTCTCTCTCTCTCT<br>CTCTCTCT/ACTCTCTCTCTCTCTCT<br>CTCTCTCTCTCTCTCTCTCTCTCTCT<br>T | ACATAATCCCAACCG<br>ACCA   | CCAAAGGGGTGAGTTT<br>TTGA    | 60.1                             | 328                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_9877069   | Ca2                                     | 9877069                       | TTATATATATATATATATATATATATA<br>TATATA/TTATATATATATATATATAT<br>ATATATATATA                  | CCGACTTTCCTTCATTA<br>ACCA | GAAGCAATTTGGGATG<br>CAAT    | 59.1                             | 724                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_9922792   | Ca2                                     | 9922792                       | CAT/CATTAT                                                                                 | ATCAATGGAGCAAGGA<br>CACC  | CATGTTTGCATTCGCA<br>ACT     | 59.9                             | 636                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca2_P4_9997900   | Ca2                                     | 9997900                       | AAATAATAATAATAATAATAATAATA<br>ATAATA/AAATAATAATAATAATAATA<br>ATAATAATAATAATA               | TAAATACGCGACGACC<br>AACA  | TTTCTGTCATAAAAAGT<br>GGCACA | 60.1                             | 407                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_100899    | Ca3                                     | 100899                        | AATATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATATA<br>TATAT                        | AACAACGACGACGTG<br>ACAT   | ACGGTAAATGCATAGC<br>CACC    | 59.1                             | 746                                           | INTERGENIC                                           | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_10091088  | Ca3                                     | 10091088                      | ACCCCC/ACCCC                                                  | CCCCAAATTCACCAAT<br>TGA    | GGCGTGAACCAAAAGG<br>TAAA  | 60.5                             | 467                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_10128061  | Ca3                                     | 10128061                      | TT/TTATTATTATTAT                                              | TCCTCCCCCTTCCTCT<br>TTTA   | CACCACTCAATGCATCT<br>TGG  | 60.0                             | 274                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_10159368  | Ca3                                     | 10159368                      | GA/G                                                          | CTAGGCTCACCAACCG<br>GATA   | CTAAGGGCGCTACAAC<br>AAGC  | 60.1                             | 354                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_10159468  | Ca3                                     | 10159468                      | T/TA                                                          | TGGGGCAAACAAAGCT<br>ATTCT  | CTAAGGGCGCTACAAC<br>AAGC  | 60.1                             | 107                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_10159672  | Ca3                                     | 10159672                      | AGGGGGGG/AGGGGGGGG                                            | CACACCAACCCCTTCG<br>TTCT   | TGCTCCACACACACA<br>AACT   | 60.0                             | 277                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_10169650  | Ca3                                     | 10169650                      | GT/GTT                                                        | CAGATGGATTCCCCTC<br>TTCA   | CTCCCCGATGAGTACC<br>AGGA  | 60.0                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_10194898  | Ca3                                     | 10194898                      | ATTTTTTTTTT/ATTTTTTTTTT                                       | TGGAGAAGAGAGGAGC<br>CAAA   | CCGTTTTCTGTTTCAC<br>AATCA | 60.1                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_1038019   | Ca3                                     | 1038019                       | AAT/AATAATCAT                                                 | GGAGCAAAATGTGTTT<br>TATGGA | GGAAACGGTCTTCCCT<br>TTTT  | 59.0                             | 173                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_10406481  | Ca3                                     | 10406481                      | CTTTTTTT/CTTTTTTTTTTTTTT                                      | GGTACGCCACACATGC<br>ATAC   | TTGAAGTTGTGGCAAT<br>GGAA  | 59.9                             | 233                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_10417401  | Ca3                                     | 10417401                      | ATTTTTT/ATTTTTTT                                              | TAAGCTTGAACACGTG<br>CCTT   | TGAGAGCATTCAAGGA<br>AGCA  | 58.6                             | 222                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                             | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                           |                           |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_10570421  | Ca3                                     | 10570421                      | GATATATATATATA/GATATATATATA<br>TATA                                                                                                                       | ACCCGAATACCTCCAA<br>GGTC  | GATCTGCAGTTGCTGA<br>TGGA      | 60.2                             | 816                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_10636003  | Ca3                                     | 10636003                      | CAAAAAAAAA/CAAAAAAAAA                                                                                                                                     | AAGACCGATTGAGATG<br>CGAC  | GGGAAAACATTGGAAA<br>ACCC      | 60.2                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_10846962  | Ca3                                     | 10846962                      | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATAT<br>ATATATATATA                                                                                     | CCAAATGACGACTTCC<br>CACT  | CAAGACGTCGTCAAAA<br>TCCC      | 60.0                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_10859593  | Ca3                                     | 10859593                      | TATATA/TATATACATATA                                                                                                                                       | TGACCTTCTATTTGCG<br>ATCA  | CACGACCAACATGTCC<br>TTTG      | 58.4                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_10923237  | Ca3                                     | 10923237                      | T/TCC                                                                                                                                                     | GCTGATTGAAATCGAG<br>CACA  | TTAAACAAGCACCAAG<br>GGC       | 60.0                             | 347                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_10973797  | Ca3                                     | 10973797                      | TTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAA/TTAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAATA                                                        | TCTCCGGATCAAAATCC<br>AAAT | TCTTTCCGACTAAGATA<br>CGATGTTT | 59.3                             | 394                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11041298  | Ca3                                     | 11041298                      | AT/A                                                                                                                                                      | TCGTGTCCCAAACTC<br>AAGG   | TTAAGTTGGTTTGGGC<br>TTGG      | 61.1                             | 830                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11044475  | Ca3                                     | 11044475                      | CAAAAAAAAA/CAAAAAAAAA                                                                                                                                     | GCATCCATCCAACGA<br>CTTT   | CATTACATCTTATTTGA<br>GGGAGAGC | 59.9                             | 286                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11104695  | Ca3                                     | 11104695                      | GTTTTTTTT/GTTTTTTTT                                                                                                                                       | TGTGGGGCTTAGAGCT<br>TTGT  | AAACTTGAGTTCCCACT<br>CATCC    | 59.9                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11213656  | Ca3                                     | 11213656                      | GTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAA/GTAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATAA<br>ATAATAATAATAA | CTCAATCCTTCAACCCT<br>CCA  | CGTTAACCAAGAAGTG<br>GGGA      | 60.0                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                                           | Forward primers (5'-3')       | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                                                         |                               |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_11247051  | Ca3                                     | 11247051                      | AAAATAAATAAATAAATAAATA/AAAA<br>TAAATAAATAAATAAATAAATA                                                                                                                                   | CTGGGGATACGTAGGA<br>GCAA      | TCCCTTAAACGGCTA<br>CCCT  | 60.1                             | 180                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11307149  | Ca3                                     | 11307149                      | TTATATATATATATATAT/TTATATAT<br>ATATATATATAT                                                                                                                                             | GTGGTACTGGAGGCCA<br>CATT      | CCAAAATGCCCCCTTTT<br>ATT | 59.9                             | 792                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11315222  | Ca3                                     | 11315222                      | TTATATATATATATATATATATATATA<br>TATATATAT/TATATATATATATATAT<br>ATATATATATATATATATATAT                                                                                                    | CTCATGATCGGGAAAA<br>TGGT      | GTTGAGAGGCATGAAG<br>AGGC | 59.8                             | 217                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11462251  | Ca3                                     | 11462251                      | ATTTTTTTTT/ATTTTTTTTT                                                                                                                                                                   | ATGATTCCCAACATC<br>CAAA       | CACGAGTCCGATAAGG<br>GTGT | 60.0                             | 149                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_1149110   | Ca3                                     | 1149110                       | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                                                                                                                                           | TGTGCAATCGTTTTAAC<br>CCA      | TGAGGGGTAATTTGAA<br>CCGA | 60.0                             | 272                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11497481  | Ca3                                     | 11497481                      | ATTATTTATTTATTTATTTATTTATTT<br>ATGTATTTATGTATTTATGTATTTAT<br>TTATTCATTTATTTATTTATTTATTTAT<br>TTATTTATTTATTTATTTATTTATTTA<br>TGTATTTATGTATTTATGTATTTATTT<br>ATTCATTTATTTATTTATTTATTTATTT | GGGTTTGCACCTTGAAG<br>GTGT     | CCTCCGAGCCAAAATA<br>CAAA | 60.0                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11519916  | Ca3                                     | 11519916                      | AT/ACAGACTTATACTGTTTT                                                                                                                                                                   | CCGAGCCAAAATCCAA<br>AATA      | AATTTCAAACGCAAACC<br>AGG | 59.9                             | 198                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11521142  | Ca3                                     | 11521142                      | TAAA/TAA                                                                                                                                                                                | TCCATCGTACGGGAG<br>ATAC       | TCGATTATGCGTAGGG<br>AAGG | 59.8                             | 235                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11537812  | Ca3                                     | 11537812                      | CTTTTTTT/CTTTTTTTT                                                                                                                                                                      | GATGCAACATCTTTTGA<br>ATCTTTGA | CCTACGTATCTCTGG<br>TGCG  | 58.8                             | 688                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11628961  | Ca3                                     | 11628961                      | TTATA/TTATATA                                                                                                                                                                           | CTCTTCCTTCACGTAG<br>GCCA      | TGGAACCAATGCTTGT<br>TGAA | 60.4                             | 800                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                 |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_11649200  | Ca3                                     | 11649200                      | TAAAAA/TAAAAA                                                                                   | ATTCATCGCTGTCTTC<br>CACC | GGTCCCTTAGCTTAATT<br>TCCG | 60.1                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11889131  | Ca3                                     | 11889131                      | GTTT/GTTTTT                                                                                     | AGGTTGGCAACATTCA<br>GGTC | AGGAGGAGCAAAAGCA<br>ACAA  | 60.0                             | 263                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11919605  | Ca3                                     | 11919605                      | GAA/GA                                                                                          | CGGAAATTGAAATCGG<br>AAAA | ATCGCGAAAGTAGTCT<br>CCCA  | 59.9                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11919676  | Ca3                                     | 11919676                      | CNNNNNNNNNNNNNNNNN/CN<br>NNNNNNNN                                                               | CGGAAATTGAAATCGG<br>AAAA | ATCGCGAAAGTAGTCT<br>CCCA  | 59.9                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_11991649  | Ca3                                     | 11991649                      | CTTTTTTTTT/CTTTTTTTTT                                                                           | TTTCCCGACTTGGTCC<br>TTTA | TCATCAAATTCGTAACG<br>CAAA | 59.5                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_12051620  | Ca3                                     | 12051620                      | GATATATATATATATATAT/GATAT<br>ATATATATATATATATAT                                                 | GCAAAAGGGAATGGAT<br>CAAA | CAGGACCTTTCATGGG<br>AAAA  | 59.9                             | 202                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_1206045   | Ca3                                     | 1206045                       | C/CTTT                                                                                          | GGCCGCCACAAAATAT<br>TAAC | TTTGAATTGGGGAGAG<br>ATGG  | 59.3                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_12167077  | Ca3                                     | 12167077                      | GGTTCGCAGAAA/GGTTGCAGAAA<br>GTTTCGCAGAAA                                                        | AACATGGAGCTGTTTG<br>GGTC | TTTCCACGATCATCTCC<br>CTC  | 60.0                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_12255918  | Ca3                                     | 12255918                      | TTATATATATATATATATATATATA<br>TATATATATATATATA/TTATATATAT<br>ATATATATATATATATATATATA<br>TATATATA | TTTCACCGCAATGCAA<br>ATAA | TCCAAACAAACCCTTC<br>GTATT | 60.1                             | 246                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_12288956  | Ca3                                     | 12288956                      | TAAAAAAAAA/TAAAAAAAAA                                                                           | TAGCAGGTGCATTGG<br>TGTA  | GTCGCACAAGGCTACA<br>GTCA  | 60.1                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)    | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                   |                          |                            |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_12392107  | Ca3                                     | 12392107                      | TAT/TATCAT                                                        | AAGGAATCATTGTCCC<br>TCCC | CCTCATCATTACCTT<br>GGCA    | 60.1                             | 419                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_12426718  | Ca3                                     | 12426718                      | AAAACCAA/AAAACCAAACCAA                                            | GTTGTGTGTTTTCCA<br>TCCC  | TTCCTAGAGGGCCAT<br>CGTT    | 60.1                             | 528                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_12659757  | Ca3                                     | 12659757                      | CATATATATATATATATATATATA<br>TAT/CATATATATATATATATATAT<br>ATATATAT | TATTTGGATTTTGCT<br>CGG   | CACCGTAGTGTGGTGG<br>TGAG   | 59.9                             | 672                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_12715466  | Ca3                                     | 12715466                      | T/TACACATTAAAG                                                    | TATCCCCGATTAATGCA<br>GCC | GTCCCGAATGCAATGT<br>CTCT   | 59.9                             | 667                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_12911294  | Ca3                                     | 12911294                      | C/CCT                                                             | TATCGAGTGTTCGG<br>TTCC   | CAGGTTCACGTGAGCA<br>AGAA   | 59.9                             | 337                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_12969818  | Ca3                                     | 12969818                      | TAAAAAA/TAAAAAA                                                   | TTACACCAATCCCCC<br>AAGA  | CATGCAAGGTTGGGCT<br>AGAT   | 60.2                             | 400                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_13096897  | Ca3                                     | 13096897                      | TCT/TCTGGAAT                                                      | TCTGGTCGACTTCTGC<br>CTTT | TCATCAGTATCGTGGG<br>TGGA   | 60.0                             | 775                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_13097036  | Ca3                                     | 13097036                      | A/AAT                                                             | CCTTCTTACGGGACC<br>CAAT  | TCATCAGTATCGTGGG<br>TGGA   | 60.2                             | 364                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_13169603  | Ca3                                     | 13169603                      | ATT/ATTTTTTT                                                      | TAGCTGGCAGGGTCTC<br>AGTT | CGAAAGAAAGTTTCCC<br>CTCC   | 60.0                             | 419                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_13236644  | Ca3                                     | 13236644                      | AATATATATATATATATATAT/AAT<br>ATATATATATATATATATATAT               | AAGACCTGTGGGATCA<br>TTGC | TTTTGTGATAGGTTCTT<br>GATGC | 59.9                             | 928                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_13359074  | Ca3                                     | 13359074                      | TAAAAAAAAA/TAAAAAAAAA                                         | AGTGATGCAATCTTCC<br>ACCC   | ACGAGGATGCGATCTC<br>CTAA    | 59.9                             | 847                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_13364914  | Ca3                                     | 13364914                      | GT/GTTGCT                                                     | AAACCCCTAACGCACAG<br>ATGG  | CGTTCTCATATGGTAG<br>AAAAGGC | 60.0                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_13417490  | Ca3                                     | 13417490                      | TAAAAAAAAA/TAAAAAAAAA                                         | TGGGAATAGGTCAGGC<br>TTTG   | TGCACGAGAGGATTG<br>TTTG     | 60.1                             | 339                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_13647076  | Ca3                                     | 13647076                      | AATATATATATATATATAT/AAAT<br>ATATATATATATATATAT                | TTGCACCTTATTTGATG<br>CGT   | TCTCTCTCATGCCAC<br>CCT      | 59.2                             | 183                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_13647375  | Ca3                                     | 13647375                      | AAGAGAGAGAGAGAGAGAGAGA<br>/AAGAGAGAGAGAGAGAGAGAG<br>AGA       | AGGGTGGCATGAGAGA<br>GAGA   | TCATAATGGTGTGTTG<br>ATTGTC  | 59.9                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_13732656  | Ca3                                     | 13732656                      | TTATATATATATATATATATATA<br>/TTATATATATATATATATATATA           | GGACTCGCAATTTATT<br>TAGGAA | TGAGAATTGCAGAAAA<br>AGCA    | 58.7                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_13802266  | Ca3                                     | 13802266                      | TAAAAAAAAA/TAAAAA                                             | TGATAAAGCTCTCAA<br>CAGCAGA | GAATTCCGATCAGATT<br>GACA    | 59.3                             | 830                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_13899750  | Ca3                                     | 13899750                      | CTTTT/CTTTT                                                   | CTAGCCCAAGCACGCT<br>TAAC   | GATCCCATTAGAATC<br>CGCA     | 60.0                             | 345                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_1390976   | Ca3                                     | 1390976                       | TAAAAAAAAA/TAAAAAAAAA                                         | AGTGGCACTGCACCT<br>TTTT    | CCAACTTGGTCCACC<br>AATC     | 59.8                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_13935710  | Ca3                                     | 13935710                      | GAT/GATAAT                                                    | CAGTACCCCTTTGGAG<br>CTTG   | ATTTTCGGGCAATTTCA<br>CTG    | 59.7                             | 127                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)                            | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                           |                           |                          |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_13996887  | Ca3                                     | 13996887                      | TTATATATATATATATATATATATAT/T<br>TTATATATATATATATATATATATATA<br>T                          | TTCCTTCGATGGTCAT<br>TGTC  | GCATAGTGCAACACCC<br>CTCT | 59.7                             | 431                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_14018560  | Ca3                                     | 14018560                      | CTTTTTTTTT/CTTTTTTTTTTT                                                                   | AGGGCAATCACGAGAT<br>TTTG  | CACGACTTGAGTGGTC<br>CAAG | 60.1                             | 635                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_14072375  | Ca3                                     | 14072375                      | TTATATATATATATATATATATATATA<br>T/TTATATATATATATATATATATATA<br>TATATAT                     | TTACCCCCATGCCATC<br>TAAT  | TTCTCCTGAAGCTGTC<br>GGT  | 60.2                             | 417                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_14138350  | Ca3                                     | 14138350                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATT/TTTATTATTATTA<br>TTATTATTATTATTATTATTATTA        | TCGCACATCTACTCAA<br>ACACG | ATAGATGATCGCATAC<br>CGGG | 59.9                             | 557                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_14205152  | Ca3                                     | 14205152                      | AATATATATATATATATA/AATATATA<br>TATATATATATA                                               | ACGGAACACAACCTTT<br>GGAG  | TGCTGCCTCTCATTCTC<br>ACA | 60.0                             | 452                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_14232110  | Ca3                                     | 14232110                      | GAAAAAAAA/GAAAAAAAAA                                                                      | TCCGTAACGCAAATTT<br>CAA   | TCAAACCTTGTGCCTG<br>AGTG | 59.2                             | 312                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_14428244  | Ca3                                     | 14428244                      | CTTT/CTTTT                                                                                | TGATTTGTGTTGGTTG<br>TTGCT | CCATAGCAGCTAGACG<br>GTCC | 59.1                             | 434                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_14429203  | Ca3                                     | 14429203                      | ATTTTTTTTT/ATTTTTTTTTT                                                                    | TGCGATGTTATCCAAA<br>ACCA  | TGCAAATATCAATTGG<br>GGGT | 59.9                             | 610                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_14441213  | Ca3                                     | 14441213                      | AATAATAATAATAATAATAATAA<br>TAATAATAAT/AATAATAAATGATA<br>ATAATAATAATAATAATAATAAT<br>AATAAT | CGGCATACAAATAACA<br>TGCG  | TGTTTGTGTTGGTGC<br>CATT  | 60.0                             | 626                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_1446842   | Ca3                                     | 1446842                       | GCC/GCACC                                                                                 | TTGAAACATTGAAGTA<br>TCCGC | TGCATTGAGGAATTC<br>ACG   | 59.1                             | 488                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')       | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|-------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                       |                               |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_14574960  | Ca3                                     | 14574960                      | CA/C                                                                  | GTTTGGTAGGTGACAG<br>GATCA     | TGTTGTGGAGTTCTAG<br>GGGC | 59.8                             | 457                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_14615841  | Ca3                                     | 14615841                      | CAAAAAACAAA/CAAAAAACAAAAA<br>ACAAA                                    | AAGACAACCATGCCTT<br>TTGG      | GGGTTGGGCTATCAAA<br>TCAA | 60.0                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_14686306  | Ca3                                     | 14686306                      | T/TC                                                                  | ATTGCATTAGGGTGTT<br>TGGC      | CCCCGTGAGATCTTCC<br>TACA | 59.8                             | 835                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_14703766  | Ca3                                     | 14703766                      | TATTCA/T                                                              | GGTCTTCAGGTTCAAT<br>CCCA      | CCACCAGGAAAAGAAG<br>GACA | 59.9                             | 821                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_14843003  | Ca3                                     | 14843003                      | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATAT<br>ATATATATATA | GAGAAAGAAGATATCG<br>GATTCTCAA | AAAAATCAACGCAGTG<br>GGAG | 59.3                             | 356                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_14874833  | Ca3                                     | 14874833                      | GCC/GCCC                                                              | AGGTCATTTTCGTCCT<br>CCCT      | CAACACACCTGTTGG<br>ATGC  | 59.9                             | 679                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_14880871  | Ca3                                     | 14880871                      | TG/TGTCG                                                              | TTTCGGTCATTTTCGTC<br>CTC      | ACACACCTATCGGATG<br>CACA | 60.1                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_1488532   | Ca3                                     | 1488532                       | TTATATATATATATATATATATA/TTA<br>TATATATATATATATATA                     | TCCAAACACCTTCACC<br>ATGA      | CTGATCAGTGCTGTGG<br>CATT | 59.9                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_14902851  | Ca3                                     | 14902851                      | GAA/GAAA                                                              | CGGTGGGGAGAACTCT<br>GATA      | TTCACATGACATCATCC<br>CGT | 60.1                             | 474                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_14919264  | Ca3                                     | 14919264                      | GTTT/GTTTT                                                            | CGATTGTGTTTGTCAC<br>AGGG      | GAAGCAAATCGATTGG<br>GAAA | 60.0                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_15038933  | Ca3                                     | 15038933                      | TG/T                                                          | CAACACGATCATGACA<br>AGCA | CCAAAGATCCCTACCA<br>ATACCA | 59.2                             | 131                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_15039270  | Ca3                                     | 15039270                      | TC/T                                                          | CAACACGATCATGACA<br>AGCA | GCATTTTGCATTGTGCA<br>ACG   | 59.2                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_15047295  | Ca3                                     | 15047295                      | TA/T                                                          | TACTTTGTGCCATGCT<br>CTGC | ACACAAGCCAACACAT<br>CCAA   | 60.0                             | 117                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_15095814  | Ca3                                     | 15095814                      | GAAAAAAAAA/GAAAAAAAAA                                         | TTGGTGCAAGCCACAA<br>ATAA | ATGATGGTGGTGATGG<br>AGGT   | 60.1                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_1533357   | Ca3                                     | 1533357                       | TCAAAA/TCAAAACTCAAAA                                          | ACCCAAAAGCTAACTT<br>GCCA | GCATCAACAAAGCAGC<br>AGAA   | 59.7                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_1534003   | Ca3                                     | 1534003                       | AACTGCAACTAACT/AACTGCAAC<br>TAACTGCAACTAACT                   | TTCTGCTGCTTTGTTG<br>ATGC | GTGGATGGGTGTTTTT<br>CATC   | 60.1                             | 774                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_15374725  | Ca3                                     | 15374725                      | ATTTTTTTTT/ATTTTTTTTT                                         | TTTGAAAGACCTGCAA<br>ACCC | GCGTAATTCCAATGATT<br>GCC   | 60.1                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_15660475  | Ca3                                     | 15660475                      | TA/TAA                                                        | AAGTGAGCTAACGGGG<br>GTTT | TGGACAGAGCAAGTGA<br>GGTG   | 60.0                             | 140                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_15660692  | Ca3                                     | 15660692                      | ATT/AT                                                        | AAGTGAGCTAACGGGG<br>GTTT | TGGGGTTGTCAGGAGA<br>AGAC   | 60.0                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_15844609  | Ca3                                     | 15844609                      | C/CTAGG                                                       | ATGGGTAGTAAGCCCC<br>GTCT | TCTTTCCAAAGGATGG<br>ATGG   | 59.8                             | 831                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                         | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                       |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_15868825  | Ca3                                     | 15868825                      | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTAT/ATATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTAT | AATCGTGCCTTTTGC<br>TTTT     | AGGATTCTCAGTGCAA<br>AGCG   | 59.8                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_16078474  | Ca3                                     | 16078474                      | ATTTTTTTTT/ATTTTTTTTT                                                                                                                 | TGAAGTCCCGTTACAA<br>TAAACC  | TTTGCTTTTGGATGAAA<br>CCC   | 59.3                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_16108101  | Ca3                                     | 16108101                      | TAAAAAAAAA/TAAAAAAAAA                                                                                                                 | AAAACAGGGCAAGAAA<br>GCAA    | AACAGCAAAAGAGAAG<br>GCGA   | 59.9                             | 292                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_16133157  | Ca3                                     | 16133157                      | GTTTTATTTATTTTATTT/GTTTTAT<br>TTTATTTTATTTTATTT                                                                                       | CGTCTCTGAAGCGAT<br>GAAA     | CATTGTTGGTCACTAG<br>CAATCA | 59.1                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_16133384  | Ca3                                     | 16133384                      | CAATAATAATAATAATAATAATA<br>ATAATAATAATA/CAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>A                                                   | CGTCTCTGAAGCGAT<br>GAAA     | ATAAGCCGTCATCTG<br>CCAC    | 59.1                             | 807                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_16133499  | Ca3                                     | 16133499                      | TA/TACACAAAGAA                                                                                                                        | TTTGCCCCATTATAAAC<br>AAAA   | ATAAGCCGTCATCTG<br>CCAC    | 57.2                             | 625                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_16137267  | Ca3                                     | 16137267                      | CATATATATATATATATATA/CATATA<br>TATATATATATATATA                                                                                       | TGGCACATCTAAAAATA<br>GGAGGA | AGAAAATCGCATCCCA<br>GAGA   | 60.0                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_16166714  | Ca3                                     | 16166714                      | TTTTG/TTGCTTTG                                                                                                                        | TCAACCATCTGGGTTG<br>GAAT    | CCCCTAGCAAAGGAAA<br>CAAA   | 60.2                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_16171083  | Ca3                                     | 16171083                      | T/TG                                                                                                                                  | TACAGCGCTTCATTCC<br>ACAG    | CGTGCATGAGCAAAAG<br>AAAA   | 60.0                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_16182804  | Ca3                                     | 16182804                      | ATTTTTTTTT/ATTTTTTTTT                                                                                                                 | CCGGCATCACCTATCA<br>GAGT    | TCCGACCTCCTTTGAG<br>AAGA   | 60.1                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)  | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                |                               |                           |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_16190775  | Ca3                                     | 16190775                      | CA/C                                                           | TCGCGGTTCTTGATGA<br>TGTA      | AGCTCGACTTATCCTTC<br>GCA  | 60.2                             | 423                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_16195131  | Ca3                                     | 16195131                      | AT/ATT                                                         | TGATAAAAGACTAACG<br>ATGCAAACA | TAAACCATCAATCTGCC<br>ACG  | 60.1                             | 655                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_16195709  | Ca3                                     | 16195709                      | AC/A                                                           | ACGTGGCAGATTGATG<br>GTTT      | GAACGTACGGAAGAGA<br>AGCG  | 60.4                             | 754                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_16212096  | Ca3                                     | 16212096                      | TAA/TAAA                                                       | AATGCACTTTGCCACT<br>GTTG      | CCAAGATTTTGCCAGA<br>TCAA  | 59.8                             | 550                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_16212378  | Ca3                                     | 16212378                      | A/AACATTC                                                      | ATGCACTTTGCCACTG<br>TTGT      | GAGGGGATGATGCTTC<br>AAAA  | 59.2                             | 879                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_16251959  | Ca3                                     | 16251959                      | ATTCA/ATTCAGTTTCA                                              | TTAATGAGGGGCTGAA<br>TTGG      | AAGCGTACCTGTGGGA<br>ATTG  | 59.9                             | 253                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_1632200   | Ca3                                     | 1632200                       | GATATATATATATATATATATATAT<br>T/GATATATATATATATATATATAT<br>ATAT | GCGACCTTCTATTGAC<br>CTCG      | CCCATTGTTTGTGTTT<br>CTTCC | 59.8                             | 363                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_16441388  | Ca3                                     | 16441388                      | GAAA/GAAAA                                                     | CGCTCGATAACCCAA<br>AATA       | ATGTCTCGTCATTCGG<br>GAAG  | 59.9                             | 441                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_16448740  | Ca3                                     | 16448740                      | TATT/TATTATTATTATTATCATT                                       | GAGGACATTGACGGGA<br>GAGA      | CTTCTTTGTGCGTCCA<br>CTGA  | 60.2                             | 568                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_16471674  | Ca3                                     | 16471674                      | CA/CAA                                                         | GTGAGGACTGGACGTA<br>ACCC      | TCCTTGCGGAGTTGTT<br>CTTT  | 59.4                             | 505                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                       | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                     |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_16476513  | Ca3                                     | 16476513                      | TNNNNNNNNNN/TNNN                                                                    | GGCTCACATGTGGAGG<br>CTAT    | CCAATGCCATACCATA<br>GAGGA  | 60.1                             | 344                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_1653851   | Ca3                                     | 1653851                       | TTTATTATTATTATTATTATTATT<br>ATTATTATT/TTTATTATTATTATTAT<br>TATTATTATTATTATTATTATT   | TTTCTAGGGTGCGACC<br>ATGT    | ACGCGTTTGGGTAGAT<br>ATGC   | 60.5                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_16544552  | Ca3                                     | 16544552                      | GTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTA/GTTATTATTA<br>TTATTATTATTATTATTATTATTA | TGCTCGACATGTTTCT<br>CCTT    | CCACACAAACTGACAA<br>CTCCA  | 58.4                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_16548843  | Ca3                                     | 16548843                      | TAAAAAAAAAAAAAAAA/TAAAAAAAA<br>AAA                                                  | TAGCCCTCCCAATCAT<br>TTTG    | CTTTAGGGGTTTTGAT<br>CGCA   | 59.9                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_16674646  | Ca3                                     | 16674646                      | ATTTT/ATTTT                                                                         | GGAGTGGAGCTGATCA<br>GAGG    | GGCCACAAAGTTTGA<br>AAAA    | 59.9                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_16793468  | Ca3                                     | 16793468                      | TTATA/TTATATA                                                                       | TAATCAAATGCCCCCA<br>ATGT    | TTGAGTTCAAGCGTGA<br>GTGG   | 60.0                             | 851                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_1685924   | Ca3                                     | 1685924                       | TTATATATATATATATATATATATA<br>TA/TTATATATATATATATATATAT<br>ATATATATATA               | CTCGCTCTCCTATATC<br>CCCC    | GGGTGAAAAATTAACC<br>AAACCA | 60.0                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_17033658  | Ca3                                     | 17033658                      | ATT/AT                                                                              | ATGCGATCATGTGGAT<br>GAGA    | TGGCTAATGCAGTTCA<br>CACA   | 60.0                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_17039245  | Ca3                                     | 17039245                      | CAAAAA/CAAAAAA                                                                      | TTCTAACTTTGCTGTCC<br>CATTTT | GGGGTAAAACCAGGAG<br>GAAG   | 59.2                             | 750                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_17039468  | Ca3                                     | 17039468                      | C/CA                                                                                | TGTTTTGAGGACAAAT<br>GTTTTGA | GGGGTAAAACCAGGAG<br>GAAG   | 59.5                             | 301                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                 |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_17135834  | Ca3                                     | 17135834                      | TCTC/TCTCTTCCCTC                                                                | CAACGCGCTTTAGAT<br>GAGA    | AAAGCTTTGAAGCAGG<br>GTCA  | 59.2                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_1719359   | Ca3                                     | 1719359                       | ATCT/AT                                                                         | TTTCCCTCCAAACACA<br>CACA   | CTTTTGATGCCCCGATT<br>AAA  | 60.0                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_17217773  | Ca3                                     | 17217773                      | TCC/TC                                                                          | ACAATCGGACACCGTT<br>TCAT   | TCATGTGGCAACACTG<br>TTCA  | 60.2                             | 253                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_17284618  | Ca3                                     | 17284618                      | TTATATATATATATATAT/TTATAT<br>ATATATATAT                                         | CCCTTCAAACTCCCA<br>AACA    | TCTTCTTCTCACCAAG<br>TCCAA | 59.9                             | 369                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_173424    | Ca3                                     | 173424                        | TAAAAAAAAAAAAA/TAAAAAAAAAAA<br>A                                                | GAGAGCGACAACACTG<br>TCAAA  | GTGGGAGGCGTGTGT<br>TATT   | 59.1                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_17413597  | Ca3                                     | 17413597                      | TTTAATTAATTA/TTTAATTA                                                           | AAGTTGGTTCGTCCAC<br>CAAG   | GAAATCGGAGAGAGGA<br>AATCG | 60.0                             | 830                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_17447451  | Ca3                                     | 17447451                      | TAAAAAAA/TAAAAAAA                                                               | TTGAGGCCGAGATTAC<br>AAAAA  | GGACAAAGGTGCAAGC<br>TCTC  | 59.7                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_17491839  | Ca3                                     | 17491839                      | AATATATATATATATA/AATATATATA<br>TATA                                             | TGAATTCATGGCTAAAA<br>AGCCT | GCAAAGATGATAATTC<br>GGCAA | 60.1                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_17706970  | Ca3                                     | 17706970                      | AATTATTATTATTATTATTATTAT<br>TATTATTATTA/AATTATTATTATTAT<br>TATTATTATTATTATTATTA | ACGGAAGCAGATGGTA<br>GTGG   | ATTTTAACAGATGGCC<br>GCAT  | 60.1                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_17712986  | Ca3                                     | 17712986                      | T/TA                                                                            | TGCAACAACTTTAGATT<br>CGGA  | ATGGAGATAATCGACG<br>TGCC  | 58.4                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |





| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_19269160  | Ca3                                     | 19269160                      | GT/GTT                                                        | CAATTGCAATGTTGTT<br>GCC   | CCGTCGTTTTGCAGTA<br>TTTG | 60.0                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19269186  | Ca3                                     | 19269186                      | CAAAAAAAAA/CAAAAAAAAA                                         | CAATTGCAATGTTGTT<br>GCC   | CCGTCGTTTTGCAGTA<br>TTTG | 60.0                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19299532  | Ca3                                     | 19299532                      | ATTTTTTTTT/ATTTTTTTTT                                         | CGCATTACAACATAAA<br>GGACG | TGTGCTCCACCTTTCA<br>TCA  | 59.6                             | 936                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19359038  | Ca3                                     | 19359038                      | TAAAA/TAAA                                                    | CGTCTTTGTTCAATCC<br>CAC   | TGAGGGCCTTTAGAAT<br>CGTG | 60.4                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19359334  | Ca3                                     | 19359334                      | CCA/C                                                         | AGGGAAATCAACGACA<br>GAGC  | TGAGGGCCTTTAGAAT<br>CGTG | 59.3                             | 365                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19362553  | Ca3                                     | 19362553                      | TAAAA/TAAAA                                                   | CCAAATGATGTTGCA<br>GGGT   | TCATCATCATTGAAAT<br>CCGT | 60.8                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19369520  | Ca3                                     | 19369520                      | TAAAAAAAA/TAAAAA                                              | AGATGTTGGCGCAGAT<br>TCTT  | CAGCAATGTTTTGTT<br>GTGG  | 59.8                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19373696  | Ca3                                     | 19373696                      | TAA/TA                                                        | GCTGAATGCGTGAAGA<br>ACAA  | GGGTAGAAAACACGCG<br>GAAT | 60.0                             | 339                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19375049  | Ca3                                     | 19375049                      | AAAAGAAA/AAAAGAAAGAAA                                         | TCTCCGTTCCATTACA<br>CGA   | AACTCCAAATCCCTGCT<br>CAA | 59.1                             | 365                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19375109  | Ca3                                     | 19375109                      | GAGAAGAAGAAGAAGA/GAGAG<br>AGAGAGAGAAGAAGAAGAAGA<br>AGA        | TCTCCGTTCCATTACA<br>CGA   | AACTCCAAATCCCTGCT<br>CAA | 59.1                             | 365                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_19376077  | Ca3                                     | 19376077                      | A/ATTT                                                        | TGACCTTGTGCATTGT<br>TTTGA  | GCAAACCTCAACCTTGC<br>CAAT      | 60.1                             | 333                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19380131  | Ca3                                     | 19380131                      | TG/T                                                          | TTGGAGAGAATACTCC<br>CCGT   | TGACGATCAGGAACAC<br>CAAA       | 59.9                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19381557  | Ca3                                     | 19381557                      | GTTATTATTAT/GTTATTATTATTAT                                    | GGAGAAAAGCATCGAA<br>AAGC   | ACCTAACCTCCAAGC<br>CAGT        | 59.0                             | 338                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19382845  | Ca3                                     | 19382845                      | TTT/TTTATT                                                    | TAGGGGCATATGGTCT<br>CGTC   | ACCACATGATGCTCTC<br>CACA       | 59.9                             | 782                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19403411  | Ca3                                     | 19403411                      | TG/TTCGGGG                                                    | AGGGTAATCCGCCAGT<br>CTTT   | GCAACATTGCTCCTCT<br>CCAT       | 60.0                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19496769  | Ca3                                     | 19496769                      | CTATAT/CTATATGTATATATATATAT<br>AT                             | CGGAAAATAAGTTAAG<br>GGACCA | AAAATACATCAAAAGTT<br>CATCATTCG | 59.4                             | 383                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_1955332   | Ca3                                     | 1955332                       | CAAA/CAA                                                      | TCATGGTTCTTTTCGAA<br>GTGG  | CACCCACTCATCCTTCA<br>CAA       | 60.1                             | 930                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19557962  | Ca3                                     | 19557962                      | AC/A                                                          | TCGGTAACCAATCCGA<br>AGAC   | ATTACCGATGCGTAA<br>ATCG        | 59.9                             | 225                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19560633  | Ca3                                     | 19560633                      | TAAAAAAAA/TAAAAAAAAA                                          | TCAGTGCGATGGAGAA<br>ATCA   | TGACATTTTAAACCTTG<br>AGTTGC    | 60.4                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19626677  | Ca3                                     | 19626677                      | GATATATATATATATATATATA/GA<br>TATATATATATATATATATATA           | TTCCCCATGCAAGGTT<br>AGAC   | TCATCGCAGGTGTACC<br>ATGT       | 59.9                             | 797                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                  | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                |                           |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_1964709   | Ca3                                     | 1964709                       | A/AT                                                                           | TCTCTTTTCTCGAACC<br>GCAT  | AAACGCAATCCTTGAG<br>TTCG      | 60.0                             | 317                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19676099  | Ca3                                     | 19676099                      | GTTTTTTTTTTT/GTTTTTTTTTTTTT                                                    | CAAACCCAAGCCATCT<br>TCAT  | TAAACTTTTGGCGGTT<br>TGG       | 59.9                             | 380                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19790164  | Ca3                                     | 19790164                      | TTATATATATATATATATATATATA<br>TA/TTATATATATATATATATATAT<br>ATATATA              | GATGGAAGTGTTGAGC<br>CTCC  | AATTTAAGCGGTGGCA<br>AATG      | 59.7                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_19960902  | Ca3                                     | 19960902                      | TAAAAAAAAAAAA/TAAAAAAAAAAAA                                                    | AGCTTTGATTCTCCAT<br>CGC   | GGTATTAGCACCCCTAC<br>GGCA     | 59.4                             | 243                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_20052639  | Ca3                                     | 20052639                      | AATTATTATTATTATTATTATTAT<br>TATTATTATTATTAT/AATTATTATTA<br>TTATTATTATTATTATTAT | ATCGTGTGCAAAGGAA<br>GGAT  | TGTGCTCAAATAAATAA<br>CGTGTCTC | 59.6                             | 856                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_20074437  | Ca3                                     | 20074437                      | CTTTTTTTTT/CTTTTTTTTT                                                          | CAAATACATGTGCCAC<br>ACAAA | TTTAACCAAATTGTGCA<br>AGGAA    | 58.0                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_20159047  | Ca3                                     | 20159047                      | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATAT<br>ATATATATATATA        | GATTGTTTATGCGCAA<br>GGGT  | TGCTTATCCCCTCCTT<br>CCT       | 60.0                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_20315844  | Ca3                                     | 20315844                      | ATTTTTT/ATTTTTTT                                                               | CGCAAACACACTTGAA<br>CTGC  | AAAGCATGTCACCAAT<br>AAGCA     | 60.5                             | 184                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_20339565  | Ca3                                     | 20339565                      | TAA/TAAA                                                                       | GGCAAAATGAATTCC<br>CTCA   | AAACGCAATCCTTGAG<br>TTCG      | 59.9                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_20349202  | Ca3                                     | 20349202                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATAT                              | ACTGCCTAGCTCACTT<br>CCCA  | GGCGATTTTCATCGTG<br>AGTT      | 60.0                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                             | Forward primers (5'-3')        | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------|--------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                           |                                |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_20378345  | Ca3                                     | 20378345                      | CAGAGA/CAGA                                                                                                               | AGGTCAATGCCTCTTC<br>TCCA       | ACCTCATGAGTTGGAA<br>ACGG     | 59.8                             | 226                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_20390519  | Ca3                                     | 20390519                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT/<br>TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTAT              | CAATGGCACAAAGATG<br>GAAA       | CAGAAATTCACATGAA<br>CCCAA    | 59.5                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_20424638  | Ca3                                     | 20424638                      | CAAAAAAAAA/CAAAAAAAAA                                                                                                     | TACATTGGTTTGTGCG<br>ATGC       | TGACTATGGGAGGTCA<br>GGAAA    | 60.5                             | 636                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_20709467  | Ca3                                     | 20709467                      | CATATATATATATATATATATATA<br>T/CATATATATATATATATATATA<br>TATATA                                                            | ATGGGCTTGGTAGGGA<br>CTTT       | CAATCCAAGCATGCAA<br>TCC      | 59.8                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_20940933  | Ca3                                     | 20940933                      | GATATATATATATATATATATATA/<br>GATATATATATATATATATATATA<br>TA                                                               | TTTTGTCACCTTGATACA<br>GCAAAA   | TGAGCATTTAAAGCC<br>CTGC      | 57.6                             | 798                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_20993915  | Ca3                                     | 20993915                      | AATATATATATATATATATATATAT<br>ATAAATATATATATATATATATA/A<br>ATATATATATATATATATATATATA<br>TATATATATAAATATATATATATAT<br>ATATA | GATTTCACGTGTTGCC<br>GTAG       | TCCGTTCTGTTTTATTT<br>CCAA    | 59.2                             | 298                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_21028328  | Ca3                                     | 21028328                      | CAAAAAAAAA/CAAAAAAAAA                                                                                                     | TGTCGTAGAAACATTT<br>GTGGG      | AGCATTCCTCGAAGAT<br>ACACG    | 58.5                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_21088951  | Ca3                                     | 21088951                      | TTATATATATATATATATA/TTATATA<br>TATATATATATATA                                                                             | AAGCGATGACATAAGA<br>ACAAC TACC | AAACGTGTATGCACAA<br>GCCA     | 60.0                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_21092785  | Ca3                                     | 21092785                      | CATATATATATATATATATATATA<br>T/CATATATATATATATATATATAT<br>ATATATATAT                                                       | GTGCGTGTGTGGAGA<br>GAAGA       | ATTGATTGTCGCATGT<br>GAA      | 60.0                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_21097843  | Ca3                                     | 21097843                      | ATTTTTTTTT/ATTTTTTTTTT                                                                                                    | GGCATTTTGATTTGATT<br>CGC       | CAAATTTGTGTTTCAA<br>AAACCATT | 60.4                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                              |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_21114306  | Ca3                                     | 21114306                      | CTAGTA/CTAGTAGTA                                                                                             | TCATGCGATCATCCATT<br>CTAA   | ATTTGCAACGATGTGA<br>ACCA  | 59.1                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_21114353  | Ca3                                     | 21114353                      | TCCCCC/TCCCCCC                                                                                               | AGTTTGTGTACACCCG<br>AGGC    | GGAGCCTTAAGTCAGG<br>TGGA  | 60.0                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_21192862  | Ca3                                     | 21192862                      | AATATATATATATATATATATATAT<br>ATATATATAT/AATATATATATATATA<br>TATATATATATATATAT                                | TGTCTTTCTCGTTTTT<br>CAATG   | TTTGTAGTTCACCAGCA<br>GGG  | 59.2                             | 414                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_21311568  | Ca3                                     | 21311568                      | GAAAAAAAA/GAAAAAAAAA                                                                                         | CACGTACATCGCAAT<br>TTTT     | CATGTCATTTCACCCA<br>CGA   | 59.6                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_21363714  | Ca3                                     | 21363714                      | CTATATATATATATATATATA/CTA<br>TATATATATATATATA                                                                | AACGGACCGTGGTCTA<br>ACAG    | AAGGTGCGTACAAGGA<br>ATGG  | 60.0                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_21481670  | Ca3                                     | 21481670                      | CTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTAT/C<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT | GCGTAGTAAATCCTTC<br>TTCCACA | TGAGACAAGAATAACA<br>CCCGA | 59.7                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_21696134  | Ca3                                     | 21696134                      | CTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATT/CTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATT     | TTTTTCAACAACCTCT<br>CCGA    | GCAAATGCAGACCAGA<br>ATCA  | 57.6                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_21892232  | Ca3                                     | 21892232                      | T/TG                                                                                                         | TGTCATCTGGGATCGT<br>TTCA    | AATTCCATCTCCTCTGG<br>GCT  | 60.0                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_21897869  | Ca3                                     | 21897869                      | ATATTATTATTATTATTATTATTA<br>/ATATTATTATTATTATTATTATA                                                         | GAGTTGAGTGTGCGCA<br>GGGT    | AGCTACCAAGCTGATG<br>GTGAA | 60.2                             | 296                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_21899233  | Ca3                                     | 21899233                      | AATCATCATCATCATCATCAT/A<br>ATCATCATCATCATCATCATCAT                                                           | CGTTGCATGATAGCTC<br>CTGA    | TGCTCATGGAATCGTA<br>CTCG  | 60.0                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                          | Forward primers (5'-3')      | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                        |                              |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_22487747  | Ca3                                     | 22487747                      | TACAGTGA/TA                                                                            | GTAATGCCCGTGAGT<br>AGGA      | CCCAATTGATTCCAAA<br>GAAA  | 60.0                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_22534501  | Ca3                                     | 22534501                      | TTTATTATTATTATTAT/TTTATT<br>ATTATTATTAT                                                | CAACGAGGGATGGGAA<br>TAGA     | GTGCACGGTACAAACC<br>TCCT  | 59.9                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_2260100   | Ca3                                     | 2260100                       | TAAAA/TAAAAA                                                                           | TGGACTTGTTGGTCC<br>ATCA      | ACCCATTTTGTGTG<br>GTGT    | 59.9                             | 293                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_22809344  | Ca3                                     | 22809344                      | TTTATTATTAT/TTTATTAT                                                                   | GGATTGGGGTCATTT<br>AGGT      | AGCGACCTCCCACTAG<br>GTTT  | 59.9                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_22932908  | Ca3                                     | 22932908                      | TATAATAATAATAATAATAATAA<br>TAA/TATAATAATAATAATAATAA<br>TAATAATAA                       | TCAGCAGAAAATGCAA<br>AACG     | CGACCGACCCATACAA<br>GTTT  | 60.0                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_23014028  | Ca3                                     | 23014028                      | CAAAAAAAAAAAAAA/CAAAAAA<br>AAAAA                                                       | GGATGTTGCACAATCA<br>AGGA     | GGCAGTGGTAGTGAAG<br>CACA  | 59.5                             | 370                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_23063614  | Ca3                                     | 23063614                      | TTATATATATATATATATATATAT<br>TATATATATATATATATATATATAT<br>A                             | GTAACCTGCACCGACC<br>CAAT     | ATGACGGTGTTTGGAG<br>ACAA  | 59.9                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_23136591  | Ca3                                     | 23136591                      | ATTT/ATTTT                                                                             | GGGTGAGTTTCTGGGT<br>CTCA     | CTTCAACAAATGGTCC<br>CTCAA | 60.1                             | 723                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_23166097  | Ca3                                     | 23166097                      | TATAATAATAATAATGATAATAA<br>TAATAATAATAAT/TATAATAATAA<br>ATAATAATGATAATAATAATAAT<br>AAT | TTTCATTTCGTTTCAA<br>GTTATCAA | TTAATGCTAACAGGGG<br>GTCG  | 59.1                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_23219721  | Ca3                                     | 23219721                      | CATTATTATTATTATTATTATTAT<br>/CATTATTATTATTATTATTATTAT<br>TTAT                          | GATTAGAGCGGCCAAA<br>ATGA     | TTTCAATTAGTCGGGT<br>GGC   | 60.2                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)        | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                      |                             |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_23253882  | Ca3                                     | 23253882                      | GAAAAAAAAA/GAAAAAAAAA                                                | TGGGTTGCGATCGTGT<br>ATTA    | TCAGTCAGTTGCAACA<br>TAGGAGA | 60.0                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_23463912  | Ca3                                     | 23463912                      | CATATATATATATATATATATATA<br>TATA/CATATATATATATATATATATA<br>TA        | TCAAATTTGGAGGAAA<br>CAACG   | TCGGAAAACCTTGTTGA<br>TGAA   | 60.0                             | 716                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_23530917  | Ca3                                     | 23530917                      | AATATATATATATATATATATATA<br>ATATATATATATATATATATATAT                 | ACCCATTAGCGTAGGA<br>GTGC    | AACGTAAATGCACTTGA<br>ACCG   | 59.2                             | 786                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_23548884  | Ca3                                     | 23548884                      | AATATATATATATATATATATA/AA<br>TATATATATATATA                          | ATGTGCATGCGTGGTA<br>CTGT    | AAAAAGTAATTGAGGC<br>CGGG    | 60.1                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_23606563  | Ca3                                     | 23606563                      | AATATATATATATATATATATATA<br>ATA/AATATATATATATATATATAT<br>ATATATATATA | TTGGTTTAATCACCCCTT<br>TTCAA | TTCAACCAATTGTGTCT<br>GGC    | 58.5                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_23653507  | Ca3                                     | 23653507                      | GTTTTTTTTT/GTTTTTTTTT                                                | AAAATAAAATGCGGTG<br>AGCG    | CCAAATGTTGTCAAAA<br>GGGA    | 60.1                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_23830553  | Ca3                                     | 23830553                      | ACTCTCTCTCTCTCTCTCTCTCT<br>CTC/ACTCTCTCTCTCTCTCTCTCTC<br>TCTCTCTCTC  | TCACGAAATTGGTCCC<br>CTTA    | GGGACCAAACTGGAG<br>AGAA     | 60.3                             | 878                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_23881356  | Ca3                                     | 23881356                      | TTATATATATATATATAT/TTATATAT<br>ATATATATATATATAT                      | ACAGCCAACAACCACA<br>TCAA    | CGTAAGTGTGACCGAC<br>GCTA    | 60.0                             | 864                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_23993355  | Ca3                                     | 23993355                      | AATAAATTATAAATTATAAATTA/AAT<br>AAATTATAAATTA                         | CCGAGCCAAAATCCAA<br>AATA    | GTTTGGGGCACAATTG<br>AGAT    | 59.9                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24004974  | Ca3                                     | 24004974                      | GAAAAAAAAA/GAAAAAAAAA                                                | TCAGGCCATCGATCAT<br>GTTA    | CTCACGACCAAGTGCA<br>AGAA    | 60.0                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                                 |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_240123    | Ca3                                     | 240123                        | GCGCCGCCGCC/GCGCCGCCGCCG<br>CC                                | GCAATTTTGTGAAGGA<br>GGGA      | GACCTTGTGGATGGCA<br>GTTT        | 60.1                             | 189                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24035775  | Ca3                                     | 24035775                      | TAAAAAAAAAAAAA/TAAAAAAAAAAA<br>A                              | TTGTGAGGTATGGACG<br>TGTGA     | GAATTACATGCGTTTGT<br>GCG        | 60.0                             | 292                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24156923  | Ca3                                     | 24156923                      | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATATAT         | CAATAGCCCAATTTTGA<br>AAGAA    | TGCTTGGGTGAGTGAG<br>AGTG        | 58.3                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24199958  | Ca3                                     | 24199958                      | ACACTCA/ACA                                                   | CACATGAAGCGTGCAA<br>TTTT      | GGTGGGTGATGACAA<br>ATTC         | 59.7                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24272959  | Ca3                                     | 24272959                      | GAATAATAA/GAATAATAATAA                                        | GCATGTCCGTTACCTC<br>CACT      | GCGATTTATTATTCAGA<br>GTTATTAGCG | 60.0                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24439636  | Ca3                                     | 24439636                      | ATTTTTTTTT/ATTTTTTTTT                                         | ACTTTGCAAGCTTTTG<br>CGAT      | AACAATGTATGCACAG<br>GCAAG       | 60.0                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24441612  | Ca3                                     | 24441612                      | AATATATA/AATATATATA                                           | GGTGCCACATCATACC<br>ATTG      | TCAAACAAAATTGGTTG<br>CTTTTT     | 59.7                             | 333                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24550785  | Ca3                                     | 24550785                      | AATATATATATATATATAT/AAAT<br>ATATATATATATATATATAT              | TCGTGCATATCAATTAA<br>ACCTAGGA | CCGGTTCAATGATGTG<br>ACCT        | 59.2                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24554701  | Ca3                                     | 24554701                      | ATGTG/ATG                                                     | GGAGTATTGTGAACCT<br>CACACG    | AGATTTTGATTGATTGG<br>CGG        | 59.5                             | 764                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24585169  | Ca3                                     | 24585169                      | ATTTTTTTTT/ATTTTTTTTT                                         | TATGTTAGACCGTCCG<br>TGGG      | TTGTACTGGTGATCATC<br>GAAAAG     | 60.8                             | 888                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_24685752  | Ca3                                     | 24685752                      | GTTGTTATGACTTTGTTATG/GTTGT<br>TATG                            | GGCTTTGATGCTTATG<br>AAGGT  | GTTCCGTTTCGTTCTT<br>TGAA   | 59.6                             | 746                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24731209  | Ca3                                     | 24731209                      | ATTTTTTTTTTTT/ATTTTTTTTTTTTT                                  | GGGGTTTCACTGGTTG<br>AAGA   | GCTTTGACCCCAGAAT<br>TCAA   | 59.9                             | 467                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24790252  | Ca3                                     | 24790252                      | AGG/AATAAATGG                                                 | TCAGCCAAAAGCTGA<br>TGTG    | AAGTTAAGGGACCACG<br>GATG   | 60.0                             | 324                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24791040  | Ca3                                     | 24791040                      | GAAAAA/GAAAAA                                                 | GGGACCACGAATGTAA<br>TTTAGC | TGCCAGCATAAGAAGT<br>TGTTG  | 59.7                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24796858  | Ca3                                     | 24796858                      | AA/AACATTATCACAACTA                                           | AAAACCAATGCTTCAC<br>ATGC   | GGCAATGACTTGTCCC<br>TGTT   | 60.0                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24850043  | Ca3                                     | 24850043                      | T/TA                                                          | TGACGTGACATGCATA<br>CGATT  | CAGCTACCAACACTCG<br>ACCA   | 60.0                             | 823                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24888413  | Ca3                                     | 24888413                      | AATATATATATATAT/AATATATATAT<br>ATATAT                         | CATGCATTCAATCAAT<br>CACA   | TGGGACAAAAACAAGC<br>TAACAA | 58.0                             | 857                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_24927543  | Ca3                                     | 24927543                      | ATATTATTATTATTATTATT/ATA<br>TTATTATTATTATTATTATTATT           | TGTTGGATTGATGTT<br>TGTA    | GTGTCACTTTAATGGA<br>CAGCAA | 60.0                             | 260                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_2494761   | Ca3                                     | 2494761                       | TAAA/TAAAA                                                    | GCATCTTTGTGGATGC<br>CTTT   | GTGCCAGTCGATTGCC<br>TAAT   | 60.1                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_2496760   | Ca3                                     | 2496760                       | A/AT                                                          | GGTTTCGAGGAAACTG<br>GACA   | GGCTTTTAGGTGGACG<br>GATT   | 60.1                             | 971                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                  | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                |                             |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_25030440  | Ca3                                     | 25030440                      | ATTTTTTTTTTT/ATTTTTTTTTT                                                       | TTGATTCCACGTCAAT<br>GTCA    | TACACACACCTTGCTC<br>GCTC     | 58.5                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_25195854  | Ca3                                     | 25195854                      | AAGAATACTCTATGTT/AAGAATACT<br>CTATGTTAGAATACTCTATGTT                           | TGCCCTAATTAAGGGA<br>ATAAATG | GTGGTTTGGGCTACTT<br>TCCA     | 58.5                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_25199115  | Ca3                                     | 25199115                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATT/TTTATTATTATTAT<br>TATTATTATTATTATTATT | AATGCACGAAGAGAGA<br>GGGA    | GAGGGAGTTGTGAAGA<br>GACAAAA  | 60.0                             | 562                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_25314505  | Ca3                                     | 25314505                      | GAAAAAAAAA/GAAAAAAAAA                                                          | CCCTCGAATTGTTTTG<br>GAA     | TGGAAATGATTGTTTT<br>TGGG     | 59.9                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_25419094  | Ca3                                     | 25419094                      | ATTTTTTTTTTT/ATTTTTTTTTT                                                       | TCACAGTTTGGATTGG<br>TGGA    | TTTCAATTTTGACCATT<br>TGTC    | 59.9                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_25519863  | Ca3                                     | 25519863                      | AATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATA<br>TAT                    | TCAGTCAACCGCACAT<br>AAAAG   | TCATCTATTCAAAAAGT<br>CTCACCG | 58.8                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_25677601  | Ca3                                     | 25677601                      | A/ATTATTATTATT                                                                 | TGCTTAAGTGAATG<br>CAAGACA   | CACCACCACTTTCC<br>CTCT       | 59.0                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_25798470  | Ca3                                     | 25798470                      | AATATATATATATATATATATAT<br>ATA/AATATATATATATATATAT<br>ATATATATATATA            | TTAAAAGGCTGCCGTT<br>ATCC    | CCTAACTCTTTAGGTC<br>GAATTG   | 59.2                             | 702                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_25872845  | Ca3                                     | 25872845                      | ACTAAATTGGTCGCTAAAT/ACTAAA<br>T                                                | TGTGTACAAGATTGTG<br>AAGGCA  | CACGTAAGATCGCCAA<br>AATC     | 59.2                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_25888060  | Ca3                                     | 25888060                      | AT/ATT                                                                         | TGTGGAAGACATCCTT<br>TACTGC  | ACCTGACCTATTTCCAC<br>CCC     | 59.2                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')        | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|--------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                                |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_25888907  | Ca3                                     | 25888907                      | GTTTTTTT/GTTTTTTT                                                       | CAGGTCATGCCAGACT<br>TTGA       | TCTGACCCGACCTGGT<br>CTAC   | 59.8                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_25889145  | Ca3                                     | 25889145                      | ATTTTTTTT/ATTTTTTTT                                                     | GTAGACCAGGTCGGGT<br>CAGA       | TGATATGTCACATTGTC<br>GCAC  | 60.1                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_25890296  | Ca3                                     | 25890296                      | TAA/TA                                                                  | CGGGACTTGATGGAAC<br>CTTA       | TTGAAACGATCGTGAT<br>GACTG  | 59.9                             | 799                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_25906200  | Ca3                                     | 25906200                      | CTATATATATATATATATATATA/C<br>TATATATATATATATATATATA                     | TTCATTTTCACTCATT<br>CAGATTTAGA | TGCAATTATCAATGACA<br>AGGAA | 59.6                             | 868                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_25937655  | Ca3                                     | 25937655                      | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATAT                       | TCGAGTATGACCAATT<br>AACCGA     | ATAAACTTTTAGGCGC<br>CGGT   | 59.5                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_25950181  | Ca3                                     | 25950181                      | AGATGGGGATGGGGATG/AGATGG<br>GGATG                                       | ACTTGCACCCCATCAG<br>TTTC       | TCCCATCTTCATCTTC<br>GTC    | 60.0                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_26020458  | Ca3                                     | 26020458                      | CATATATATATATATATAT/CATAT<br>ATATATATATATATATATAT                       | CCCACTAAAGGCCCAT<br>ATCA       | TTCAAATTCACGCCCT<br>AAC    | 59.8                             | 789                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_26159882  | Ca3                                     | 26159882                      | CATATATAT/CATATAT                                                       | TTGACCAGACCGAGAT<br>CACA       | GGGGCATTATGGACTT<br>GAAA   | 60.2                             | 779                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_26215938  | Ca3                                     | 26215938                      | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATATA<br>TATATATATATAT | TTTATGGGAGCTCTTG<br>CCAC       | TTGACCCTCAAAGAG<br>ATGG    | 60.2                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_26437635  | Ca3                                     | 26437635                      | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>A             | TTTTTGAAAACCTGCTG<br>CCT       | GCTTGAGCACACAGCC<br>ATTA   | 59.9                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_2653586   | Ca3                                     | 2653586                       | GTTTTTTT/GTTTTTTT                                             | TGTTTTGCAGCAAGAT<br>GTCC     | TGGAGATGGTTAGCAA<br>TGGA  | 59.8                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_26695279  | Ca3                                     | 26695279                      | AATATATATATATATATATATATAT<br>AT/AATATATATATATATATATATA<br>T   | AAGTCATCATCACTCAT<br>TTGAAGA | GTACCGGAGCAGTGGA<br>TTGT  | 57.9                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_26823353  | Ca3                                     | 26823353                      | AAATACAATAC/AAATAC                                            | CGAAAATGTTGAGGGG<br>CTAA     | GTTTTGGTGCGGTTTC<br>TTGT  | 60.1                             | 979                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_26872317  | Ca3                                     | 26872317                      | CAGAGAGAGAGAGAGAGAGAGAGA<br>G/CAGAGAGAGAGAGAGAGAGAGA<br>GAGAG | CAATGTGCTCGATTTC<br>TCCA     | TTACATTCCTTGCCTCG<br>TCA  | 59.8                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_27188795  | Ca3                                     | 27188795                      | AATATATATATATATATATAT/AAAT<br>ATATATATATATATATAT              | CCAAATGACGACTTCC<br>CACT     | TTACTACATTTCTGCC<br>CCG   | 60.0                             | 865                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_27221901  | Ca3                                     | 27221901                      | AATTAT/AATAATTATTAT                                           | TGGCCTAAAAATGACC<br>GACT     | TGTGCGCTGATAGGCA<br>TTAG  | 59.6                             | 929                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_2724739   | Ca3                                     | 2724739                       | AATATATATATATATATATA/AATA<br>TATATATATATATATA                 | GCGCAATACTCAAATG<br>CAGA     | GTGCACTTGCGGTCTT<br>ATCA  | 60.0                             | 338                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_27277791  | Ca3                                     | 27277791                      | CATATATATATATATATATATA/CA<br>TATATATATATATATATATATAT<br>ATATA | GCGAAGCGCCATACTA<br>ACTC     | AAGCCCAAACCTCCCTTT<br>TTC | 60.0                             | 858                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_27378702  | Ca3                                     | 27378702                      | CAA/CAAA                                                      | GTCGGGGACTAGTGGA<br>CTCA     | CGGGGAAGTTCTAAGG<br>TGCT  | 60.1                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_27551834  | Ca3                                     | 27551834                      | TTATATATATATATATATATA/TTATA<br>TATATATATATATATA               | TCTTTGGATGGGTTCC<br>ATGT     | TTGTTGACACCGAATTA<br>GCG  | 60.2                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                           |                              |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_27572261  | Ca3                                     | 27572261                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATATATAT                                     | ACATGCCTACTCGTGT<br>CGTG     | TTTTCCTTTTATTTTCT<br>TTGTGA | 59.8                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_27573773  | Ca3                                     | 27573773                      | ATATATATCTATATAT/ATATATAT                                                                 | TGAATTTTCATGTGCGT<br>TTGA    | TTCTCTTGACATTAGG<br>CTCC    | 60.1                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_2762503   | Ca3                                     | 2762503                       | GTTTT/GTTTTT                                                                              | CTCTACCCAAGAAGA<br>TCGC      | TTGGAACAAACACCT<br>GCAA     | 60.0                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_27743850  | Ca3                                     | 27743850                      | TAAAAAAAA/TAAAAAAAA                                                                       | TAATGGACCACAATTG<br>CACC     | AATTGCACCGCTGAGT<br>TTTT    | 59.3                             | 216                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_27844143  | Ca3                                     | 27844143                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>TTATTATTATTATTATTATTATT<br>TTATTA | TCCACACAGTCCCACT<br>ACCA     | TGTTACCACCACCAGA<br>ACCA    | 60.0                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_27853892  | Ca3                                     | 27853892                      | A/ATTT                                                                                    | TGGATTGACATAAATTG<br>AAAGAAA | AAAATAGACCCCAAT<br>GCC      | 57.8                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_27854154  | Ca3                                     | 27854154                      | TGG/TG                                                                                    | TCGATAATGAGTGATT<br>GGTGGG   | ACCTCACCTCGAATG<br>TCAC     | 60.2                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_27854804  | Ca3                                     | 27854804                      | T/TA                                                                                      | GGATTGAGAGGGGAG<br>AAAGG     | TTTGAAAGCAAGAGCG<br>TCAA    | 60.0                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_27854997  | Ca3                                     | 27854997                      | ATTTTTTTTTT/ATTTTTTTTT                                                                    | GGATTGAGAGGGGAG<br>AAAGG     | TTTGAAAGCAAGAGCG<br>TCAA    | 60.0                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_27856755  | Ca3                                     | 27856755                      | TAAAAAAAA/TAAAAAAAA                                                                       | CGAAGATGAAGAGGCT<br>TGAAA    | CAACAACCTTCTGATGCT<br>CGC   | 59.6                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                                 |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_27867074  | Ca3                                     | 27867074                      | TCAC/TCACAC                                                   | TGAGATAACCAGCGAA<br>TCCC  | ATTCGGGATAAGTGG<br>ACCC         | 60.0                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_27867135  | Ca3                                     | 27867135                      | AT/ATT                                                        | TGAGATAACCAGCGAA<br>TCCC  | ATTCGGGATAAGTGG<br>ACCC         | 60.0                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_27882658  | Ca3                                     | 27882658                      | TAAAAAAAA/TAAAAAAAA                                           | TTTGTGCAAGGACTCT<br>GACG  | TGGAAACCTGTGTGC<br>AAAA         | 60.0                             | 747                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_28113252  | Ca3                                     | 28113252                      | ATTTTTTT/ATTTTTTT                                             | TCCTTCTCCTCTTCCTT<br>CCA  | TGTTTGTGCAATTGAAT<br>TATAGTTATG | 58.9                             | 849                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_28188438  | Ca3                                     | 28188438                      | CAAAA/CAAAA                                                   | ACCCATAACGCACTCG<br>TTTC  | TCCTCCATTTTTCGTTT<br>TCG        | 60.0                             | 434                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_28193661  | Ca3                                     | 28193661                      | AT/ATGTGT                                                     | GGTAAGGGCTCCTTCC<br>AAAC  | ATTCCCCATTCTTAACG<br>CCT        | 59.9                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_28262436  | Ca3                                     | 28262436                      | ATTATTTATTT/ATTATTT                                           | TACTTTTACCCCCATTG<br>CCA  | AAACACCCATCCCACG<br>TATG        | 60.2                             | 414                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_28262509  | Ca3                                     | 28262509                      | GTTTTTTTT/GTTTTTTTTT                                          | TACTTTTACCCCCATTG<br>CCA  | AAACACCCATCCCACG<br>TATG        | 60.2                             | 414                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_28293830  | Ca3                                     | 28293830                      | TAAAAAAAAA/TAAAAAAAAA                                         | GATTACTGCTAGGGCC<br>CAAAT | ATCCCACTTGCAACACT<br>TCC        | 59.5                             | 147                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_28294648  | Ca3                                     | 28294648                      | AATATATATATATATATAT/AAAT<br>ATATATATATATATATAT                | TACCAGTACCAGGAGG<br>CAGG  | TGGTGGGTAATCCGAT<br>GAAT        | 60.1                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)    | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                   |                         |                         |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_2884020   | Ca3                                     | 2884020                       | AA/AATAATAATAATTA                                                 | TCGAGAAAATTGAACG GACA   | AACAAAATAAAGCGGA CAGTCA | 59.2                             | 565                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_29028379  | Ca3                                     | 29028379                      | TTATATATATATATATATATATATATATATATATAT/TTATATATATATATATATAT         | CACAGGCTCGAAACAC ACAT   | TTATTTTTCTTGATGCA ATGGA | 59.8                             | 302                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_29051833  | Ca3                                     | 29051833                      | AATTATTATTATTATTATTATTAT/AA TTATTATTATTATTATTAT                   | CCCACCTCTACCACCG ACTA   | TCTGAACCGTCTTGATT CGAT  | 60.0                             | 387                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_29087544  | Ca3                                     | 29087544                      | GAAATATATA/GA                                                     | GCTGGAAGCTTCTAAT GGCA   | AAACCGCCTTTTCAGAA CAT   | 60.5                             | 471                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_29087580  | Ca3                                     | 29087580                      | TATATATAA/T                                                       | GCTGGAAGCTTCTAAT GGCA   | AAACCGCCTTTTCAGAA CAT   | 60.5                             | 471                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_29089899  | Ca3                                     | 29089899                      | TTATATATATATATATATATATATATA T/TTATATATATATATATATATATATA TATATATAT | CACCCCACATGCAAAC ACTC   | CCTTTGGCAATCGAGG TAAA   | 60.0                             | 399                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_29091788  | Ca3                                     | 29091788                      | TAAAAAA/TAAAAAAA                                                  | TTTTGGAAAAGCGCTG TAAAA  | CTTCGACACTGTAGCA CCCA   | 59.9                             | 852                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_29174780  | Ca3                                     | 29174780                      | TTATATATATATATAT/TTATATATAT ATATATATATAT                          | ATCCACCCACATTCA AATC    | GGAGAGAAATACGCGT GGAG   | 59.5                             | 439                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_29224433  | Ca3                                     | 29224433                      | ATTTTTTTTT/ATTTTTTTTTTT                                           | TGCAATTTGTTGGAGC GTTA   | TTGCTCCAAATTTCAA GGC    | 60.3                             | 394                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca3_P4_29334875  | Ca3                                     | 29334875                      | TTATATATATATATATATATAT/TTAT ATATATATATATATATATATAT                | GGGTGGCTCATGAAGC TTAG   | TCTCAACCGTTTTGGT GACA   | 59.8                             | 576                                           | INTERGENIC                                  | --                               | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                    | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                                  |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_29362184  | Ca3                                     | 29362184                      | AAGAGAGAGAGAGAGAGAGAGAGA<br>GAGAGAGAGAGAGAGAGAGAGAGA<br>GAGAG/AAGAGAGAGAGAGAGAGAGA<br>GAGAGAGAGAGAGAGAGAGAGAGA<br>GAGAGAGAGAGAGAGAGAGAGAGAG                      | ACCACAATCTGAAGCC<br>AACC  | GTTGCACTGTGGGAT<br>CTTT      | 60.0                             | 679                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_29512683  | Ca3                                     | 29512683                      | AATATATATATATATATATAT/AAATAT<br>ATATATATATATAT                                                                                                                   | TGCAATGAATGGAATC<br>TTGG  | TCCAAAACAACAAGGA<br>CACG     | 59.5                             | 380                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_29534996  | Ca3                                     | 29534996                      | CAAAAAAAAA/CAAAAAAAAA                                                                                                                                            | TCAATGACCTATTGTC<br>GCCTT | TGGATAGCATCACATG<br>AATAAAAA | 59.6                             | 736                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_29552129  | Ca3                                     | 29552129                      | AATATATATATATATATATATATATAT<br>ATATA/AAATATATATATATATATAT<br>ATATATATATATA                                                                                       | AAAACACAGTTGGAGG<br>TGCC  | TATCAGTCGGCTGTGT<br>TTGG     | 60.0                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_29636957  | Ca3                                     | 29636957                      | TTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATA/TTAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAA | CCTTTGAATTATCACG<br>GAAGC | TTTAGAGTTGAGAGG<br>GGTGG     | 58.7                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_29809142  | Ca3                                     | 29809142                      | ATAT/AAATTAT                                                                                                                                                     | GCTCATGCCTCCTTCA<br>AAAA  | AAGCAGCCATAATGAC<br>AGGG     | 60.3                             | 856                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_29829081  | Ca3                                     | 29829081                      | CAAAAA/CAAAA                                                                                                                                                     | TTCATTCATCGCATTGA<br>GGA  | CTTTGAATCCTTGCCCA<br>AAA     | 60.2                             | 337                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_29849306  | Ca3                                     | 29849306                      | AATTATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTATTAT<br>TATT/AAATTATTATTATTATTATTAT<br>ATTATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATT                | TGGCAATCATTGCTTT<br>TTG   | AGAGGCATTGACTTTG<br>GTGG     | 59.7                             | 228                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_29919321  | Ca3                                     | 29919321                      | AATATATATATATATATATATATATAT<br>ATATAT/AAATATATATATATATATA<br>TATATATATATATAT                                                                                     | TCAGCCCTCGCCTTAC<br>TTAG  | TTTCAACATTTTCTCCC<br>CATT    | 59.6                             | 585                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_29949453  | Ca3                                     | 29949453                      | TAAAAAA/TAAAAA                                                                                                                                                   | TGTGGAGGTTATTTT<br>GGGC   | AAGCCGGCAGTGTAGT<br>GTCT     | 59.8                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                      | Forward primers (5'-3')      | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------|------------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                    |                              |                                 |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_30061370  | Ca3                                     | 30061370                      | CTTT/CT                                                                            | CCAAAAATGACATTAAT<br>CTTGGC  | ATCACAAATTTGGTGCA<br>GTTTT      | 59.7                             | 194                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30072887  | Ca3                                     | 30072887                      | AGGTG/AGGTGTGTGGTG                                                                 | CACCTCACGCACCACA<br>TTAC     | CACCAATTATGCCCTT<br>GTC         | 60.0                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30114026  | Ca3                                     | 30114026                      | AAGA/AA                                                                            | CCGTTGAGAATGGTGA<br>GGTT     | AAAAAGAAGAGAGTTC<br>CCCCT       | 60.0                             | 681                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30291152  | Ca3                                     | 30291152                      | CAAAAAAAAA/CAAAAAAAAA                                                              | GCTGAATTTTGTGGTA<br>GCCC     | CCGATTAGAAAAGCGGT<br>TGAA       | 59.6                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30339047  | Ca3                                     | 30339047                      | AAATAATAATAATAATAATA/AAA<br>TAATAATAATAATAATAATA                                   | CCTCCTCCAACCATGA<br>AATG     | CCTGTGTGGTCAGAAA<br>GGGT        | 60.3                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30420653  | Ca3                                     | 30420653                      | TTATATATATATATATAT/TTATATAT<br>ATATATATATAT                                        | TGATCAAAAGAAAAGG<br>TCTGAGAT | TGCACGTAAGTCAAAT<br>GCAA        | 58.5                             | 813                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3050975   | Ca3                                     | 3050975                       | AATATATATATATATATATATATAT<br>ATATATATATA/ATATATATATATATA<br>TATATATATATATATATATATA | TGGCCTAAGCTTCTCC<br>CTTT     | TGTGCTCCAATTACTTC<br>TTTAGCA    | 60.3                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30564227  | Ca3                                     | 30564227                      | TTA/TTATA                                                                          | GCTGACGTGGACCTCT<br>TCTC     | TGTCGATATTTATGAGT<br>GATTAGGTGA | 60.0                             | 333                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30602332  | Ca3                                     | 30602332                      | CTTTT/CTTT                                                                         | GCCCTCAGATGAGAGT<br>CAGG     | AAATTAAACCCTCATCC<br>CCG        | 59.9                             | 842                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30646834  | Ca3                                     | 30646834                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                                          | TTTCCGGTACACAATT<br>CCA      | CGCCTTCTACGACATT<br>CACA        | 58.9                             | 260                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_30729039  | Ca3                                     | 30729039                      | TTATATATATATATAT/TTATATATAT<br>ATAT                           | CGAAGTTTTATGGTCC<br>CCAA   | CCTCGCGCGATAAAAA<br>GTTA      | 59.8                             | 763                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30760574  | Ca3                                     | 30760574                      | TTATATATATATATATATATATATAT/<br>TTATATATATATATATATATATAT       | GCACCAAGTTCTTCTTT<br>GCC   | GGGAATTGGAGCACTT<br>GAAA      | 59.9                             | 258                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30784930  | Ca3                                     | 30784930                      | TAAA/TAAAA                                                    | CACACACAATTAACATT<br>TGCCA | TTGTAACCAATGAGGT<br>GTTGAAA   | 59.4                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30811197  | Ca3                                     | 30811197                      | ATTTTTTTTT/ATTTTTTTT                                          | TCACGCGTCTTCTTAG<br>GGTT   | TTCAATTGGCCATATCA<br>CTTTG    | 59.9                             | 798                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3082418   | Ca3                                     | 3082418                       | TTT/TTTATT                                                    | CCGTTTATCATTTTTGG<br>GGTT  | TTTGACAAAAATGATGG<br>GTTCA    | 59.9                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30875852  | Ca3                                     | 30875852                      | TTATATATATATATATAT/TTATAT<br>ATATATATATAT                     | CATGTACTATTGCGGC<br>AAACA  | CCAAACCAACCATGAG<br>TTCAC     | 59.6                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30890215  | Ca3                                     | 30890215                      | ATTTTTTTTTT/ATTTTTTTTTT                                       | CATCAACAATATTCGCA<br>CGG   | CAATGCAGACCGTCAA<br>TCAC      | 60.0                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30930504  | Ca3                                     | 30930504                      | GTTTTTATTTTTATTTT/ATTTT<br>TTTTTA                             | GCATGGACCGTTTAAA<br>ATTG   | TTTAGGTGGAAAATTCA<br>TTAGAAAA | 58.0                             | 818                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30936561  | Ca3                                     | 30936561                      | ATTTTTTTT/ATTTTTTTTTT                                         | TGAGGCAGAATTCTC<br>GTTG    | TGTTACGGGGTATTTA<br>GCGG      | 59.2                             | 427                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_30939663  | Ca3                                     | 30939663                      | GTATATATATATATATAT/GTATATAT<br>ATATATAT                       | TTGTTTATTTGGGGTA<br>CACGG  | ATTTGTCGGGATGTCA<br>ACCA      | 59.6                             | 271                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                   |                               |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_30942170  | Ca3                                     | 30942170                      | ATTTTTTTTT/ATTTTTTTTT                                                             | ACACTCAAGAGGTGGC<br>ATCC      | TGTCTTGCGACTATTT<br>CAATTT | 60.1                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31026529  | Ca3                                     | 31026529                      | TG/TGG                                                                            | ATTCGCTATAGGCCGA<br>CACA      | CGAGTGAGGGGATTTA<br>TGGA   | 60.6                             | 708                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31059721  | Ca3                                     | 31059721                      | TAAAAAAAA/TAAAAAAAA                                                               | CGTTAACCTGTGACCC<br>GTTT      | CAGTGATGGCAGGCAA<br>ACTA   | 59.9                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31105400  | Ca3                                     | 31105400                      | AATATATATATATATA/AATATATA<br>TATATATA                                             | AGGAAAAATGATGGAG<br>GGGT      | TTTTTGGTGAAATTGAC<br>GTG   | 59.6                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3113742   | Ca3                                     | 3113742                       | TATAATAATAAT/TATAATAATAA<br>T                                                     | ACGGTGATGAAAGGAA<br>AACG      | TGGGATAAGCTTTCAA<br>ATCCA  | 60.0                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31183194  | Ca3                                     | 31183194                      | AATATATATATATATATATATAT<br>ATATATATATATATATAT/AATATATA<br>TATATATATATATATATATATAT | CACCGTATTACACCAA<br>AACGA     | TTTCGACGACAACAAC<br>AAGG   | 58.5                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31201179  | Ca3                                     | 31201179                      | TTAATAATAATAATAATAATAAT<br>AATAATA/TTAATAATAATAATAAA<br>TAATAATAATAATAATAA        | AAGCTATTTTAGTGG<br>GAGAACTTTT | TTGGTGACACTCTAGC<br>AAAGGA | 58.6                             | 371                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31253675  | Ca3                                     | 31253675                      | CTTTTTTTTT/CTTTTTTTT                                                              | AATTGCAGGTATGAGG<br>ACGG      | GTTTCGGAGTGTGGCA<br>TTTT   | 60.0                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31263318  | Ca3                                     | 31263318                      | ATGTTGTTGT/ATGTTGT                                                                | GACGCAAAATGTTGAC<br>CCTT      | AATCCGGTTGTTGTCT<br>GGAA   | 60.0                             | 395                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31264246  | Ca3                                     | 31264246                      | TTATATATATA/TTATATATATATA                                                         | AAAAACGAGTGGATGC<br>GTTC      | AGAAGACCATCTCTCG<br>TTAGGC | 60.1                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_31266098  | Ca3                                     | 31266098                      | TC/T                                                          | TGCGTGCGTCTTTGAT<br>TAAC | TAGCCCAAGTCAACCG<br>AATC       | 59.9                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31291540  | Ca3                                     | 31291540                      | ATTATTTTATT/ATTATTTT                                          | ATTTGCCGTGACCCTA<br>TGAA | TGGTCTTAAATATGAA<br>GAAAAGAAAA | 60.3                             | 743                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31292520  | Ca3                                     | 31292520                      | TGATGAGTGACGGA/TGATGAGTGA<br>CGGATGAGTGACGGA                  | TTGGGACATCAAGCCA<br>ATTT | TCGTTTATTTCACCGC<br>CTT        | 60.3                             | 286                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31293455  | Ca3                                     | 31293455                      | TG/TGG                                                        | TGGGATGTTTGAGAAA<br>AGCA | ATCCCATCCCAAC<br>AATA          | 59.2                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31293569  | Ca3                                     | 31293569                      | AT/ATT                                                        | TGGGATGTTTGAGAAA<br>AGCA | CCCACATCGTTTATCC<br>CATC       | 59.2                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31293673  | Ca3                                     | 31293673                      | G/GA                                                          | TGGGATGTTTGAGAAA<br>AGCA | CCCACATCGTTTATCC<br>CATC       | 59.2                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31294489  | Ca3                                     | 31294489                      | GTTTTTTTTTTTT/GTTTTTTTTT                                      | CGTTAAATGTCACGCT<br>GTCG | CGCTGTTTAAAGAATTG<br>TGTACG    | 60.3                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31325736  | Ca3                                     | 31325736                      | ATTT/ATTTT                                                    | ATTAATTGGGCTGACG<br>TGGA | GTCCACATTAGGGACA<br>CGCT       | 60.3                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31326387  | Ca3                                     | 31326387                      | GTTTT/GTTT                                                    | CGGGTACAGCCGGTAA<br>GTAA | GGGTGCCTTTAAAGT<br>TGGA        | 60.0                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31336604  | Ca3                                     | 31336604                      | T/TC                                                          | AGCAGGCCTGGACCTT<br>TACT | GGAATGCCAACGAATG<br>AAAA       | 60.3                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_31338630  | Ca3                                     | 31338630                      | ATTT/ATT                                                      | TATCGTTCGTTGCTCT<br>CGTG  | GGCCGAAAGTTATTAC<br>GTGG   | 60.0                             | 870                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31339236  | Ca3                                     | 31339236                      | T/TC                                                          | CCAACCCATGTACCGA<br>CATT  | AGAGACCGTTTCATGA<br>GATTTG | 60.5                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31339678  | Ca3                                     | 31339678                      | ATT/ATTT                                                      | CAATCTCATGAAACG<br>GTCTCT | ACGTTATCCTCACCGT<br>GGAC   | 58.3                             | 266                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31341112  | Ca3                                     | 31341112                      | GTATATATATATATAT/GTATATATAT<br>ATATATAT                       | TCACTCTGATCACAGG<br>AACCC | AATCACGGCGTTTCTG<br>ATTC   | 60.1                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31344262  | Ca3                                     | 31344262                      | ATTTTT/ATTTTTTTT                                              | CGAACCTAGACTTGAG<br>CATGG | TCTCTCATCCACCCA<br>GAGG    | 59.9                             | 441                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31345376  | Ca3                                     | 31345376                      | AAATGGAAT/AAAT                                                | ATGGAAAGCCAGCTGA<br>AGAA  | CTATGTTGTGGGAAGG<br>TGGG   | 60.0                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31348024  | Ca3                                     | 31348024                      | AC/A                                                          | GGTCAACAACATCAAT<br>TGCG  | TAGGGGACCAAACTG<br>AGGA    | 60.0                             | 924                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31350700  | Ca3                                     | 31350700                      | TCATG/TCATGCATG                                               | TCTTAGCGTAGATTCG<br>CCGT  | AACATCTGGGCTAATC<br>GGTG   | 60.0                             | 280                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31364505  | Ca3                                     | 31364505                      | CTTTTTTT/CTTTTTTTTT                                           | ACCAATGTCTCGCAAG<br>CTCT  | GGTAAACATTGCATC<br>GTTGG   | 60.0                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31365869  | Ca3                                     | 31365869                      | GTTTT/GTTT                                                    | AATTAACCCGTGCAA<br>ATTCC  | AAATGACATGCGATCC<br>AACA   | 60.1                             | 209                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_31368075  | Ca3                                     | 31368075                      | TA/T                                                          | TGATTAAGGCAAGGTG<br>ATCCA | AGCCGCTTCATGTAAC<br>CAAT     | 60.5                             | 219                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31375853  | Ca3                                     | 31375853                      | TAATAAATAAATAA/TAATAAATAAAT<br>AAATAA                         | TGGTTGTCAGAGCAGG<br>TTCA  | CATATGTGAACCATGG<br>CAGC     | 60.4                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31389756  | Ca3                                     | 31389756                      | C/CG                                                          | AAATATTCAGTCGGAG<br>GGGG  | TTTTATCTACGTTTACA<br>AAACACC | 60.1                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31392191  | Ca3                                     | 31392191                      | A/ATAAAT                                                      | CACCCATTTTGTATC<br>GAGTT  | TCTTGCTCATGGTGCT<br>TCTG     | 58.8                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31392713  | Ca3                                     | 31392713                      | TGGG/TGGGG                                                    | CAGAAGCACCATGAGC<br>AAGA  | TGTCGGCAGTTAAGTT<br>GGTG     | 60.1                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31399757  | Ca3                                     | 31399757                      | A/AC                                                          | TGTGTGAGCACGATTT<br>CTCC  | TTTGTTCACAGCGCAT<br>TTC      | 59.8                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31402077  | Ca3                                     | 31402077                      | TAAAA/TAAAAA                                                  | TGTACACGTCGGTGAA<br>CAACT | TGTGGCGACAACAAAC<br>TTTGA    | 59.1                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31415275  | Ca3                                     | 31415275                      | T/TG                                                          | GTAGCTAACCAACCG<br>GTGA   | GGGCCCGTTATATATT<br>GGCT     | 60.0                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31448365  | Ca3                                     | 31448365                      | TTTATT/TTTATTATT                                              | GACCTTACATGCTCCA<br>ACGC  | TGGCCACACAAAAGT<br>ACCA      | 60.7                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31448937  | Ca3                                     | 31448937                      | ATTT/ATTAGAAAGTTT                                             | TGGCCACCACTAACAC<br>AAAA  | ACAGGTGATCCTCTTT<br>CCCC     | 60.0                             | 757                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_31467437  | Ca3                                     | 31467437                      | ACC/AC                                                        | GCCCTTGAAATCTCAT<br>CCAA  | GCTCTCGCAAGAACA<br>AACC  | 60.0                             | 177                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31475167  | Ca3                                     | 31475167                      | ATTAATTTAATTTAATT/ATTAATTTA<br>ATT                            | AACACCGCAACAAGTC<br>ACTG  | AAATGACGGCACGACA<br>AGAT | 59.8                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31476091  | Ca3                                     | 31476091                      | TAAT/TAATCATTAGTTTTCAAAT                                      | TGGTTCAGATTTGTTT<br>GGTGA | CAACGTGAGTGAAAC<br>AACCA | 59.0                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31476641  | Ca3                                     | 31476641                      | TACAA/T                                                       | TGGTTGTTTCACTCAC<br>GTTTG | AGGGTGTCACAAATGG<br>AAGC | 59.6                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31482581  | Ca3                                     | 31482581                      | CTAAT/CTAATTAAT                                               | TGCTCATGTGCCAAGA<br>GTTG  | TAGGGCCACAAATCA<br>AAAG  | 61.0                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31494186  | Ca3                                     | 31494186                      | ACTCTCTC/ACTCTCTCTC                                           | TTCAGTCTCGATCATG<br>AAGGG | GAGTGGCTACGATTTA<br>CGGC | 60.2                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31519164  | Ca3                                     | 31519164                      | C/CT                                                          | TACACGTGGCCTCAAA<br>CAAA  | TCAAGCATGGTTCCAA<br>TCAG | 60.1                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31535563  | Ca3                                     | 31535563                      | GAAAAA/GAAAAA                                                 | ACACCCCAATCCCAAA<br>AATA  | CCTTGGAACGATGACG<br>TTTT | 59.0                             | 761                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31560705  | Ca3                                     | 31560705                      | A/AAG                                                         | TGTTCACTGCCAACT<br>CTGC   | GCAGTGCACTGAT<br>GGTT    | 60.0                             | 585                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31578353  | Ca3                                     | 31578353                      | CTTTTTTT/CTTTTTTTTT                                           | TGTGGGGGTACATGT<br>ATT    | CCCAATCTTCATGTCC<br>TGC  | 58.5                             | 681                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_31604401  | Ca3                                     | 31604401                      | TCTTACTTA/TCTTA                                               | GATGAGCAAAGGCAT<br>GATT   | CAAATCAGCAGATTCC<br>AGCA    | 60.0                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31664819  | Ca3                                     | 31664819                      | TGA/TGAGA                                                     | CAAGAGAATGTTGGAC<br>GGGT  | TTCTTTCCAATTTTGCC<br>CAC    | 60.0                             | 441                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31775359  | Ca3                                     | 31775359                      | TAAAAAAAAA/TAAAAAAAAA                                         | CGAATGCGACTGTTGA<br>GAAA  | GTACCACCCGAAATT<br>TGAA     | 60.0                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3185857   | Ca3                                     | 3185857                       | TAAAAAAAAA/TAAAAAAAAA                                         | CGCCTCTCTTTTCTAT<br>GCG   | TGTTGCTGTTGTTGCC<br>TCTC    | 60.1                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31895120  | Ca3                                     | 31895120                      | CTAATATCTTAA/CTAATATCTTAATA<br>TCTTAA                         | GCCCATCAAACCTCTGT<br>GGAT | ATCGGGTGTC AATTGT<br>CGAT   | 59.9                             | 771                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31918341  | Ca3                                     | 31918341                      | TAATCTGTGAAAT/TAATCTGTGAA<br>TCTGTGAAAT                       | TGGTCCAAAAACCACT<br>CACA  | TGAATCACCAATTGCCA<br>GAA    | 60.0                             | 761                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31939842  | Ca3                                     | 31939842                      | T/TG                                                          | GCACGGAAACAGCGAT<br>TTTA  | CGCAAATTC AAAAGAAT<br>TCAAA | 61.1                             | 607                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_31970085  | Ca3                                     | 31970085                      | ATTTTTTT/ATTTTTT                                              | TCTCGTATCAGCCATT<br>CCAA  | ATTTCCAACGTGCCTTT<br>GTC    | 59.2                             | 743                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3235341   | Ca3                                     | 3235341                       | AGCTTCAGTCGCT/AGCT                                            | TGGAGTGAGCTGTGGT<br>TGAG  | TGGTCACCACTTGGTG<br>TTTG    | 60.0                             | 840                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3235471   | Ca3                                     | 3235471                       | TAAA/TAA                                                      | ATAGGCCAAGCAACCA<br>AAGA  | GACGATGGTGAAGATG<br>ACGA    | 59.7                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_3235549   | Ca3                                     | 3235549                       | GCACACA/GCACACACA                                             | ATAGGCCAAGCAACCA<br>AAGA       | GACGATGGTGAAGATG<br>ACGA    | 59.7                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_32387176  | Ca3                                     | 32387176                      | TAAAAAAAAA/TAAAAAAAAA                                         | TCTCGCATTATCTTCT<br>ATCCTCA    | AAGGTAAACTTCCGAA<br>ATGCAA  | 59.4                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_32506988  | Ca3                                     | 32506988                      | TG/T                                                          | ATTGCGAGAATTGTGG<br>GATG       | TTTGAAAAATGCACATA<br>GCCC   | 60.9                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_32541478  | Ca3                                     | 32541478                      | ATTGT/ATTGTTGT                                                | TCCAATACCGAATTCAA<br>CACTT     | TCACTAAGGCCTCTCA<br>TGCC    | 58.5                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_32559515  | Ca3                                     | 32559515                      | TAAAAA/TAAAAA                                                 | TGGTTCGGGTTCGAAT<br>TTAT       | TTCTGAGTTTCGACTG<br>CCCT    | 59.3                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_32560640  | Ca3                                     | 32560640                      | ATTTTT/ATTTT                                                  | TTTAATAGTTCAGTGTG<br>TTGATTGTC | TCACGTGGTAAGTCCG<br>CATA    | 58.8                             | 139                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_32563568  | Ca3                                     | 32563568                      | TTATATATATATATATAT/TTATAT<br>ATATATATATATATATAT               | CGAAAGAAAAAGAAAA<br>CATCGC     | GAAGGTGGCTCGGCAT<br>ATAA    | 60.2                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_32591698  | Ca3                                     | 32591698                      | CTT/CTTT                                                      | CTTTATGGGTGGAGA<br>TGGG        | TCCAATACACCTGTCTT<br>CCAAAT | 59.2                             | 314                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_32616318  | Ca3                                     | 32616318                      | GTTTTTTTTTTTT/GTTTTTTTTTT                                     | TGTGGTTGTTGTGGGC<br>TTAG       | CGAATGTGAGTTTGG<br>GACT     | 59.6                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_32651806  | Ca3                                     | 32651806                      | TAAAAAAAAAAAAA/TAAAAA<br>AAAAA                                | GCCAGCACTGCACTAA<br>AACA       | TCCTTTAGCAAGGGCT<br>GAGA    | 60.1                             | 256                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                 |                           |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_32683395  | Ca3                                     | 32683395                      | ACTTTC/ACTTTCATGCATCTTTAT<br>CTTTC                                                              | GGTGCATAGTATCAG<br>TGCG   | TTTGGGTAAATCAGGA<br>CCCA      | 60.2                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_32691639  | Ca3                                     | 32691639                      | A/ACCT                                                                                          | AATACCCACATGGCCA<br>AAAA  | CCGACAACATATGTGCA<br>CCTTT    | 60.1                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_32795871  | Ca3                                     | 32795871                      | ATTTTT/ATTTTTT                                                                                  | TTGATGGGTCTGGATG<br>TTTT  | TTGAAATATCCAAAAC<br>TGTTACAAA | 57.8                             | 297                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_32836823  | Ca3                                     | 32836823                      | AATATATATATATATATATATATAT<br>ATATATATATAT/AATATATATATATA<br>TATATATATATATATATATATATAT<br>ATATAT | TATGGATGAAGCTTTC<br>GCCT  | TGGTTATTTAATTTGGG<br>CCATT    | 59.8                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_32871592  | Ca3                                     | 32871592                      | TTATATATATATATATATATA/TTATA<br>TATATATATATATATATA                                               | AGGAAATTTTGGTTCG<br>GCTT  | TTTCAACCCTGTCCTTT<br>TGG      | 59.9                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_32921141  | Ca3                                     | 32921141                      | AT/A                                                                                            | AGCAGTTGTAATGAGG<br>CAGGA | TCCTCAAACAACCCCT<br>CAC       | 59.9                             | 726                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33043917  | Ca3                                     | 33043917                      | TAAAAAAAAA/TAAAAAAAAA                                                                           | GAAGCGAAAACTTTTG<br>CAGG  | GGCCTGTTTGAGGAAT<br>TCAA      | 60.0                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33062899  | Ca3                                     | 33062899                      | ATTTTTTTTT/ATTTTTTTTTT                                                                          | TAATGGTTGGTTGGTG<br>GTTG  | TTGGGACTAAATCACTA<br>TGCCA    | 59.1                             | 321                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33099785  | Ca3                                     | 33099785                      | TAAAAAAA/TAAAAAAA                                                                               | GCTTTTCACTCTCGG<br>TTGC   | ATATGAGTTACGGGAT<br>GCGG      | 60.0                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3317901   | Ca3                                     | 3317901                       | AATATATATATATATATATA/AATA<br>TATATATATATATA                                                     | TGTTTTGAATTGCACC<br>GTTTA | GGGGATCAGTTGACTT<br>CAAGA     | 59.1                             | 773                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_33192861  | Ca3                                     | 33192861                      | CATATATATATATATATATA/CATA<br>TATATATATATATATA                                 | CCTCACTTCACCCCA<br>ACTA  | CACTCTTAACCCGCC<br>TCAC  | 60.0                             | 274                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33224456  | Ca3                                     | 33224456                      | TA/TAA                                                                        | TGCAATAGGGCAATGG<br>AAAT | GGCCTGGCCTACTTAT<br>AGCC | 60.3                             | 216                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3339537   | Ca3                                     | 3339537                       | TTT/TTTTCTT                                                                   | GCATTAAGAGGTTCCC<br>CCTC | TATCGATTTGGGGAAA<br>AACG | 59.9                             | 872                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3340030   | Ca3                                     | 3340030                       | AG/A                                                                          | AATTCCTTCCACACAA<br>CCA  | ACCACACTACGGTGCT<br>AGGG | 60.2                             | 173                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33418554  | Ca3                                     | 33418554                      | GTAATAATAATAATAATAATAAT/<br>GTAATAATAATAATAATAATAAT<br>AATAAT                 | GGTTTGTGAGCGAAAA<br>AGGA | TTATTTACCCTCGTGT<br>CCA  | 60.2                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3354325   | Ca3                                     | 3354325                       | CGAGAGAGAGAGAGAGAGAGAGAG<br>AGAGAGAG/CGAGAGAGAGAGAGA<br>GAGAGAGAGAGAGAGAGAG   | TAGGATAAGGTGAGAC<br>GGCG | CAACCTGTCCAAGGCA<br>TTTT | 60.2                             | 246                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33559268  | Ca3                                     | 33559268                      | TAAAAAAAAAAAA/TAAAAAAAAAAAA                                                   | CCGAGCCAAAATCCAA<br>AATA | GAAGCCACAAATGGAC<br>AGGT | 59.9                             | 801                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33576979  | Ca3                                     | 33576979                      | AATATATATATATATATATATATAT<br>ATATATA/AATATATATATATATAT<br>ATATATATATATATATATA | GCTTAGGCAGCCACAA<br>AATC | TCTTGTGCTTGTGTCAC<br>TCG | 59.9                             | 909                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33579150  | Ca3                                     | 33579150                      | AAAGNNNNNNNNNAAG/AAAG                                                         | TGTGGGAGCTGAAAGT<br>GTTG | TTCTTGCCATGTCAC<br>CATA  | 59.9                             | 175                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33693334  | Ca3                                     | 33693334                      | AATATATATATATATATATAT/AA<br>TATATATATATATATAT                                 | CTCACCATAAACCA<br>CACG   | CGTCCCGTCCAAATCT<br>TCTA | 61.2                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                           | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                         |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_33695196  | Ca3                                     | 33695196                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                                                                                           | CTACGGAGGAAAGGG<br>GATGT  | CGTTTTGAATTGATGGA<br>GCA  | 60.3                             | 819                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33748791  | Ca3                                     | 33748791                      | TAGTTTCAG/TAGTTTCAGTTTCAG                                                                                                               | AGGTGCCAAAATTGAT<br>GAGG  | CCTAGAAGGTCGCATC<br>TCCA  | 59.9                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33827405  | Ca3                                     | 33827405                      | GATAATAATAATAATAATAATAAT/G<br>ATAATAATAATAATAATAATAAT<br>AATA                                                                           | CTCATATCCCAGGTG<br>CAAT   | CTCAATCGTGGGTGAC<br>CTTT  | 59.8                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33828272  | Ca3                                     | 33828272                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>/TTTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATT                              | AGAGGCAACAAGAAC<br>CGAA   | TGCATATAAGGAATTGA<br>CGCC | 59.9                             | 318                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33877257  | Ca3                                     | 33877257                      | AATATATATATATAT/ATATATAT<br>ATATATATAT                                                                                                  | CTCACTTCGCTCATG<br>TCAA   | ATATGGCAAGGATGGG<br>AAAA  | 60.0                             | 287                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33884499  | Ca3                                     | 33884499                      | TAAAAAAA/TAAAAAA                                                                                                                        | CAATTTTCGCAAGTCA<br>CACAA | CGAACCTTAATGGTCG<br>GAAA  | 59.8                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3392479   | Ca3                                     | 3392479                       | TTG/TTGAAAGAGTG                                                                                                                         | AATGCATTTGGGTTTT<br>CAA   | GGCAATCCTCGTTCAC<br>ACTT  | 60.2                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33954378  | Ca3                                     | 33954378                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATAT                                                                                         | GGCTTCAAAGCCAACA<br>TCAT  | TTTGTGCTGCCAACATT<br>TTC  | 60.1                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33954528  | Ca3                                     | 33954528                      | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATT/ATATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATT | GGCTTCAAAGCCAACA<br>TCAT  | TCATACAAAACCAAC<br>GGG    | 60.1                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_33996297  | Ca3                                     | 33996297                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                                                                                           | TATTACACCAGAGCCC<br>CCAA  | CCAGCAATGCAACAA<br>CAAT   | 60.3                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_34474422  | Ca3                                     | 34474422                      | TAAAAAAAA/TAAAAAAA                                                      | AAAAATCAATTTATGCC<br>GTTGT  | TTATGCCGATTGACA<br>CTCTT  | 57.7                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_34578013  | Ca3                                     | 34578013                      | AGAGG/AGAGGAGG                                                          | CCAAACCGCAAGATTG<br>ATTT    | TTTCCCAATATTCTGCC<br>TCG  | 59.9                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_34813314  | Ca3                                     | 34813314                      | GTTTTTTTTTTT/GTTTTTTTTTTTTT                                             | AAAAATGCAAAAACACC<br>ATGAA  | AAGTCGCCATTTGAAA<br>CTCG  | 59.4                             | 340                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_34879718  | Ca3                                     | 34879718                      | ATTTTTTT/ATTTTTT                                                        | GGTAAAAGGTGTAACC<br>GAAGAAA | GCAATTAGATGGGTCA<br>CGCT  | 58.7                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_34943152  | Ca3                                     | 34943152                      | TTATATATATATATATATA/TTATATA<br>TATATATATATATA                           | TGCATTTTTGTGATTGT<br>GTGTG  | GCTGGCTCTTTGGGTA<br>TGAG  | 60.5                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35016413  | Ca3                                     | 35016413                      | ATTTTTTTTT/ATTTTTTTTT                                                   | AGGCTTAAGAGAGGGG<br>TCCA    | CCCTAAAATTTTGTGG<br>GCTT  | 60.2                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35171574  | Ca3                                     | 35171574                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATAT                             | GTGCACGGTACAAAAC<br>CCTT    | CAGCACCATACTCAATT<br>GTCA | 59.9                             | 965                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35172088  | Ca3                                     | 35172088                      | CATATATATATATATATATATATA<br>TATATA/CATATATATATATATATA<br>TATATATATATATA | TGACAATTGAGTATGG<br>TGCTG   | TTCTTCAGAAACCG<br>ATACA   | 57.2                             | 184                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35179411  | Ca3                                     | 35179411                      | TAAAAAAAAA/TAAAAAAAAA                                                   | AATGGTGCAACTACA<br>TCCC     | TGGTATTGCGATAATGT<br>CCCT | 59.7                             | 309                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35250926  | Ca3                                     | 35250926                      | TAAAAAAAAA/TAAAAAAAAA                                                   | TTCGGTGGCCAATAGA<br>TTTC    | TGTGTATGGTGAGGGA<br>CGAA  | 59.9                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                   | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                 |                            |                           |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_35254569  | Ca3                                     | 35254569                      | CAAAAAAAAA/CAAAAAAAAA                                                                                           | TGAGCAAGTTGTCCGA<br>TTCA   | GTA CTGCGCGGTAGG<br>TAAG  | 60.4                             | 909                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_35264037  | Ca3                                     | 35264037                      | GAAAAAAAA/GAAAAAAAA                                                                                             | GAATCCAAGGTTGGTT<br>GGTG   | ATGCTTAGGCATGCTG<br>GATT  | 60.2                             | 566                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_35302305  | Ca3                                     | 35302305                      | ATTTTTTTTT/ATTTTTTTTT                                                                                           | GAATCCATGGGCACT<br>TGTT    | TTGGATTGGGACATG<br>GATT   | 60.0                             | 708                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_35440962  | Ca3                                     | 35440962                      | CTTTTTTTTT/CTTTTTTTTT                                                                                           | TGTCAGGAGACCAGGA<br>GAGG   | CCGGGGTCTTTGATGA<br>CTAC  | 60.4                             | 540                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_35533352  | Ca3                                     | 35533352                      | TTATATATATATATATAT/TTATAT<br>ATATATATATAT                                                                       | AATCCAGCCACAACAA<br>GTCC   | CGAATTTGAATGGCTTA<br>GCTC | 60.0                             | 378                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_35584605  | Ca3                                     | 35584605                      | TAATACAA/TAATACAAATACAA                                                                                         | CATCCCTTTCATTTTCC<br>CCT   | TTTTATGGGTTATTGG<br>CCG   | 60.1                             | 230                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_35629460  | Ca3                                     | 35629460                      | TTATATATATATATATAT/TTATAT<br>ATATATATATATAT                                                                     | ACTGTGGGGCATATTG<br>GTGT   | TGCCCTTGCTATTG<br>GTTA    | 60.1                             | 660                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_35662143  | Ca3                                     | 35662143                      | GTTTTTTTT/GTTTTTTTT                                                                                             | CATCATGGTGTGTCCA<br>CTTGA  | TTTTGAAGGCATAGG<br>ACCG   | 60.4                             | 676                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_35662446  | Ca3                                     | 35662446                      | GAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATA/GA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TA | TTTGATTATAAATGGGA<br>CCACA | TTTTGAAGGCATAGG<br>ACCG   | 59.2                             | 274                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_35665629  | Ca3                                     | 35665629                      | TAAAAAAAA/TAAAAAAAA                                                                                             | TTCACATGAATCCCGT<br>CAAA   | TCATGGCTGTGAGAA<br>GGTTT  | 59.9                             | 712                                           | INTERGENIC                                           | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_35699071  | Ca3                                     | 35699071                      | CTGTAATGTAAT/CTGTAAT                                          | ACGAATCTCTCAACCA<br>TCGG   | TGAGGCTCTTTGTG<br>ACTTTG | 60.1                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35703302  | Ca3                                     | 35703302                      | TAAAAAAAAA/TAAAAAAAAA                                         | CGGATATGCGGACAAA<br>AACT   | TTAGCTTTGGGGTTTG<br>ATGG | 60.0                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35787583  | Ca3                                     | 35787583                      | AATATATATATA/AATATATATA                                       | ATGGAGAAGCATGTCC<br>CTTG   | TCAATGGCCTAAGGTG<br>AAGG | 60.1                             | 305                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35792530  | Ca3                                     | 35792530                      | CTT/CT                                                        | GCTTCATGCATACG<br>CCAA     | CCACCAAAAACACATCA<br>CCA | 59.7                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35834316  | Ca3                                     | 35834316                      | GATATATATATATATAT/GATATAT<br>ATATATATATATAT                   | GCTCCCCCTTCATGTG<br>ACTA   | CCTTTTCGCCATCTTG<br>TGT  | 60.1                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35861277  | Ca3                                     | 35861277                      | ATTTTTTTTT/ATTTTTTTTT                                         | TGCAAACTTGGAGAAA<br>AGGG   | ATGGAGACAAATGGCT<br>GTCA | 60.2                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35863496  | Ca3                                     | 35863496                      | A/AG                                                          | CGTGAAGATATTGTTG<br>CTTTGG | CCTTTCTACGACCAATT<br>CCG | 59.6                             | 383                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35863677  | Ca3                                     | 35863677                      | CACATTAAACATTAAAC/CACATTAA<br>AC                              | CGGAATTGGTCGTAGA<br>AAGG   | TGCAATTCAGGTCTG<br>ATGC  | 59.6                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35863925  | Ca3                                     | 35863925                      | CTT/CT                                                        | CGGAATTGGTCGTAGA<br>AAGG   | TGCAATTCAGGTCTG<br>ATGC  | 59.6                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35878677  | Ca3                                     | 35878677                      | TAAAAAAAAA/TAAAAAAAAA                                         | TCCCTTCCCTTTGTTGT<br>GTC   | TTTTATGTTTCGCGGG<br>GATA | 59.9                             | 753                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_35886280  | Ca3                                     | 35886280                      | GAAAAAAAA/GAAAAAAAA                                           | CATGATGTGGTCGAAA<br>AGGA | TGCAAGCAATGATGAA<br>AACTC   | 59.5                             | 209                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35950711  | Ca3                                     | 35950711                      | ATTTA/ATTTAAATTACATGCAATT<br>TA                               | CATGCGATGGAAGTGA<br>ATTG | GTAAAGTTGGCACAGG<br>GGAA    | 60.1                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35963610  | Ca3                                     | 35963610                      | G/GA                                                          | AGCTGTCTCAAGCACC<br>GAAT | TGCTCTGAATACTTTGT<br>CCGC   | 60.0                             | 823                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35963663  | Ca3                                     | 35963663                      | CT/CTAT                                                       | AGCTGTCTCAAGCACC<br>GAAT | TGCTCTGAATACTTTGT<br>CCGC   | 60.0                             | 823                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_35979815  | Ca3                                     | 35979815                      | TT/TTAT                                                       | TAGTGGCTGGGTAACG<br>GAAC | CTTGGGACCCACGAAA<br>TAGA    | 60.0                             | 296                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36000041  | Ca3                                     | 36000041                      | CTCATG/CTCATGTCATG                                            | TCCAAATCATCCGCAC<br>ATAA | TGATATGGGCCTTCAC<br>ATTG    | 59.9                             | 182                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36000193  | Ca3                                     | 36000193                      | AATATATATA/AATATATATATA                                       | TCCAAATCATCCGCAC<br>ATAA | TGGGTAAATAAGTTTT<br>GGACACA | 59.9                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36019725  | Ca3                                     | 36019725                      | GAAA/GAA                                                      | ACCTTTGGATTCATGG<br>TTGG | CCGATAGCCATTTGGA<br>CACT    | 59.6                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36025831  | Ca3                                     | 36025831                      | TAAAA/TAAAAA                                                  | ACGCCAGTCACACAGA<br>CAGA | CATTAGGGGCGTAGC<br>AAAT     | 60.5                             | 875                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36027335  | Ca3                                     | 36027335                      | A/AT                                                          | GCTGATTCAAAAAGCC<br>CTCA | TGTGCATTTTATTTTTG<br>TTGGAA | 60.3                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')          | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                  |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_36028102  | Ca3                                     | 36028102                      | TGAGCTTTAAAA/T                                                | TCACAAATTTTCCAAA<br>ATAACG       | TGCCTCAAATTTCTTT<br>TCCA    | 58.2                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36031623  | Ca3                                     | 36031623                      | TAAAAAAA/TAAAAAA                                              | CATGATATTTGCAGGT<br>CGGA         | TGGTTACCAATACCGA<br>GGAAA   | 59.5                             | 918                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36032000  | Ca3                                     | 36032000                      | TAATTTGAAATTTGAAATT/TAATTTG<br>AAATT                          | TGGTAAGGACAAAAAG<br>AGTTCCA      | AACGCTGAACCAAAAT<br>GACC    | 60.0                             | 801                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36041204  | Ca3                                     | 36041204                      | ATT/AT                                                        | TTCACTCTCCAGTTT<br>GGA           | AAGTCGACGTTTGTGA<br>AGAGTTC | 59.4                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36041601  | Ca3                                     | 36041601                      | A/AAAC                                                        | CACGTGTAAAAATTTCTT<br>GTAAATCAAA | CGAGTGTTCGAAAGGA<br>TCAA    | 59.8                             | 620                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36042558  | Ca3                                     | 36042558                      | ATTTTT/ATTTTTTT                                               | CTCCAGTTTTGGACCC<br>TCAA         | TTTCCAAAATAAACTCG<br>ACGC   | 60.1                             | 430                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36044328  | Ca3                                     | 36044328                      | CAT/CATAT                                                     | TGTCAAATATCAAGGG<br>GGATG        | TGATGCTTTAAGCCGT<br>CACA    | 59.6                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36052612  | Ca3                                     | 36052612                      | GTCACCTTCACCTTT/GTCACCTTT                                     | CATCAATGCACGACCC<br>ATAC         | TAAGTGAGCGCATCCA<br>TTTG    | 59.8                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36076512  | Ca3                                     | 36076512                      | AGAATT/A                                                      | GCATTTGTTTCAACAAG<br>GTAAGG      | TTTGGAGGACAAAAAC<br>TGGG    | 59.9                             | 395                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36089210  | Ca3                                     | 36089210                      | CAAAAAAAA/CAAAAAAAA                                           | GGGCTTTGTTTGTGTTT<br>GGA         | AATAAAGGGGAAAAGG<br>CCAA    | 60.0                             | 185                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_36089976  | Ca3                                     | 36089976                      | AC/A                                                          | AATACGAATCATTGGA<br>GCTTTT | AAACTGGTTTGAGTGA<br>CGGC     | 58.3                             | 167                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36090173  | Ca3                                     | 36090173                      | GTTTTTTTT/GTTTTTTT                                            | ATGAATCCATTGGCG<br>CTAC    | GAAGCGTCAAGTATCC<br>TCCG     | 59.9                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36093211  | Ca3                                     | 36093211                      | CGG/CG                                                        | TTTTGGAAGGTTGCAG<br>CATA   | TGAAACCATCAATATCC<br>TTATTCG | 59.3                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36105355  | Ca3                                     | 36105355                      | CTTTTT/CTTTTT                                                 | GAGTGTGGGAAGGATC<br>GAAA   | CCTGGAGAAGGCTGTC<br>AAAG     | 60.1                             | 372                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36105726  | Ca3                                     | 36105726                      | TC/T                                                          | CTTGACAGCCTTCTC<br>CAGG    | AGGCTCATAAACGCC<br>TCAA      | 60.0                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36107618  | Ca3                                     | 36107618                      | GA/GAA                                                        | AGATCGGACGCTCCTC<br>ACTA   | TGGCGAAGTTAAAGGG<br>ATTG     | 60.0                             | 325                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36126613  | Ca3                                     | 36126613                      | A/AT                                                          | GACCCATCAATGAAGC<br>GACT   | GTAGGCATGTGGAGCC<br>AAGT     | 60.1                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3613355   | Ca3                                     | 3613355                       | TAAATTTAAATTTAAATTTAAAT/<br>TAAATTTAAATTTAAAT                 | GCCCATTA CTGCTGG<br>TTAG   | TTTCTCACC ACTCCAC<br>TCC     | 59.7                             | 178                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36139586  | Ca3                                     | 36139586                      | CT/CTGT                                                       | ATGCAAATTACCCAAG<br>ACGC   | TTATACCGGCTTCGTT<br>GACC     | 60.0                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36139755  | Ca3                                     | 36139755                      | TTAT/TTATATAT                                                 | ATGCAAATTACCCAAG<br>ACGC   | TTATACCGGCTTCGTT<br>GACC     | 60.0                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_36140094  | Ca3                                     | 36140094                      | CAA/CAAA                                                      | GGTCAACGAAGCCGGT<br>ATAA    | CGAAAAATAACACCAAT<br>GCAAA | 60.0                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36140610  | Ca3                                     | 36140610                      | CTCTTCCTTCTT/CTCTTCCTTCTTC<br>CTTCTT                          | TTTGCATTGGTGTTATT<br>TTTCG  | TTGGATCAGCCTTGCT<br>CTTT   | 59.9                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36151877  | Ca3                                     | 36151877                      | T/TG                                                          | TCCAATGTGTGGTTGG<br>ATAAAA  | TTTTTCCAAATTGACAG<br>CCA   | 60.1                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36163828  | Ca3                                     | 36163828                      | GTTTTTTTTTTT/GTTTTTTTTTTT                                     | AATCGTTTGAAAGACG<br>TCGAA   | TCAAACGGACCTCTCC<br>ATAAA  | 59.7                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36184874  | Ca3                                     | 36184874                      | AAAAA/AAAAAGAAAA                                              | AACTGTCAACACGTTG<br>AGTATCG | GGCGTACACATGTCTT<br>TGGA   | 59.2                             | 395                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36185797  | Ca3                                     | 36185797                      | AT/A                                                          | CGGAATGTAGTGTGA<br>CCCC     | CAGTGACAGTGAGACG<br>TGGG   | 60.2                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36187853  | Ca3                                     | 36187853                      | AT/ATTGAGATTAATAATT                                           | GCTAAAGTCAGCCCAA<br>ACCA    | TCAATGGAACATCCAAA<br>GCTC  | 60.2                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36201223  | Ca3                                     | 36201223                      | ATTTTT/ATTTTT                                                 | CTAATTGTTGAAGCCG<br>GGAA    | CCCTTTTGTGAAGTG<br>GCAT    | 60.1                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36201355  | Ca3                                     | 36201355                      | ATTTTT/ATTTTTTT                                               | CTAATTGTTGAAGCCG<br>GGAA    | CCCTTTTGTGAAGTG<br>GCAT    | 60.1                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36219342  | Ca3                                     | 36219342                      | GTTT/GTT                                                      | CATGTGGCGAAGAGAG<br>TGAA    | GTATTCCTTTGGGCG<br>TGAA    | 60.0                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_36224870  | Ca3                                     | 36224870                      | AAGAGAGAGAGAGAGAGAG/AA<br>GAGAGAGAGAGAGAGAGAGAG<br>GAG        | ACCTGTGTGACTCTGA<br>GGGG  | CCCAGTAACCGCTCTC<br>TCTG     | 60.2                             | 721                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36227106  | Ca3                                     | 36227106                      | AATATATA/AATATATATA                                           | CACGAAATCCGAAATG<br>GAAC  | CTTTATGTCGCACAAG<br>CTGC     | 60.3                             | 758                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36240433  | Ca3                                     | 36240433                      | TAAAAAAAA/TAAAAAAAA                                           | TTGTTTTGAATTGGG<br>CCAG   | TTCCAAAATCTCACCAT<br>TCATT   | 60.8                             | 859                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36241503  | Ca3                                     | 36241503                      | AAT/AATGAT                                                    | TAATGAAGGGGACTGC<br>AACC  | TTCGACTCCGAGATAT<br>AACATTCA | 59.9                             | 789                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36241653  | Ca3                                     | 36241653                      | CC/CCAC                                                       | TTCGCAGAAAACTAT<br>GCCC   | TCCGTATTCGAATTGA<br>GACAA    | 60.2                             | 808                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36242951  | Ca3                                     | 36242951                      | GTTTTTTT/GTTTTTTT                                             | TGCTGCAAAAGACAAT<br>TTCG  | AAGTGGTGGTGTGTT<br>TTCC      | 60.0                             | 907                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36251816  | Ca3                                     | 36251816                      | TTATAT/TTAT                                                   | CGTCAAAAACAACAGG<br>CAGA  | CAGAAGCTTGCAGCTA<br>CCCT     | 59.9                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3625461   | Ca3                                     | 3625461                       | CTT/CTTT                                                      | CGGCCTAGCCTACGTT<br>AGAGT | TCCTTCACTAGCTGGTT<br>TTCC    | 59.9                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36264735  | Ca3                                     | 36264735                      | TA/TAA                                                        | ATCACCTGCAACATGG<br>ATCA  | TTAATTAGGCACACCAC<br>GCA     | 59.9                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36286597  | Ca3                                     | 36286597                      | ATTTTTTT/ATTTTTTT                                             | TCATTTTGGCACTTAC<br>CACC  | TGCCTGAATTTATTGG<br>GAATG    | 59.9                             | 754                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_36287175  | Ca3                                     | 36287175                      | TAAAAAAAAA/TAAAAAAAAAAAAA                                     | CATTCCAATAAATTCA<br>GGCA   | CGGGCATTAGAGATCC<br>ACAT        | 59.8                             | 202                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36289361  | Ca3                                     | 36289361                      | TTATATATATATATATAT/TTATAT<br>ATATATATAT                       | GTGCTTTTGCGATTTC<br>ATCA   | TGTAAGAAAATGCATG<br>CGATAGA     | 59.8                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3628980   | Ca3                                     | 3628980                       | TAAAAA/TAAAAA                                                 | CCACCATTAGTTAACG<br>GAGTCA | TTGTCTAAAGAAATTGA<br>AATCATGTTG | 59.0                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36289807  | Ca3                                     | 36289807                      | T/TTGATACCTAGATC                                              | CGCATGCATTTCTTAC<br>AACA   | GCGTTTTGTGTTTCC<br>GTCT         | 59.8                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36290753  | Ca3                                     | 36290753                      | CA/C                                                          | AAAATCTCAAAATTCGC<br>CTTTG | TGAGTGGGGTAAATAA<br>ACTCTGAA    | 59.6                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36303360  | Ca3                                     | 36303360                      | ATTTTT/ATTTTTTT                                               | GCAAACATGGTAAATT<br>GGCA   | CAAAATTGTCACGTC<br>GGTG         | 59.4                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36303469  | Ca3                                     | 36303469                      | GTTTTTTTTT/GTTTTTTTTT                                         | GCAAACATGGTAAATT<br>GGCA   | CAAAATTGTCACGTC<br>GGTG         | 59.4                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36303688  | Ca3                                     | 36303688                      | AT/A                                                          | GCAAACATGGTAAATT<br>GGCA   | CAAAATTGTCACGTC<br>GGTG         | 59.4                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36308195  | Ca3                                     | 36308195                      | T/TC                                                          | TTTGCCACTTGATACA<br>GCAGA  | TTGAACCTAAACGATGA<br>CACCTT     | 59.5                             | 309                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36324828  | Ca3                                     | 36324828                      | T/TG                                                          | TCCATGAAACATTCCC<br>CATT   | CGCACTAAAACGACGA<br>ACAA        | 60.0                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_36326063  | Ca3                                     | 36326063                      | TAAAAAAAAA/TAAAAAAAAA                                         | CGCTGAGCAAAATGA<br>CAAA      | CTCAAACCAATCAAGC<br>CCAT | 60.0                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36326214  | Ca3                                     | 36326214                      | ATTTTTT/ATTTTTTT                                              | TTGCAAAATGGTCCAT<br>CAAA     | CTCAAACCAATCAAGC<br>CCAT | 59.9                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36326321  | Ca3                                     | 36326321                      | ACT/ACTCT                                                     | TTGCAAAATGGTCCAT<br>CAAA     | GCAGTGTGATGCAAAA<br>ATGG | 59.9                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36327195  | Ca3                                     | 36327195                      | ATTTTTTTTT/ATTTTTTTTT                                         | CACTTTCTCCTTGCAAC<br>CAA     | TGGAGAAACAATGCAA<br>ATGG | 58.9                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36328591  | Ca3                                     | 36328591                      | GAAA/GAA                                                      | CACGATGAAATCACTA<br>TGAAAAGC | CGTTCCAGACCTCCAT<br>TGTT | 60.0                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36342426  | Ca3                                     | 36342426                      | GAAAAA/GAAAAAA                                                | AGTATTGAAGCATCAC<br>CGCC     | TCGAGGCATTGTCTG<br>AGAG  | 60.1                             | 195                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36347468  | Ca3                                     | 36347468                      | CTTTTTTT/CTTTTTTT                                             | AAGCACCAGAAGGTCC<br>TGAA     | TGGAAAAGGGAAATTC<br>GTTG | 59.8                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36348447  | Ca3                                     | 36348447                      | GTTT/GTTTTTT                                                  | TCAAGAATGCCAACAA<br>CAAAA    | TTCGACCTTGGAAT<br>GTCA   | 59.2                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36349322  | Ca3                                     | 36349322                      | TTCTC/TTCTCTC                                                 | TGACATTTTCCAAGGT<br>CGAA     | GTTGACGGTCGATTGA<br>AACA | 59.1                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36350064  | Ca3                                     | 36350064                      | TAT/TATAAT                                                    | GGTTTCCCCAATATTC<br>CGTT     | GATGGCAAGCTTTTGT<br>CCTT | 59.9                             | 492                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_36350864  | Ca3                                     | 36350864                      | TA/TAA                                                        | AAGGACAAAAGCTTGC<br>CATC  | TTGTCCCAATGTTGG<br>TCTT   | 59.3                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36351279  | Ca3                                     | 36351279                      | TA/TAA                                                        | AAGACCAACATTGGGG<br>ACAA  | CGATTCAAGTGTGCGA<br>TGTC  | 60.2                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36351563  | Ca3                                     | 36351563                      | TAAAAAA/TAAAAAA                                               | AAGACCAACATTGGGG<br>ACAA  | GCCTGCAATGAACCGT<br>AAGT  | 60.2                             | 873                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36351613  | Ca3                                     | 36351613                      | AA/AACA                                                       | GACATGCGACACTTGA<br>ATCG  | GCCTGCAATGAACCGT<br>AAGT  | 60.3                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36361613  | Ca3                                     | 36361613                      | GACA/GA                                                       | ACTCATCTCCAACAG<br>AGGG   | TTGCTGCTGATTTTCT<br>GTC   | 60.1                             | 769                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36362897  | Ca3                                     | 36362897                      | A/AC                                                          | AGGAAATTCTCCGACG<br>TTGA  | TTCCGTCCATATGCATT<br>GATT | 59.7                             | 920                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36363081  | Ca3                                     | 36363081                      | CG/C                                                          | TGTGTAGCGATGTCAC<br>ACTTG | TTCCGTCCATATGCATT<br>GATT | 58.3                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36370183  | Ca3                                     | 36370183                      | GA/GAAA                                                       | TGGAGAAAATGCGAGA<br>TTCC  | AAAACGGATCCCCTAC<br>CAAC  | 60.2                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36371742  | Ca3                                     | 36371742                      | ATTTTTTT/ATTTTTTT                                             | GGGTTTTCTAGTCCCC<br>CAAG  | TGTTTTTCATTATGTGC<br>CCG  | 59.8                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36371828  | Ca3                                     | 36371828                      | GT/GTTAT                                                      | GGGTTTTCTAGTCCCC<br>CAAG  | TGTTTTTCATTATGTGC<br>CCG  | 59.8                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                 |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_36668334  | Ca3                                     | 36668334                      | GTTTT/GTTTTT                                                                                    | TGGGTAAAAGCTCGAG<br>TTCC   | CAGTGGTGGAAGG<br>CAAT     | 59.3                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36740169  | Ca3                                     | 36740169                      | GATATATATATAT/GATATATATATAT<br>AT                                                               | TGCGTTGCGACACAAT<br>AAAT   | CCACACCTTAGTTTC<br>CACCC  | 60.1                             | 783                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_36829016  | Ca3                                     | 36829016                      | TAAAAAAA/TAAAAAA                                                                                | CGTTCCTTGAATGAGT<br>GACCAA | AGTGCAAAGAGGTTGC<br>AAGG  | 60.1                             | 321                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_37017817  | Ca3                                     | 37017817                      | AATATATATATATATATATATATATAT<br>ATATATATA/AATATATATATATATAT<br>ATATATATATATATATATATATATA<br>TATA | CAGAAGGCCAGGAGAA<br>GAAA   | TGTGCGTGAAGTTTCA<br>TG GT | 59.5                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_37150587  | Ca3                                     | 37150587                      | GAAAAAAAAA/GAAAAAAAAA                                                                           | TGCTTGC GTGAAAATT<br>GAAA  | TCCCATGTTCCGTATAT<br>CCAA | 60.4                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_37191129  | Ca3                                     | 37191129                      | TAAAAAAAAA/TAAAAAAAAA                                                                           | TGGTTTCATTCATCTTT<br>TGCAG | GCCCAATCAACCCAT<br>TTTA   | 60.1                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_37192959  | Ca3                                     | 37192959                      | T/TCA                                                                                           | TCAAATTCATGTGCG<br>CTGT    | TAATAGTCCGGCCAC<br>TTTG   | 60.3                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_37245566  | Ca3                                     | 37245566                      | GTATATATATATATATATATATATAT/<br>GTATATATATATATATATATATAT                                         | TCAAATGTCTCCGTCTA<br>CGCT  | GGGTGACATGCATCTT<br>TG TG | 59.9                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3725109   | Ca3                                     | 3725109                       | AC/ACC                                                                                          | TGTGGTGGTGGAGAAC<br>AGAG   | CGGTCTTTGTGGTGAT<br>TCCT  | 59.7                             | 357                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_37378120  | Ca3                                     | 37378120                      | GAGAAGAAGAAGAAGAAGAA/G<br>AGAAGAAGAAGAAGAA                                                      | ACCTCAGATTCCAAAC<br>GTGC   | GCTGCATTGTGGATAA<br>GGGT  | 60.1                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_37384200  | Ca3                                     | 37384200                      | GAAAAAAAAA/GAAAAAAAAA                                                         | GGTTGACCGACAAAAT<br>CGAG  | TCTTGTAGCCAATCCAA<br>CCA  | 60.5                             | 826                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_37396352  | Ca3                                     | 37396352                      | CAATTGGGAATTGG/CAATTGGGAA<br>TTGGGAATTGG                                      | CCTTTGCCTTTCTGAG<br>ATGG  | GCGGTGAATATCCAAA<br>GGAC  | 59.8                             | 481                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_37428682  | Ca3                                     | 37428682                      | T/TGGA                                                                        | TTGAGGATCAGCTACA<br>CCCC  | TGGAACAATTTTGGTG<br>GTGA  | 60.1                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_37484993  | Ca3                                     | 37484993                      | TATAATAATAATAATAATAATAT<br>TAATAATAATA/TATAATAATAATAAT<br>AATAATATTAATAATAATA | CCCGCGTAAATATCAA<br>TGCT  | GGTGGTGGTTTGACG<br>TAAC   | 60.0                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_37594905  | Ca3                                     | 37594905                      | TTATATATATATATATATATATA/T<br>TATATATATATATATATATATA                           | GTCCGCCCTAAAAAGG<br>TAGC  | TCAAAACACCACATCAA<br>AAGC | 60.1                             | 188                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_37719535  | Ca3                                     | 37719535                      | TGG/TGGG                                                                      | TTGGGTCAAGAATTCA<br>TCTCG | CCCAAAATGTGGCTTG<br>AAAT  | 60.1                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_37756750  | Ca3                                     | 37756750                      | ATTTTTTTTT/ATTTTTTTTTT                                                        | AATAGGCCAGGTCAGG<br>CTTT  | GGATTGTTGATGATG<br>GCTT   | 60.1                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_37828643  | Ca3                                     | 37828643                      | CCAGAC/CC                                                                     | GGGAATAGGCTAGACC<br>GTCC  | GCTTGGCCTACGACCT<br>ATCA  | 59.9                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_37875029  | Ca3                                     | 37875029                      | GT/GTT                                                                        | ATGGCGTGACTGAACA<br>TGAA  | AAGGGCAAGATCCCAA<br>AAAC  | 60.1                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_38007387  | Ca3                                     | 38007387                      | TTCTCTCTCTCTCTCTCTCTCTCT<br>/TTCTCTCTCTCTCTCTCTCTCTCT<br>TCT                  | AAACAATACGCAAAACC<br>GGAG | CTTCTCCAACAAGAGC<br>GACC  | 60.0                             | 245                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_3804824   | Ca3                                     | 3804824                       | TAAA/TAA                                                      | AGTCAGACGCTACTCG<br>GCAT       | ATTAGGGGAGCATGCA<br>TTTG        | 60.0                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_38129457  | Ca3                                     | 38129457                      | CATATATATATATATA/CATATATATA<br>TATATATA                       | CAAAAGCCGGACCAAA<br>ATTA       | GGGCATGGGCAATAAT<br>CTAA        | 59.9                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_38142353  | Ca3                                     | 38142353                      | TCGACGAC/TCGAC                                                | ATCAATTGGTCGCACC<br>TTTC       | CATGATGGCAAATTCAT<br>AGGC       | 59.9                             | 387                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_3818047   | Ca3                                     | 3818047                       | G/GGA                                                         | ATGCTCTGCACCTTGCA<br>GCTA      | TTCATCGCCTCAAAGT<br>GTTG        | 59.9                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_38182761  | Ca3                                     | 38182761                      | TTGATATGATAT/TTGATAT                                          | AAACAACGTCATGAAG<br>AAAATTGA   | GGTTTTGCCAACATCT<br>GCTT        | 59.9                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_38182839  | Ca3                                     | 38182839                      | AGTGTGTGTGTGTGTGT/AGTGTGT<br>GTGTGT                           | AAAGCGTCTTTCATTAA<br>TAGTGTGTG | GGTTTTGCCAACATCT<br>GCTT        | 60.0                             | 319                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_38183210  | Ca3                                     | 38183210                      | TTAAATTAATAAATTAATAAA/TTAAA<br>TTAATAAA                       | AATCAAGCAAGCCGTT<br>GACT       | TAAAGGTTTTGTGCGT<br>GTCG        | 59.9                             | 356                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_38240907  | Ca3                                     | 38240907                      | ATTTTTTTTTTTTTT/ATTTTTTTTTT<br>T                              | GGCTCCTCTCCTCTAA<br>CGGT       | GACAAGTGCAACAATTT<br>TCATCA     | 59.8                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_38241297  | Ca3                                     | 38241297                      | TTTATT/TTT                                                    | TTGATGAAAATTGTTGC<br>ACTTG     | TTGCTAACACAAAAGTA<br>TTTGAATGTC | 58.7                             | 189                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_38322519  | Ca3                                     | 38322519                      | GTGAT/GT                                                      | CCTTGGCAGTCGTTGT<br>TTCT       | GCCATACACGTGTCTC<br>CCTT        | 60.3                             | 122                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                 |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_38406107  | Ca3                                     | 38406107                      | AATATATATATATATATATAT/AA<br>TATATATATATATATATATATAT                             | CTCTCAAAGTGCTGAA<br>GAGACC  | GGGACTGCATACCAAT<br>AGCTG | 58.3                             | 775                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_38693651  | Ca3                                     | 38693651                      | TAA/T                                                                           | GCCTTTCACATCAAAC<br>CGAT    | GAGAGAGCATCCCGAA<br>AACA  | 59.9                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_38729935  | Ca3                                     | 38729935                      | CTTTTTTTT/CTTTTTTTTT                                                            | AAAAGGCAAATGTGTG<br>TCATTG  | CATTGGCCACAGAAC<br>ATTG   | 59.9                             | 856                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_38735945  | Ca3                                     | 38735945                      | TTTTATTTATTTATTTAT/TTTTATTTA<br>TTTATTTATTTATTTAT                               | GGGTTTGCTTATTGA<br>GAATACTG | GAATCTAGCAGCAGGA<br>GCCA  | 58.3                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_38900161  | Ca3                                     | 38900161                      | GACAACA/GACA                                                                    | GCCATTCCATTAAAGG<br>GTCA    | TCTGCCTAATCAAACAT<br>GCC  | 59.8                             | 891                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_39010533  | Ca3                                     | 39010533                      | AG/AGG                                                                          | CGGGCTTTCCTGTTAC<br>ACAT    | GCAGAGAAAGGAACAG<br>AGCG  | 60.0                             | 309                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_39248121  | Ca3                                     | 39248121                      | CATATATATATATATATATATATA<br>TATATA/CATATATATATATATATATA<br>TATATATATATATATATATA | CCAAGTTGGCTAAACC<br>TTGC    | CATACCACCATTCTTTC<br>CCG  | 59.7                             | 783                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_39355870  | Ca3                                     | 39355870                      | TAAAAAAAAA/TAAAAAAAAA                                                           | TGCGAGATCGAAGATT<br>TGG     | CGACGCGACTGGATTG<br>TAA   | 59.9                             | 725                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_39401096  | Ca3                                     | 39401096                      | ATTTTTTTTT/ATTTTTTTTT                                                           | ATTTGGGTCAAGGATG<br>ATGC    | GCTTTGCTTGCCCATTT<br>TTA  | 59.8                             | 940                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_39417852  | Ca3                                     | 39417852                      | AAT/A                                                                           | TGAGTTGTGAGATGCT<br>TCCCT   | CCTTGC AATTTTCTTT<br>GCC  | 59.9                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                            | Forward primers (5'-3')  | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------|--------------------------|---------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                          |                          |                                 |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_39419535  | Ca3                                     | 39419535                      | C/CAATAAAATA                                                                                             | CCTAACTCAGCATGGG<br>GAAA | TTAATTAATTGTTGGGG<br>TTTTGTT    | 60.1                             | 431                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_39419619  | Ca3                                     | 39419619                      | TAATATGAATATGAATAT/TAATATG<br>AATAT                                                                      | CCTAACTCAGCATGGG<br>GAAA | GCGTGACAATAGTAAG<br>ATAATTGTTCC | 60.1                             | 506                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_3963300   | Ca3                                     | 3963300                       | CAAAAAAAAA/CAAAAAAAAAAAAA                                                                                | TCCATTGTGTGCCACA<br>GTCT | TCTAGTCCGCGACTCA<br>ACCT        | 60.2                             | 505                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_39670282  | Ca3                                     | 39670282                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATAT                                                          | TGGTGCGACAATCATT<br>AACC | TGGATATCGAACCCTC<br>ACCT        | 59.4                             | 720                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_39706199  | Ca3                                     | 39706199                      | TTATATATATATATATATA/TTATATA<br>TATATATATA                                                                | TGCTCAAACCAAATAT<br>GGCA | TTGGGCAAAACTCCAT<br>CTTC        | 60.1                             | 770                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_39813917  | Ca3                                     | 39813917                      | AATATATATATATATAT/AAATAT<br>ATATATATATATAT                                                               | GAGGTTGGTCACCGGT<br>AAGA | TTGTAGGCGGTGTGTC<br>AAAT        | 60.0                             | 550                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_39988476  | Ca3                                     | 39988476                      | GTTTT/GTTT                                                                                               | AGAACAGAGCTGGCCT<br>CAAA | ATTGCAAGAAAACCAG<br>CACC        | 60.1                             | 148                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_4017573   | Ca3                                     | 4017573                       | TAA/TAAA                                                                                                 | ACCACAGATCACCAGT<br>CGCT | ACGTCCAAGGTAAGGG<br>CTTT        | 60.7                             | 683                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_4073796   | Ca3                                     | 4073796                       | CT/CTT                                                                                                   | CTCAACATCCACCATG<br>CAAT | TGCAAAATTCATCAAA<br>GCATAA      | 59.4                             | 746                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_4076583   | Ca3                                     | 4076583                       | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATT/ATA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATT | ATAGTCCTCACCCACG<br>CATC | AAGCGTACCTGTGGGA<br>ATTG        | 60.0                             | 607                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                      | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                    |                             |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_4132392   | Ca3                                     | 4132392                       | TTATATATATATATATAT/TTATAT<br>ATATATATATATATATAT                                    | CGTGTGAGAAAACCTC<br>GACA    | GAAGGCCAACTTCCAA<br>ATGA      | 59.9                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_4137886   | Ca3                                     | 4137886                       | TTATATATATATATATATATATATA<br>TATATATATA/TATATATATATATATA<br>TATATATATATATATATATATA | ATGTTCTCCTCCCTTT<br>TCA     | GTTCCGACGAAAACGA<br>CATT      | 58.6                             | 783                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_4152638   | Ca3                                     | 4152638                       | CTTTTTTTTT/CTTTTTTTTT                                                              | TGATGCAAAGTGTGCT<br>GTGA    | TTTTTGGTTGGGTGGG<br>TAAA      | 60.0                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_4180993   | Ca3                                     | 4180993                       | AATATATATATATATAT/AATATAT<br>ATATATATAT                                            | TTCAATTTACTTGT<br>GATGTAGCA | AAATTTTGATGACCGCA<br>TCC      | 59.2                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_4194452   | Ca3                                     | 4194452                       | GTTTTTTT/GTTTTTTT                                                                  | TGGCCTCTTAGACAA<br>TGCC     | TCGGTGGTTTGAATC<br>ATT        | 60.2                             | 159                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_4280022   | Ca3                                     | 4280022                       | CTTTTTTT/CTTTTTTT                                                                  | GCAAACCAACTCGAAT<br>GACA    | ATCTTGGTGGCATTGG<br>AAAG      | 59.7                             | 145                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_4365472   | Ca3                                     | 4365472                       | TC/TCC                                                                             | ATCCAATGCGAGCAGT<br>TCTT    | TGAGGGACAAAATAT<br>GGGAA      | 59.8                             | 792                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_4491629   | Ca3                                     | 4491629                       | TGAAAATGAGAAA/TGAAAATGAGAA<br>AGTAGAAAATGAGAAA                                     | ACAGGCACCGTTCAA<br>TAGG     | GATGTCGTGAGTGACA<br>TGGG      | 60.0                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_451560    | Ca3                                     | 451560                        | ATAACGTGATCTTA/ATA                                                                 | AGCAGAAAGGGAGAA<br>GGGT     | ACGGTGAAGCTCCGAA<br>AATA      | 60.1                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_454494    | Ca3                                     | 454494                        | AGGG/AGG                                                                           | GGATTGGAGTGTTCA<br>GCAT     | TTGTCATTAGTTTCAAT<br>CTCACCAA | 59.9                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_454633    | Ca3                                     | 454633                        | GATATATATATATAT/GATATATATAT<br>AT                             | GGATTGGAGTGTTCAG<br>CCAT   | TTGTCATTAGTTTCAAT<br>CTCACCAA | 59.9                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_458081    | Ca3                                     | 458081                        | TTATATATATATATAT/TTATATATAT<br>ATAT                           | GCGGTTTCCTTTAATT<br>TGGA   | GAGGGAACGCAGAAAG<br>TTCA      | 60.3                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_4689138   | Ca3                                     | 4689138                       | TAAAAAA/TAAAAAA                                               | CAGCTTGCAATTGCTTT<br>TGA   | TTGCTCCTACGTATCTC<br>CCG      | 60.1                             | 888                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_47457     | Ca3                                     | 47457                         | ATAGTGTAGTGTA/ATAGTGTA                                        | GCGTACTGGGCTGAG<br>ATGT    | TTTTAGATGCATGTGTG<br>CGG      | 60.3                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_488374    | Ca3                                     | 488374                        | ATTTTTTTTTT/ATTTTTTTTTT                                       | TTTGC GTTACGAATTTG<br>ATGA | ACAAAATACCAAGTGC<br>CCCA      | 59.2                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_4929398   | Ca3                                     | 4929398                       | ATTTTTTTTTT/ATTTTTTTTTT                                       | GGCTTGTCACATCAGC<br>TCAA   | TCAGAACCATGTCAAC<br>GAGTTC    | 60.0                             | 681                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_4965548   | Ca3                                     | 4965548                       | ATTTT/ATTTT                                                   | CGGGGAATGTGATTGA<br>TAGG   | GTTGGAGAGATCGGTG<br>GAAA      | 60.1                             | 948                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_4965624   | Ca3                                     | 4965624                       | AATT/AATTGAGGATT                                              | TGCAAATCTGGAGCAG<br>AGAA   | GTTGGAGAGATCGGTG<br>GAAA      | 59.7                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_4966098   | Ca3                                     | 4966098                       | CTTTTTTT/CTTTTTT                                              | TTTCCACCGATCTCTC<br>CAAC   | AAACCCGCTCCTTCAA<br>AAT       | 60.1                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_4975195   | Ca3                                     | 4975195                       | AATATATATATATATA/AATATATATA<br>TATATATATATATA                 | CAAAGTTCAATACGCC<br>AGCA   | AGGTTTTGGCGTAACT<br>CCCT      | 59.9                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                             |                          |                              |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_5092682   | Ca3                                     | 5092682                       | TTTT/TTTTGTTT                                                               | TCTGGATTCAAACCC<br>ACTC  | GTGGAAGGGTGCAAG<br>ACAT      | 59.9                             | 260                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_5269970   | Ca3                                     | 5269970                       | CAAACAATAA/CAA                                                              | GATTGGCACGTCGATT<br>AACA | TTCTCGCTTTCGTTTCG<br>TTT     | 59.5                             | 563                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_5270123   | Ca3                                     | 5270123                       | GAA/GA                                                                      | ACGAAACGAAAGCGAG<br>AAAA | CGACCTCGAAATAATC<br>GGAA     | 60.0                             | 521                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_5270478   | Ca3                                     | 5270478                       | TATCAATC/TATC                                                               | ACGAAACGAAAGCGAG<br>AAAA | CGACCTCGAAATAATC<br>GGAA     | 60.0                             | 521                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_5286221   | Ca3                                     | 5286221                       | ATTT/ATT                                                                    | CACCCCTCCCAAAACA<br>TCT  | TTGTGAGTGCATTGAT<br>TTTGTT   | 59.8                             | 876                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_5286324   | Ca3                                     | 5286324                       | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                               | CCTGAACCCAAATCA<br>AAACA | TTGACAAAGTTGAAATA<br>TGGGAAA | 59.8                             | 569                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_5288032   | Ca3                                     | 5288032                       | AATATATATATATATATATATAT/A<br>ATATATATATATATATATAT                           | AGAAGGTCGCATCTCC<br>AAGA | TGGCACTTGTATTCATC<br>CGC     | 60.0                             | 456                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_5288343   | Ca3                                     | 5288343                       | ATT/ATTGTTGTT                                                               | GCGAGTGAATACAAGT<br>GCCA | TAGAAGATCGCATCCC<br>CAAG     | 59.9                             | 549                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_5347423   | Ca3                                     | 5347423                       | CAATAATAATAATAATAATAATA<br>ATAATAATAA/CAATAATAATAATAAT<br>AATAATAATAATAATAA | TTGCTCTACGTATCT<br>CCCG  | TTGTGACAATTTGATGG<br>TTCTAAA | 60.2                             | 563                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_5389213   | Ca3                                     | 5389213                       | AATTATTATTATTATTATT/AATTATT<br>ATTATTATTATTATT                              | AAGAGACTTCGCGTCC<br>AAAA | CAAGTTTCAACAAATAA<br>ATGCACA | 60.0                             | 229                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                   | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                                 |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_540167    | Ca3                                     | 540167                        | CTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>A/CTAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT | CAGAGGCAGCAAACAA<br>TGAA | GGAAAATCATCGAAAA<br>GCAGA | 60.0                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_5502243   | Ca3                                     | 5502243                       | TG/T                                                                                                                                                            | TGCGTTTTTCTGCATT<br>CTG  | ATTCTGCGCGACTATC<br>AACC  | 60.0                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_5520403   | Ca3                                     | 5520403                       | GTATATATATATATATATATATAT<br>A/GTATATATATATATATATATATA                                                                                                           | CAATGACGACGACGA<br>TGAC  | GAATGATGACAATGCG<br>GTTG  | 60.1                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_5520464   | Ca3                                     | 5520464                       | TTATATATATATATAT/TTATATATAT<br>ATATATAT                                                                                                                         | CAATGACGACGACGA<br>TGAC  | GAATGATGACAATGCG<br>GTTG  | 60.1                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_5643374   | Ca3                                     | 5643374                       | TCCC/TCC                                                                                                                                                        | GAGAAATGGAGGCAAT<br>GGAA | GCAACACTCATTTGCC<br>CTTT  | 60.0                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_5689033   | Ca3                                     | 5689033                       | CT/CTT                                                                                                                                                          | TTGGTCAATGTGGCTT<br>CTCA | TGAACTCTGAGCGTGT<br>GACC  | 60.2                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_5689239   | Ca3                                     | 5689239                       | GA/GATTATGTTA                                                                                                                                                   | TTGGTCAATGTGGCTT<br>CTCA | TGAACTCTGAGCGTGT<br>GACC  | 60.2                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_5689325   | Ca3                                     | 5689325                       | ATTT/ATT                                                                                                                                                        | TTGGTCAATGTGGCTT<br>CTCA | TGAACTCTGAGCGTGT<br>GACC  | 60.2                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_5689863   | Ca3                                     | 5689863                       | GTTT/GTTTT                                                                                                                                                      | GGTCACAGCTCAGAG<br>TTCA  | GAAGCAAATCGATTGG<br>GAAA  | 60.0                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_5698499   | Ca3                                     | 5698499                       | TTATAT/TTATATAT                                                                                                                                                 | GAGGATTTGGGGGAGA<br>AGAG | AGAAGGGAGGAGATGG<br>AAGC  | 60.0                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_5729374   | Ca3                                     | 5729374                       | TAAAAAAAAAAAAA/TAAAAAAAAAAAA<br>A                             | TCGTGTTTCACTATCCA<br>ACCC | TTCCAGCACATTGTCTT<br>CCA     | 59.8                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_5769480   | Ca3                                     | 5769480                       | ACC/AC                                                        | TAATGGTTTTTCAGGCC<br>AACA | TACGGTGCTAGGGAAC<br>CAAC     | 60.0                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_5805263   | Ca3                                     | 5805263                       | GT/GTT                                                        | CAATTGGTCGAAAGAC<br>GGAT  | TTCGAATGAACATAATT<br>GAACTTT | 59.9                             | 164                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_5805325   | Ca3                                     | 5805325                       | TAAAAA/TAAAAA                                                 | CAATTGGTCGAAAGAC<br>GGAT  | TTCATCTTCGTCAACAA<br>TGAAAA  | 59.9                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_5921705   | Ca3                                     | 5921705                       | GT/GAGAT                                                      | GGCGTTGGTTTCACTC<br>AAAT  | TCAGTCAACGCACAC<br>AAAA      | 60.0                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_6057834   | Ca3                                     | 6057834                       | TTATATATATATATAT/TTATATATAT<br>ATATATAT                       | AATTCATAGAAAGCA<br>GGGGG  | TCTTTGCCTGGTCTGA<br>CCTT     | 59.5                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_6352791   | Ca3                                     | 6352791                       | AATATATATATATATATAT/AAATAT<br>ATATATATATATAT                  | TTTTTATGTTGGGCC<br>ATGT   | ATGCGCTTGACAAGAA<br>TGTG     | 60.1                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_6432046   | Ca3                                     | 6432046                       | TAAAAAAAAAAAAA/TAAAAAAAAAAAA                                  | TCCTGATGGCAATGCA<br>AATA  | AATAAGGTTGTCGTTT<br>GCG      | 60.0                             | 172                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_6466373   | Ca3                                     | 6466373                       | TTAATAATAATAATAATAA/TTAA<br>TAATAATAATAATAATAA                | GAACCCCTGTAAACAC<br>CAGA  | GGAGAACGTTAAGGCA<br>GCAG     | 59.8                             | 443                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_6548012   | Ca3                                     | 6548012                       | CT/CTT                                                        | TTATGCCGTTTGGAGT<br>TTCC  | TTCAATTGCCTTGTGG<br>CATA     | 59.9                             | 615                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')    | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|----------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                            |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_6664320   | Ca3                                     | 6664320                       | TAAAAA/TAAAAA                                                           | TGAAATTATGGGTGGG<br>CATT   | GCTGAAAAAGTGCCGA<br>AGAA        | 60.0                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_6723619   | Ca3                                     | 6723619                       | T/TAATAATAATA                                                           | TGGAAAGCTTGTTAGC<br>AAATG  | AACGCACGAGCAAATT<br>CTTT        | 58.1                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_6730727   | Ca3                                     | 6730727                       | CTTTTTTTTTTT/CTTTTTTTTTTT<br>T                                          | TTTAGGATTTTCCAACC<br>ACCA  | TGGGGAGATAGGGTTG<br>ATTTT       | 59.3                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_6790470   | Ca3                                     | 6790470                       | T/TA                                                                    | GGCTGGCTACTTAGGG<br>ATCA   | GACCTCGTCCAGCTTT<br>TCAG        | 59.3                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_6814196   | Ca3                                     | 6814196                       | AATATATATATATATATATATAT/AAT<br>ATATATATATATATATATATAT                   | CATGAACCTCATCAC<br>TCCG    | AACCATCCTAATTTGAC<br>ACCAA      | 59.9                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_6821813   | Ca3                                     | 6821813                       | TCCC/TCC                                                                | GAAACTTGTAGGGGAG<br>GGGA   | ATTGTAGCTTGGGATC<br>ACGC        | 60.3                             | 304                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_6921816   | Ca3                                     | 6921816                       | AATATATATATATATATATATATAT<br>AT/AATATATATATATATATATATA<br>TATATATATATAT | TGTTTATGTTTGTTACG<br>CCTGC | GGAATTGGGAAAAATG<br>GGAT        | 60.1                             | 168                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_6961692   | Ca3                                     | 6961692                       | TTAATAATAATAATAATAATAA/T<br>TAATAATAATAATAATAATAATA<br>A                | GCCAAAACAAATTGGA<br>GAGG   | TCCTAGATCTGGAAC<br>AGAGGTCA     | 59.5                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_7118164   | Ca3                                     | 7118164                       | AATATATATATATATATATATATAT<br>AT/AATATATATATATATATATATA<br>TATATAT       | AAAGCATGTCTTCGGT<br>TTTCA  | TGAATATCAAACAATCA<br>ACTATCAACA | 59.7                             | 849                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_7330455   | Ca3                                     | 7330455                       | GTTTTTTTTTTTT/GTTTTTTTTTT<br>T                                          | CCAACAAAGGACGGA<br>AGAA    | TTTTGTCCCAACAATCT<br>CCC        | 60.1                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                    | Forward primers (5'-3')   | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------|---------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                  |                           |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_7377309   | Ca3                                     | 7377309                       | TAAAAA/TAAAAA                                                                                                                    | CATATTCGCATTCCCA<br>ACC   | ACCTGCAAACCAACT<br>CAAC        | 60.2                             | 306                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_7456958   | Ca3                                     | 7456958                       | TTATATATATATATATA/TTATATA<br>TATATATATATATA                                                                                      | CACATACCGCGGTTAG<br>AACA  | ACCATTTCACGTGATT<br>GCT        | 59.6                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_7494196   | Ca3                                     | 7494196                       | T/TC                                                                                                                             | TTGCTTTGGTTTGATGT<br>GGA  | GAAGTTGCCTTAGTGG<br>CAGG       | 60.1                             | 694                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_7636434   | Ca3                                     | 7636434                       | TTATTATTA/TTATTACTATTATT<br>A                                                                                                    | TGGCCTTGTTGTGATT<br>GCAT  | CTGAATTGCGTGTGTC<br>TGGT       | 60.0                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_7749695   | Ca3                                     | 7749695                       | G/GACT                                                                                                                           | GCTTGGTTTTCTGGGT<br>TTGA  | ACCTTGAATCGTGCC<br>TCTA        | 60.1                             | 870                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_7773838   | Ca3                                     | 7773838                       | AATATATATATATAT/AATATATAT<br>ATATAT                                                                                              | CATGCGAGTTGTAACA<br>CCCT  | CGTGCATACTTAATATC<br>AGTCAAGTG | 58.7                             | 365                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_7792015   | Ca3                                     | 7792015                       | TAT/TATTATCTTCCCTAAT                                                                                                             | TAGGTAAAGGTGGTTT<br>GCCG  | TGAGGGATAGATGCAG<br>GTCA       | 60.0                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_7959750   | Ca3                                     | 7959750                       | TTAATTTGATTATGTTAAGTAATTTG<br>ATTATGTTAA/TTAATTTGATTATGTT<br>AAGTAATTTGATTATGTTAAGTAATT<br>TGATTATGTTAA                          | TTGGCATAGGTCATGG<br>AAGTT | TTTGCCAATGTTGCTAG<br>CTG       | 59.4                             | 848                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_805419    | Ca3                                     | 805419                        | CTTTATTTATTTATTTATTTATTTATT<br>TATTTATTTATTTATTTATTT/CTTTA<br>TTTATTTATTTATTTATTTATTTATT<br>ATTTATTTATTTATTTATTTATTTATT<br>TATTT | GAACGTATGAGTTGTG<br>CGGA  | GGAGGTGATTTCAAAG<br>GCAA       | 59.7                             | 260                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_8061977   | Ca3                                     | 8061977                       | T/TC                                                                                                                             | CTGAAAAAGTTCGACG<br>AGCC  | AATTGTGCTTGCTCCC<br>ATTC       | 60.0                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                   |                           |                            |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_8088284   | Ca3                                     | 8088284                       | CT/CTCTCTTCACAT                                                                   | TCTTCCACCCAGTTT<br>GACC   | ACATAACACGTGGCCT<br>GTGA   | 59.9                             | 477                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_8146397   | Ca3                                     | 8146397                       | AT/A                                                                              | TCAAGAAGGATGGAGG<br>ATCG  | TCCTTTTGCACATGCTT<br>CAC   | 60.2                             | 448                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_8245494   | Ca3                                     | 8245494                       | TCT/TCTTCTGCT                                                                     | TGCGCCTCTTCTAAAT<br>CGT   | TATCGCAATCAGAGGA<br>ACCC   | 60.0                             | 670                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_8393314   | Ca3                                     | 8393314                       | GTATATATATATATATAT/GTATAT<br>ATATATATATATATATAT                                   | GTTGGTTCCCTAGCAC<br>CGTA  | TATTTTGGATTTTGGCT<br>CGG   | 60.0                             | 602                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_8523296   | Ca3                                     | 8523296                       | ATTTTTTTTT/ATTTTTTTT                                                              | CACATGACAAATTGG<br>TGGAA  | CGTTAAGGCACATCTC<br>ACTCC  | 59.3                             | 508                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_8544653   | Ca3                                     | 8544653                       | CG/C                                                                              | ACCTGCGGTTACTTCC<br>ACAG  | TTTCTGCACTCTGCCA<br>CATC   | 60.2                             | 600                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_8602266   | Ca3                                     | 8602266                       | AATATATATATATA/AATATATATATA<br>TATA                                               | GCTCAACAGAGACCAC<br>CACA  | CGTATTCGTGTGTGAA<br>AGCG   | 59.9                             | 835                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_8611127   | Ca3                                     | 8611127                       | ATATTATTATTATTATTATTATTA<br>TTATTATTATTAT/ATATTATTATTAT<br>TATTATTATTATTATTATTAT  | AGAATTAATGGTTGCG<br>GTCG  | CTCCAGGTGCAATAGG<br>GAAA   | 60.0                             | 434                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_8775439   | Ca3                                     | 8775439                       | GTATATATATATATATATATATAT<br>ATATATATAT/GTATATATATATATAT<br>ATATATATATATATATATATAT | AGTCGCATCTTCGTGCG<br>TTTC | GGCATCGGGAGTCTGT<br>TTTA   | 60.4                             | 537                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca3_P4_8942193   | Ca3                                     | 8942193                       | AT/ATT                                                                            | TGGGGAAAAACCTTA<br>CCTT   | CACATGATTTCAATTGG<br>CTTTG | 59.7                             | 326                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_9186815   | Ca3                                     | 9186815                       | CTATATATATATATATATATATA/C<br>TATATATATATATATATATATATATA       | TCCACAAACACGATAA<br>CATTGA | TGTAACAAGCATTGTG<br>GGG     | 58.9                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_9215609   | Ca3                                     | 9215609                       | TAAAAAAAA/TAAAAAAAA                                           | AAATCCCAAGTTGTA<br>CGGC    | TTGGATGTGTTGGCTT<br>GTGT    | 59.0                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_9289555   | Ca3                                     | 9289555                       | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATATATAT       | GAACCAAGTTGCATGG<br>GAAT   | CCTAGGGACTTCGTGG<br>TTGA    | 59.8                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_939073    | Ca3                                     | 939073                        | GTT/GTTTT                                                     | ATTGGTTCTGCTCTGG<br>GTTG   | GGGACCACAGCACCTA<br>TGTT    | 60.1                             | 296                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_9416399   | Ca3                                     | 9416399                       | AG/AGG                                                        | CCCAAGAGAACGCAAT<br>TCAT   | TCTCACGGTTGTGAGG<br>ACTG    | 60.1                             | 811                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_9426071   | Ca3                                     | 9426071                       | CAAAAAAAAA/CAAAAAAAAA                                         | CCATAAAACCATTTCCA<br>TTGC  | TACTCTAGCAACCACC<br>GCCT    | 59.2                             | 262                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_9427257   | Ca3                                     | 9427257                       | TTTA/T                                                        | CATGCGTTCCTTGTTG<br>TAGA   | GGCCTAAGATCATAGC<br>AATTCAA | 59.7                             | 165                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_9500843   | Ca3                                     | 9500843                       | CAATCGATTTC/CAATCGATTCCA<br>AATCGATTTC                        | CCCGTGAGATCCTCCT<br>AACA   | CATGCAGGAATTCAGC<br>AAAA    | 60.1                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_9735715   | Ca3                                     | 9735715                       | TC/T                                                          | GGAATATTGATCCACT<br>CGCC   | GAAAAAGCGCTGTAA<br>TGCC     | 59.3                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_9827185   | Ca3                                     | 9827185                       | TAAAAAAAAAAAA/TAAAAAAAAAAAA                                   | GAAGGCTACCGTTACG<br>CAAT   | CGGGAGATACGTAGGA<br>GCAA    | 59.3                             | 756                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3') | Reverse primers (5'-3')  | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|-------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                 |                         |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_9846827   | Ca3                                     | 9846827                       | AATATATATATATATATATATATATATATATATATATA/AATATATATATATATATATATATATATATATATATATATA | GTGGCTTTCGTTGAATGGTT    | CAAAATGCCACAAACTCTGATG   | 60.0                             | 280                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_9940560   | Ca3                                     | 9940560                       | A/AT                                                                            | ACCGGTATTGTAACACCCCA    | CCTTATGCGGTAATCCCTGA     | 60.0                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca3_P4_9953160   | Ca3                                     | 9953160                       | GAAAAAA/GAAAAAAA                                                                | TGCCACGTTTCTATTTCCT     | ATCACGCCATAAGCACCTTC     | 59.6                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10033685  | Ca4                                     | 10033685                      | TTATATATATATATATATAT/TTATATATATATATATATATATAT                                   | CTAGTTCGTAACCCGTGCGT    | AGGCATGGTGTGGAGTCAT      | 60.2                             | 248                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10035522  | Ca4                                     | 10035522                      | GT/GTT                                                                          | AAGGGAGACGCAAGAAATGA    | CATCACGATCTTTGTCCACG     | 59.8                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10092984  | Ca4                                     | 10092984                      | GTTTTTTTT/GTTTTTTTTT                                                            | CGCACGAGTAACACGTCATT    | ACGCGGAACAAATATTGTCA     | 59.8                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10147217  | Ca4                                     | 10147217                      | GTTTTTTTTT/GTTTTTTTTT                                                           | TGAATGCGCGTATTGTGAAT    | AAAAATGACAAACGAAACATAAAA | 60.1                             | 728                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10173137  | Ca4                                     | 10173137                      | ATTTTTTTT/ATTTTTTTTT                                                            | CCCGTTATTTTGTACGAAACA   | TGTGTTGAGTGGTGGCATTT     | 59.9                             | 791                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10208528  | Ca4                                     | 10208528                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                                   | CCACCAATCCCAAAAATTG     | CCCAACACCTTTGGCTTTTA     | 60.0                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10223331  | Ca4                                     | 10223331                      | AATATATATATATATATATATATATATATATAT/AAATATATATATATATATATAT                        | ACGTGAAGTCCAAATCTGCC    | TTCGACTGTCCACGTATATCTCA  | 60.1                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)      | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                    |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_10233239  | Ca4                                     | 10233239                      | GACAATTATTTGGTACAATTAT/GAC<br>AATTATTTGGTACAATTATTTGGTAC<br>AATTAT | TGTCGGTTGTTGCTTG<br>AAGA  | ATACAATCATTTTCCCG<br>CCA   | 60.4                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10241994  | Ca4                                     | 10241994                      | TAAAAAAAAA/TAAAAAAAAA                                              | CCTGCACCATTCTCTT<br>GGT   | TTTCTGGTAACTCGGA<br>CCC    | 60.1                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10247608  | Ca4                                     | 10247608                      | CAATATTGTAAAATA/CAATATTGTA<br>AAATAATATTGTAAAATA                   | GAGTTAGGGTTGGTGA<br>GGCA  | TTTTTCACGTCGCATAA<br>ATCT  | 60.1                             | 236                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10253630  | Ca4                                     | 10253630                      | GAAAAAAA/GAAAAAAA                                                  | TGTGTTTGAATGGGCA<br>AAAA  | CTTCATTTAAACGCCCC<br>AAA   | 59.9                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10261671  | Ca4                                     | 10261671                      | ATTTTTT/ATTTTT                                                     | TGGATTTGGACTTGG<br>TCTTG  | AACAACACGTGATTTGA<br>ATTGC | 60.0                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10329029  | Ca4                                     | 10329029                      | AC/A                                                               | GAGTTACGGATCCACA<br>ACCAA | TTTTTAACTTTCGGGT<br>GGT    | 59.8                             | 414                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10456572  | Ca4                                     | 10456572                      | ATTTTTTTT/ATTTTTTTT                                                | ATCGATCAAACCCGT<br>GAAG   | CGTTGTTGGTAAGGGA<br>ATCG   | 59.9                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10460005  | Ca4                                     | 10460005                      | ATTTTTTTTTT/ATTTTTTTTTT                                            | TCAAATCAAATCCAAAG<br>GGC  | TCGTCTCTTTGTGGTAA<br>TCGTG | 59.9                             | 687                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10555606  | Ca4                                     | 10555606                      | TTA/TTAATA                                                         | TGTTGAAATGTGGTGT<br>GGCT  | CAGCTTAGCTCGGGT<br>TTTG    | 60.0                             | 764                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10586036  | Ca4                                     | 10586036                      | CATATATATATATATAT/CATATAT<br>ATATATATATATAT                        | GTAGCCGAGCAGGAAA<br>TGAG  | CATGCGAGTTAATGAC<br>GGAG   | 60.0                             | 860                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                              | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                            |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_10612304  | Ca4                                     | 10612304                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATT/TTTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATT             | AATCACGCAAAACAAGT<br>GTCG    | AGCGACATAAATGGCT<br>GCTA   | 59.8                             | 408                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10648356  | Ca4                                     | 10648356                      | CTTTTTTTTT/CTTTTTTTTT                                                                                      | GGCCATCTATGGGTCC<br>TACA     | GGTTGATCCAACAAGT<br>TCAAAA | 59.8                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10649251  | Ca4                                     | 10649251                      | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATATATA<br>TAT                                              | TGAGTCACTTAGAGGG<br>AGGGA    | CCCAACAAATAAACCC<br>CCTT   | 58.9                             | 295                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10793822  | Ca4                                     | 10793822                      | AT/ATGGT                                                                                                   | TGGTGAAAATAGATTA<br>GGACGAGA | CTGAACATTGCGTGCT<br>CTCA   | 59.2                             | 943                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10879888  | Ca4                                     | 10879888                      | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTA/ATATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTA | TTGAGAAAGAAGGGGA<br>AGACA    | AATCCTGCCAGCTAG<br>AGTT    | 58.9                             | 390                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10954430  | Ca4                                     | 10954430                      | AATATATATATATATATATATA/AATA<br>TATATATATATATATATATA                                                        | TTCGTGAATTAGTTTT<br>CGTGA    | TAACGTAACATGCCATT<br>GCC   | 59.6                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_10993124  | Ca4                                     | 10993124                      | CAAAAAA/CAAAAAA                                                                                            | CCTAAAACCCTAACCC<br>CCAA     | AGCACCCCAAAAAGA<br>AAGT    | 60.0                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11083084  | Ca4                                     | 11083084                      | ATTTTT/ATTTTT                                                                                              | GTTTTGGTGTGAAGC<br>GGAT      | TGCAATTTTGACCGATA<br>CCA   | 60.0                             | 905                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11216489  | Ca4                                     | 11216489                      | TAAAAA/TAAAAA                                                                                              | CTTCGCGCCAGTGTCT<br>TAAT     | TCAAACCAAGGATGAT<br>GCAA   | 60.4                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11216964  | Ca4                                     | 11216964                      | TAAAAA/TAAAAA                                                                                              | TTGCATCATCCTTGTT<br>TGA      | TCATTCCCTACGTACTC<br>GGC   | 60.0                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_11225146  | Ca4                                     | 11225146                      | GTG/GTGGCTTTG                                                 | TGGGGAGAAACAAAT<br>GGAG    | AGTGTGCTTTCGGCTA<br>AGGA  | 59.9                             | 607                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11263983  | Ca4                                     | 11263983                      | CAAAAAAAAA/CAAAAAAAAAAAAA                                     | CGCATGTGTGCTTGAA<br>TCTC   | TCCACCAATTTTGCAAT<br>GAA  | 60.4                             | 786                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11264215  | Ca4                                     | 11264215                      | TA/TAA                                                        | TGTGGGATCAATTGGG<br>AAGT   | TCCACCAATTTTGCAAT<br>GAA  | 60.2                             | 171                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11268024  | Ca4                                     | 11268024                      | AAAGAA/AAA                                                    | TAGTGCCCTCCAAAG<br>GATG    | GCGTTGAGGTGTCAAC<br>TGTG  | 60.1                             | 733                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11270494  | Ca4                                     | 11270494                      | CATATAT/CATAT                                                 | TGTTGACAAACACAAA<br>GACCG  | ATCCACCATCAATGCC<br>ATCT  | 59.6                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11282146  | Ca4                                     | 11282146                      | T/TA                                                          | TCGAACCATGTATTGAT<br>TTTGC | ACGCCACTTTGTCAAA<br>CACA  | 59.8                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11291506  | Ca4                                     | 11291506                      | GAAACAACTT/G                                                  | GATGAAAGTTTTTGGT<br>GTGGC  | CATTCGGATGGACACT<br>CTCA  | 59.5                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11298187  | Ca4                                     | 11298187                      | CTTTTTTTTTTT/CTTTTTTTTT                                       | AAATGCTCCAAAACCC<br>AACG   | ATTAAAAATGCCAGCAGT<br>GGG | 60.0                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11300403  | Ca4                                     | 11300403                      | ATATTATT/ATATT                                                | GTGTTACTTCGCGCT<br>TGAT    | TGTCAAGTTGTTTCATG<br>CTGC | 60.0                             | 185                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11300962  | Ca4                                     | 11300962                      | C/CG                                                          | GCAGCATGAAACAAC<br>TGACA   | TTTCTTAATGTGCGCAA<br>TGG  | 59.9                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_11318155  | Ca4                                     | 11318155                      | ATTTTTTTTT/ATTTTTTT                                           | ATTCTCATGGCAAGGG<br>ATTG    | TGCGTAATGGACCAAT<br>TCAA    | 59.9                             | 909                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11319252  | Ca4                                     | 11319252                      | GGGAG/GG                                                      | ATGACCTTTTTCTGC<br>CCTT     | CGCACACAGACGCAAT<br>ACTT    | 59.9                             | 313                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11319307  | Ca4                                     | 11319307                      | TGCG/TG                                                       | ATGACCTTTTTCTGC<br>CCTT     | CCACCACCAAAGTCCA<br>AAGT    | 59.9                             | 733                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11321165  | Ca4                                     | 11321165                      | AT/A                                                          | ATGATGATGATGCTAC<br>CGCA    | TGGTTAATTGAAACGG<br>TGAAGTT | 60.1                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11321437  | Ca4                                     | 11321437                      | ATTTT/ATTTT                                                   | AACCTCACCGTTTCAAT<br>TAACCA | CAGAGAATCCGACTCC<br>GAAA    | 59.8                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11321691  | Ca4                                     | 11321691                      | ATT/ATTT                                                      | AACATGTGGCTAACA<br>CCCTT    | CAGAGAATCCGACTCC<br>GAAA    | 58.5                             | 316                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11322366  | Ca4                                     | 11322366                      | ATTT/ATTTTT                                                   | TTGTGAGGAATGCAAA<br>CTGC    | ACAATCATCATGCCATC<br>GAA    | 59.8                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11322920  | Ca4                                     | 11322920                      | AAGCTCCTCTTC/A                                                | TCGATGGCATGATGAT<br>TGTT    | AAGAGGATTGGAGATA<br>GGAGAGC | 59.9                             | 371                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11338339  | Ca4                                     | 11338339                      | AAGA/AAGAGA                                                   | ACGGATAAAATGCCCA<br>TTGA    | ATTGGTGTGAGTGCTG<br>TGGA    | 60.2                             | 821                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11341314  | Ca4                                     | 11341314                      | TAAA/TAA                                                      | TGCATTGCCTTCTCAAA<br>CTG    | TCAGCTTATCACTGGG<br>GTCC    | 60.0                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_11341357  | Ca4                                     | 11341357                      | AATATATATATATATATATAT/AA<br>TATATATAT                         | TGCATTGCCTTCTCAAA<br>CTG    | TCAGCTTATCACTGGG<br>GTCC  | 60.0                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11348371  | Ca4                                     | 11348371                      | ATG/A                                                         | CGAACTTTGTCCACCC<br>CTAA    | TTTGTGGCATCGCTTA<br>TTG   | 60.0                             | 849                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11352038  | Ca4                                     | 11352038                      | GAGAGAGAGA/GAGAGAGAGAAAG<br>AGAGAGA                           | TGCCCATGTTTACCAC<br>AAAA    | CCCTCTCTCTCTCTCTC<br>TCGG | 59.8                             | 898                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11354394  | Ca4                                     | 11354394                      | CAACAATAACAATAACAATAACAATA<br>ACA/CAACAATAACAATAACAATAAC<br>A | GATGTTCTTTGCCCC<br>ATAA     | AGAGACAAATTCAGGG<br>TGGG  | 59.8                             | 720                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11354532  | Ca4                                     | 11354532                      | ATGTTGTTGTTG/ATGTTGTTGTTGT<br>TGTTG                           | GATGTTCTTTGCCCC<br>ATAA     | AGAGACAAATTCAGGG<br>TGGG  | 59.8                             | 720                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11357023  | Ca4                                     | 11357023                      | C/CA                                                          | GCCTCGTTGATTACCC<br>AAAA    | GGCATGGACGTAGGCT<br>AGAG  | 59.9                             | 809                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11359837  | Ca4                                     | 11359837                      | ACCC/ACC                                                      | TGTTGCGGTTGTATGG<br>TGTC    | TGACATTGGGGGATTC<br>ATT   | 60.4                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11368276  | Ca4                                     | 11368276                      | CG/C                                                          | TGATGAATTTTCATTCA<br>CCAATC | TCCCAAGGTCAATTAG<br>GCAG  | 58.8                             | 116                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11370496  | Ca4                                     | 11370496                      | TAAAAAAAAA/TAAAAAAAAA                                         | GAGATGGTGAAATCCA<br>ACGC    | TTTGAAGGGTTTAGA<br>GGGG   | 60.5                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11370815  | Ca4                                     | 11370815                      | TAAA/TAAAAA                                                   | GAGATGGTGAAATCCA<br>ACGC    | AGGGAGGGGATGAGA<br>GAAAA  | 60.5                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_11376655  | Ca4                                     | 11376655                      | TGGGG/TGGGGG                                                  | ACTGTGTTGAAGTGAG<br>GGGC   | CGTTTGATAAGATTTC<br>GCA    | 60.2                             | 753                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11377196  | Ca4                                     | 11377196                      | TAAAAAA/TAAAAAAA                                              | TTGCGGAAATCTTATCA<br>AACG  | GATGAAGTTCACCCAC<br>CACA   | 60.1                             | 331                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11377416  | Ca4                                     | 11377416                      | CAAAAA/CAAAA                                                  | TTGCGGAAATCTTATCA<br>AACG  | TGCTGGACCATAAACC<br>CATT   | 60.1                             | 783                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11383319  | Ca4                                     | 11383319                      | GTTTTT/GTTTTTTT                                               | CAAGATTAACGGTGAC<br>TGCAT  | GATCCACCTTTGGACA<br>GAGC   | 57.8                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11393203  | Ca4                                     | 11393203                      | GCAT/GCATCAT                                                  | ACAAACATGCCACCA<br>CAAA    | TCCATTGCTCACATTG<br>GAA    | 59.9                             | 585                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11443015  | Ca4                                     | 11443015                      | AATT/A                                                        | GGCTTGGTGTGGGTTT<br>ACAT   | AGGCCCTTAGTTGTC<br>TCGT    | 59.7                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11444419  | Ca4                                     | 11444419                      | GAAAAAA/GAAAAAAA                                              | AAACGGGCGATTGTGTT<br>TTTA  | GGAAGGAACCATCAAG<br>CAAA   | 59.5                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11446405  | Ca4                                     | 11446405                      | A/ACAT                                                        | TTAATGCGGTTGAAAT<br>GGTG   | AATATGGCATTCCCATC<br>CAA   | 59.4                             | 438                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11447422  | Ca4                                     | 11447422                      | TTAAT/TT                                                      | GCCACAGCTACATCCA<br>AAAA   | GCATTGCTATCATTACT<br>GTGCG | 58.8                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11447651  | Ca4                                     | 11447651                      | AAAAAAGTAAAAAGTAAA/AAAAAAG<br>TAAA                            | TCGCACAGTAATGATA<br>GCAATG | TGGATAATATGGGCGG<br>TGAT   | 58.9                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_11449130  | Ca4                                     | 11449130                      | C/CT                                                          | TCCTTGTGTCATCAC<br>CTTCA    | CACAATCAACATGCAC<br>TCG      | 59.1                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11449776  | Ca4                                     | 11449776                      | ATTTTTTT/ATTTTTTT                                             | CTTGATCGAGTGCATG<br>TTTGA   | AGCTCGATGGTAAAGG<br>CGTA     | 59.9                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11459960  | Ca4                                     | 11459960                      | CTAAGT/CTAAGTAAGT                                             | GAGATCCAAATCAAG<br>GGCA     | TTCATGCATCTGCAGG<br>GTAG     | 60.0                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11468609  | Ca4                                     | 11468609                      | AAATTGAAAATAATT/AAATT                                         | TTTGAATGGACGGATG<br>TGTA    | TTGACGAGGAACCTTG<br>AATGAA   | 58.9                             | 264                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11472250  | Ca4                                     | 11472250                      | ATTTT/ATTTT                                                   | TGTCATCACTCGTGTG<br>GTATCT  | CCAACCGAGGAGACAA<br>GAAA     | 58.1                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11473446  | Ca4                                     | 11473446                      | GTTTTTTT/GTTTTTTT                                             | ACATTTGGAAGGCTTG<br>AACG    | CCCATCAACGGAATTT<br>GAC      | 60.1                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11473509  | Ca4                                     | 11473509                      | CA/CAAA                                                       | ACATTTGGAAGGCTTG<br>AACG    | CCCATCAACGGAATTT<br>GAC      | 60.1                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11478077  | Ca4                                     | 11478077                      | CTT/CT                                                        | CCGCTTCTCTTCAATG<br>CTCT    | AACACACCCAATTTG<br>CATT      | 59.7                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11478441  | Ca4                                     | 11478441                      | TTATTAATTGTATATTAATTGTATAT<br>TAATT/TTATTAATTGTATATTAATT      | AATGCAAATGGGGTG<br>TGTT     | TCACATATTATAATTT<br>CTGCACCG | 60.1                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11479120  | Ca4                                     | 11479120                      | AT/ATTTT                                                      | AATTGAAGGTTATTTT<br>GGAATCA | AGTGTCAATGCGCACAC<br>AAAT    | 58.1                             | 372                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_11482459  | Ca4                                     | 11482459                      | TA/TAA                                                        | TGGGGAGACAAGGGA<br>GTATG | TGGGATTAAGCCCTT<br>GACA      | 59.9                             | 252                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11483405  | Ca4                                     | 11483405                      | AC/A                                                          | AAAGATTGGCCTGCTT<br>TTGA | TTCAATGCCTCTCAAGT<br>AATTGTT | 59.8                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11492296  | Ca4                                     | 11492296                      | CTTTTT/CTTTTT                                                 | GCAACTTATCCAGGGC<br>TCAA | TGCTTCTTTGGGTGTG<br>TGAG     | 60.2                             | 174                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11492735  | Ca4                                     | 11492735                      | CAAAAAAAAA/CAAAAAAAAAA                                        | CTCACACACCCAAAGA<br>AGCA | AACATCATGGTCAGCA<br>CCAA     | 59.9                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11492800  | Ca4                                     | 11492800                      | AAAACAA/AAAACAATAAACAAACAA                                    | CTCACACACCCAAAGA<br>AGCA | AACATCATGGTCAGCA<br>CCAA     | 59.9                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11493423  | Ca4                                     | 11493423                      | ATTTTT/ATTTTTT                                                | CAAAGAAGCTGACCTT<br>GGAG | CCCATACTGGATGGG<br>AGAA      | 60.0                             | 679                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11493841  | Ca4                                     | 11493841                      | AT/ATT                                                        | GTTGCGACACCTACCA<br>ATGA | CAGAAATGCTTGCCTC<br>GTTA     | 59.6                             | 242                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11494266  | Ca4                                     | 11494266                      | GAA/GAAAAA                                                    | TAACGACGCAAGCATT<br>TCTG | GGTGCAGAGAGAAAA<br>CCTG      | 60.0                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11494600  | Ca4                                     | 11494600                      | ATAAATTTAAATTTAAATTTA/ATAAA<br>TTTAAATTTA                     | CAGGTTTTCTCTCTCG<br>CACC | CAACACAACCCGTGAA<br>CATC     | 60.0                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11494725  | Ca4                                     | 11494725                      | TAAAAAAA/TAAAAAAA                                             | CAGGTTTTCTCTCTCG<br>CACC | CAACACAACCCGTGAA<br>CATC     | 60.0                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_11505808  | Ca4                                     | 11505808                      | GACA/GACAAAAACA                                               | GCAATGATGACGGTGT<br>ATCG  | CATGAACCATGATGTC<br>GAGG     | 60.0                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11506583  | Ca4                                     | 11506583                      | CTTA/CTTAATTA                                                 | CTCGACATCATGGTTC<br>ATGG  | CGGATCTATGCATGGG<br>ATAA     | 59.9                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11514114  | Ca4                                     | 11514114                      | AAAACA/AAAACAAACA                                             | TGGATTTATGTAATGG<br>GCTGG | TCGCCGAGTTTCAACT<br>CTTT     | 59.7                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11514377  | Ca4                                     | 11514377                      | GATT/G                                                        | AAAAGGATCCAACGG<br>TTCA   | TCGCCGAGTTTCAACT<br>CTTT     | 59.4                             | 102                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11536367  | Ca4                                     | 11536367                      | T/TA                                                          | GTGAGGGAATGCATG<br>TG TG  | TTGATTTTTATCTGCAA<br>TTACCGT | 60.0                             | 811                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11539392  | Ca4                                     | 11539392                      | TA/TATGA                                                      | TGCGGTTTTCACAAAT<br>GAC   | CAACGGTTCATGATCC<br>AATCT    | 59.6                             | 192                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11544878  | Ca4                                     | 11544878                      | TAAAAAA/TAAAAAA                                               | CAGATTCCTTGCCATC<br>GATTA | AAGTTGCCCTTGCCATC<br>CTAA    | 60.0                             | 131                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11545907  | Ca4                                     | 11545907                      | GAATTTTTTT/GAATTTTTTTAAATTT<br>TTTT                           | TGCACCGCTTTTACTTT<br>TACC | GGATTTTGAGGTGTAG<br>GGCA     | 59.3                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11549203  | Ca4                                     | 11549203                      | CTTTTTTTTT/CTTTTTTTTTTT                                       | AGAAGGACGAGGAGG<br>AGGAG  | CGGTGGACCTTACGA<br>ATTT      | 59.9                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11549653  | Ca4                                     | 11549653                      | TAA/TAAAA                                                     | AAATTCGTAAAGGTCC<br>ACCG  | CCAACGGTGTGCATAA<br>TGAG     | 58.9                             | 729                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                         | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                       |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_11550605  | Ca4                                     | 11550605                      | TAAAAAAAAAAAAA/TAAAAAAAAA                                                                             | CTCATTATGCACACCG<br>TTGG   | GTGGCAAAGGGAATT<br>TGAA    | 60.0                             | 991                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11579781  | Ca4                                     | 11579781                      | AATATATATATATATATATATA/AATA<br>TATATATATATATATA                                                       | AGGGTCCTACCCCGAT<br>TATG   | ATATTCAACCGTGGTTC<br>CCA   | 60.0                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11585549  | Ca4                                     | 11585549                      | TAAAAAAAAA/TAAAAAAAAA                                                                                 | AACACTCACAAAAGCC<br>ACGA   | TTGTTTCTGGATTTGT<br>CCC    | 59.3                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11602402  | Ca4                                     | 11602402                      | TTATATATATATATATATATATATA<br>/TTATATATATATATATATATATAT<br>ATATA                                       | GCTTCAAGACAATCTTT<br>GACCA | AATTAATGGCGGAG<br>GACC     | 59.4                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11611162  | Ca4                                     | 11611162                      | AATATATATATATATATATATATAT<br>ATATATATATATATAT/AATATATA<br>TATATATATATATATATATATATAT<br>ATATATATATATAT | TCACACATACACCACA<br>CACACA | GAACAAAAGTTCGTGA<br>ACCACA | 59.4                             | 190                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11615556  | Ca4                                     | 11615556                      | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>A                                           | TCACACATACACCACA<br>CACACA | TCGAATAAGTTTTCGTG<br>AACCA | 59.4                             | 187                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11769762  | Ca4                                     | 11769762                      | TA/T                                                                                                  | TCCATAGTGAGATGC<br>GACA    | GGAACATGCGAATCAC<br>AAAA   | 60.2                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11818956  | Ca4                                     | 11818956                      | CAAA/CAAAA                                                                                            | CCAAAACATGAAAGCA<br>ACAAAA | TAACATTGATGGCAGA<br>GGCA   | 60.0                             | 170                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_11988786  | Ca4                                     | 11988786                      | TAAAAATTAATAAAAAA/TAAATTA<br>ATAAAAAATTAAATAAAAAA                                                     | TCTTTAACAAGTGTCTG<br>GCCA  | GGCAACTGGGAAGCAA<br>ATAA   | 59.4                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12015084  | Ca4                                     | 12015084                      | CATATATATATATATATATATAT/C<br>ATATATATATATATATATATATATA<br>T                                           | ACCATAAAACAGCCTC<br>CACG   | GTGTTGCGATTTTGGT<br>GTTG   | 60.0                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                               | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                             |                            |                            |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_12082492  | Ca4                                     | 12082492                      | AATATATATAT/AATATATATATAT                                                                                                                                   | GGACTCAGCATCGTGT<br>TCCT   | TTTCTTTAGGTTAGGCC<br>CTCC  | 60.3                             | 561                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_12090377  | Ca4                                     | 12090377                      | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATATA<br>TAT                                                                                               | ATTTGGTCTGCGTTT<br>GACC    | ACTAGGTTGGAGCATG<br>AGGC   | 60.0                             | 567                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_12092916  | Ca4                                     | 12092916                      | GTCTCTCTCTCTCTCTCTCTCTC/<br>TC/GTCTCTCTCTCTCTCTCTCTC<br>TC                                                                                                  | ACTAAACCGACCACCA<br>CACC   | TGTACCTCCATTTGCCA<br>TGA   | 59.7                             | 534                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_12127716  | Ca4                                     | 12127716                      | AAATAATAATAATAATAATAATA<br>AT/AAATAATAATAATAATAATAA<br>T                                                                                                    | CATTCGGTGGACCTTT<br>TACG   | TGAAGAGACGAAGCTG<br>CAAA   | 60.4                             | 343                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_12197670  | Ca4                                     | 12197670                      | AAATAATAATAATAATAATAATA<br>ATGATAATGATAATAATAAT<br>AATAATAATAATAATAATAATA<br>TAATAATA/AAATAATAATAATAA<br>TAATAATAATGATAATGATAATG<br>ATAATAATAATAATAATAATAAT | CGGTGGTGGAGGAAG<br>TAAAA   | TGCATCTGCTTTACCA<br>TGA    | 60.0                             | 329                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_1236798   | Ca4                                     | 1236798                       | AACACACACACACACACA/AACA<br>CACACACACACACACACA                                                                                                               | TGATGGGTGGTGAAT<br>GAAA    | AAAGAGGGGATGTTCC<br>TTGG   | 59.9                             | 673                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_1237884   | Ca4                                     | 1237884                       | AATATATATATATATATATATATA/<br>AATATATATATATATATATA                                                                                                           | GTGGTCTGGAACATCG<br>TCCT   | TTGCAGTTGCAATATC<br>GTTG   | 60.0                             | 863                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_12477637  | Ca4                                     | 12477637                      | TAAAAAAAA/TAAAAAAAAAAAA                                                                                                                                     | GGATTCAAATCATTCAC<br>CCG   | TGGTTTAAGGTTTGG<br>GTTGA   | 60.1                             | 536                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_12479950  | Ca4                                     | 12479950                      | AGTA/AGTAGTA                                                                                                                                                | GATGCCCCACAACCAC<br>TACT   | CGACCATGTAAAGCAA<br>AACTTG | 59.9                             | 599                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_12480535  | Ca4                                     | 12480535                      | CAT/CATACAAAAT                                                                                                                                              | CAAGTTTTGCTTTACAT<br>GGTCG | AAGTTGTGCTTTTGTG<br>CCC    | 59.7                             | 438                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_12483472  | Ca4                                     | 12483472                      | CAA/CA                                                        | TCTACGGTCCAATACC<br>CGAG  | GGTCCGTGGAGAAAAT<br>TTGA     | 59.9                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12505498  | Ca4                                     | 12505498                      | ATATATATAT/ATATATATATGTATAT<br>ATAT                           | GCAAGGACAAGGGATG<br>TAGG  | TCAACCGCAATTGAGA<br>TTTTC    | 59.6                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12507863  | Ca4                                     | 12507863                      | AAAAGAAA/AAAA                                                 | ATTGAGCACATGCCAC<br>TGTC  | CCTTCAATGTGGTGGT<br>AGGG     | 59.7                             | 827                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12520618  | Ca4                                     | 12520618                      | AATATATATATATAT/AATATATATAT<br>ATATAT                         | TCAAAGCTGCATTTTGT<br>TGC  | TTGCTATGCTATGCAC<br>GCTC     | 60.0                             | 441                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12528813  | Ca4                                     | 12528813                      | CATA/CATAATA                                                  | TAACGCTAGGGTCCCA<br>TGTC  | TCGTTTTGATCATTTAT<br>CGTTTTT | 60.0                             | 720                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12528995  | Ca4                                     | 12528995                      | CTTTT/CTTT                                                    | TAACGCTAGGGTCCCA<br>TGTC  | TCGTTTTGATCATTTAT<br>CGTTTTT | 60.0                             | 720                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12529201  | Ca4                                     | 12529201                      | TAAAAAAAAA/TAAAAAAAAA                                         | CATGGCTCCAAGAAGC<br>TTAAA | TTGTTTTGATCATTTA<br>TCGTTTT  | 59.5                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12561884  | Ca4                                     | 12561884                      | AATAT/AAT                                                     | TCGTCTATGCGAGTCG<br>TAACA | TTCAAACCTAAGCCACT<br>GCAT    | 59.5                             | 727                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12563798  | Ca4                                     | 12563798                      | GTTTTT/GTTTT                                                  | TGTGATATTGGGTCCA<br>TTGGT | TCACAAATCGAAATGC<br>GGTA     | 59.9                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12566243  | Ca4                                     | 12566243                      | TTTATTATTATTATTATTATTATT<br>/TTTATTATTATTATTATTATTAT<br>TATT  | GTTGTGAATCAACTTG<br>GCCC  | GGGACTGCACCTATTT<br>TATGC    | 60.4                             | 834                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_12566497  | Ca4                                     | 12566497                      | CTTTTTTT/CTTTTTTTTT                                           | CCGTCCGTCATGACCT<br>ATAA    | CATCTCAAACAACTCG<br>GACA   | 58.4                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12566654  | Ca4                                     | 12566654                      | AG/A                                                          | TCAGTCTTTCCATATTC<br>TCTCCG | AAAACCCAGGAGGTCA<br>GCTT   | 59.7                             | 619                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12567928  | Ca4                                     | 12567928                      | AATATATATAT/AATATATAT                                         | ATTCTGGCAATTCTACC<br>CCTT   | GAGGTAGAGCTCGACG<br>ATGG   | 59.8                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12571781  | Ca4                                     | 12571781                      | ACCCC/ACCCCC                                                  | ACATCCAATGACCAAG<br>AGCC    | CCACTTTCGGAACAATT<br>TTGA  | 59.9                             | 394                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12571941  | Ca4                                     | 12571941                      | AA/AATTTA                                                     | ACATCCAATGACCAAG<br>AGCC    | TTGTTTTGCATGCTCTT<br>CCA   | 59.9                             | 820                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12586849  | Ca4                                     | 12586849                      | TTAATATAATATAAT/TTAATATAATA<br>TAATATAAT                      | AACCTAATAAGCCCG<br>AAGC     | GACAAAAGTGTGGCG<br>GTTT    | 59.6                             | 916                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12588357  | Ca4                                     | 12588357                      | TAAAAAAAAA/TAAAAAAAAAAAAA                                     | ACAATTCGAAGATAC<br>CCCC     | GATGTGGTCGTTGTGCG<br>AGTG  | 60.0                             | 506                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12589362  | Ca4                                     | 12589362                      | CTTTTTTTTT/CTTTTTT                                            | CAATGGTTCTTTTGGG<br>GTTT    | ACAACGTCTTCCATTAC<br>GCC   | 59.3                             | 615                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12604453  | Ca4                                     | 12604453                      | ATTTT/ATT                                                     | AGTCCATGCTTTCTGC<br>TGCT    | ATTTCACAAATGGGCG<br>TGAG   | 60.2                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12606654  | Ca4                                     | 12606654                      | CAT/CATAT                                                     | GGGTGCTAATGCCATT<br>GTTT    | GGGATTGATTGTAAAG<br>GAAGGA | 59.8                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                 |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_12607155  | Ca4                                     | 12607155                      | ATTTTTTT/ATTTTTTTTTTT                                                           | TCCTTCCTTACAAATCA<br>ATCCC  | AATTTTTGCGACTTTGA<br>CCG   | 59.3                             | 194                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12700885  | Ca4                                     | 12700885                      | GAAAAAAAA/GAAAAAAAAA                                                            | TTGCAAAACAACTCACA<br>ACATTC | TCCACTCAATTCAATAC<br>CATCA | 60.1                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12788740  | Ca4                                     | 12788740                      | TTATATATATATATATATATATA/TTA<br>TATATATATATATATATATATATAT<br>A                   | TCACATGCGTCCAATTT<br>TTG    | AAACGTGTGGCCAGC<br>TAAC    | 60.5                             | 845                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12795892  | Ca4                                     | 12795892                      | TTATATATATATATATATATATATA<br>TATATATATATATAT/TTATATATATA<br>TATATATATATATATATAT | TTTTCCCTTTTCACCC<br>AAG     | TCTGAAAAAGCGCCGT<br>AAAT   | 59.0                             | 291                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12797194  | Ca4                                     | 12797194                      | GAAGAGAAAGAG/GAAGAG                                                             | ACAATAGGGTTATGGC<br>GCAG    | AATCATCTCCATTGCGA<br>ACC   | 60.0                             | 347                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12836741  | Ca4                                     | 12836741                      | AATATATATATATATATATATATAT<br>ATATAT/AATATATATATATATATATA<br>TATATATATAT         | TCGTTCAATCGAGGAA<br>AACC    | CTTTGTTGGGCTAATCA<br>CGG   | 60.1                             | 886                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12852660  | Ca4                                     | 12852660                      | AATATATATAT/AATATATATATAT                                                       | CATTCTCTCTATGCCAC<br>GCA    | AACTTGTGTCTTCAAG<br>GGG    | 60.0                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12918326  | Ca4                                     | 12918326                      | GAAAAAAAAA/GAAAAAAAAAAAAA                                                       | TGATTCAAAACATGCG<br>AGAAA   | TATCCATAAACACCCCT<br>CCG   | 59.3                             | 793                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_12918976  | Ca4                                     | 12918976                      | GATATATATATATATATATATATA<br>TATAT/GATATATATATATATATAT<br>ATATATATATAT           | TTAATGCACGGTCATG<br>TGCT    | GCTATTTGCAAAGGTG<br>GCTT   | 60.1                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1310245   | Ca4                                     | 1310245                       | ATTTTTTTTTTT/ATTTTTTTTTTT                                                       | TGAAATTGCTTGATTTT<br>GCTTT  | CGACCGATTTTATCCG<br>TCTC   | 58.9                             | 825                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                           | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                         |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_13133292  | Ca4                                     | 13133292                      | AT/ATATATTT                                                                                             | CAGCCGCCTCCAAC<br>TTAC     | CCATCCATGCAATTGAA<br>CAC | 59.7                             | 408                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13133678  | Ca4                                     | 13133678                      | CTTTTT/CTTTTTT                                                                                          | TGTTCAATTGCATGGA<br>TGGT   | TTTAGGGCACCGTTTG<br>AAGT | 59.8                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13149119  | Ca4                                     | 13149119                      | CATTATTATTATTATTATTATTAT<br>TATTATTATT/CATTATTATTATTATT<br>ATTATTATTATTATTATT                           | AGCAGCAGTTGTATGG<br>GCTT   | GCCATGCATTCCGAAA<br>ATAA | 59.9                             | 211                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13191736  | Ca4                                     | 13191736                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAA/AAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAA | CAAGTCGTTTACTTTG<br>GCACA  | TTTTCGCACATCTACCC<br>ATT | 58.9                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13210889  | Ca4                                     | 13210889                      | GA/GCCATCTGATTCTA                                                                                       | TTGTCTTTTGGGCTG<br>CTCT    | GGTCACACACAAATGC<br>CAAG | 60.0                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13352277  | Ca4                                     | 13352277                      | CAG/CAGGAAG                                                                                             | TTTTCCAAATATGGTCG<br>CAA   | AATTTCAAGCCATCGAC<br>CAC | 59.0                             | 797                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13433311  | Ca4                                     | 13433311                      | TA/T                                                                                                    | CGAGCAAACACAATGA<br>ATGG   | TTGGTTGGTTCATTGG<br>TTGA | 60.1                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13446467  | Ca4                                     | 13446467                      | CAAAAAATAAAAAAAATAAAAA/C<br>AAAAAAATAAAAA                                                               | TGAGATGCTGCATTAC<br>CTGC   | ATCCAATGTTCTGGAC<br>GGTG | 60.0                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13478987  | Ca4                                     | 13478987                      | ATTA/ATTTGAAATTACCTTA                                                                                   | CACTGGGATCTTCAAT<br>GTTTCA | CGTAGTTTAAATTTGG<br>GGTG | 59.6                             | 733                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13494856  | Ca4                                     | 13494856                      | GGTAGT/GGTAGTAGT                                                                                        | CGAAGGCATGGGATAA<br>AAAT   | TTTCTAGGCCACCCAT<br>CTTG | 58.9                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_13509527  | Ca4                                     | 13509527                      | ATTTT/ATTTTATTAATAAATTTATTT<br>TT                             | CCTCTTCACGGTGCTC<br>ATT    | CCTCGTTTTAAGCCCA<br>ATCA  | 60.3                             | 158                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13556277  | Ca4                                     | 13556277                      | TTAATAATAATAATAA/TTAATAATAA<br>TAATAATAATAATAA                | GTCGCAAGTGTTTATC<br>GCAA   | GGCTAGACGAGTTCGA<br>CGAC  | 59.9                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13577543  | Ca4                                     | 13577543                      | GTATATAT/GTATATATAT                                           | TTGGCATAGCAAGACA<br>ACCA   | TGAACCAGTGATGATT<br>GCAGA | 60.3                             | 358                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13578691  | Ca4                                     | 13578691                      | TTACAATTAATAA/T                                               | TTTTCCGAAATTTCTG<br>CTG    | CTTAAGAAGGGCAAGG<br>GCAT  | 60.2                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13579909  | Ca4                                     | 13579909                      | ATTT/AT                                                       | TTCCCAATTTTCTTTC<br>AATTTT | GCACTACCAAGCAAT<br>AGCA   | 58.2                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13582008  | Ca4                                     | 13582008                      | GTTTATTTATTTATTT/GTTTATTTAT<br>TT                             | TTGTGATCGCCGAAAA<br>TACA   | CAATCATGGTGCTGCG<br>ATAC  | 60.1                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13582915  | Ca4                                     | 13582915                      | GAAATAAAAA/GAAATAAAAAAATA<br>AAAA                             | CCATTGCTGAGATCAT<br>GGTG   | TGCATGCATCAGACAA<br>CAGA  | 60.1                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13604124  | Ca4                                     | 13604124                      | GA/G                                                          | TTCAGACCCAGTTTC<br>ATCA    | GACATGTATCGTGTGC<br>GGTC  | 59.1                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13608282  | Ca4                                     | 13608282                      | ATTTTTTTT/ATTTTTTTTTT                                         | TCTTTGTCCAAAGGCC<br>AATC   | CACATTTTGCAAGGTTT<br>GTG  | 60.1                             | 795                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13608641  | Ca4                                     | 13608641                      | ATT/ATTT                                                      | GGTGACGTGGCTTACT<br>CTCC   | CCCTTTCTGCATGGAC<br>AAGT  | 59.7                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_13610617  | Ca4                                     | 13610617                      | AAAGCCA/AAAGCCAAGCCA                                          | GATGAAGCCAAACTAC<br>CCCA   | ACGCTGAAGGAAGAAA<br>GCTG  | 59.9                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13610669  | Ca4                                     | 13610669                      | AG/A                                                          | GATGAAGCCAAACTAC<br>CCCA   | ACGCTGAAGGAAGAAA<br>GCTG  | 59.9                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13612409  | Ca4                                     | 13612409                      | AACAATCAACACAATCA/AACAATCA                                    | GCACCCTAACACTTCT<br>TGCAT  | CACCAAATTCACGAGA<br>ACCA  | 59.3                             | 329                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13619118  | Ca4                                     | 13619118                      | AC/A                                                          | TTGTAATGCCAAAATTG<br>CGA   | TTGCCTCCAAAATCAAC<br>CTC  | 60.1                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13621014  | Ca4                                     | 13621014                      | GTTTTT/GTTTTTT                                                | TTTGCTAACTTGCTCC<br>CACC   | GCGAGAGGCCCATGTA<br>ACTA  | 60.2                             | 723                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13627308  | Ca4                                     | 13627308                      | A/AT                                                          | TTGGCGTGAAAGACAA<br>CATT   | TGTTGGGTGAGTTTTTC<br>CACA | 59.2                             | 938                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13630632  | Ca4                                     | 13630632                      | AA/AAGAGTCTA                                                  | TATGCAGGCCCAAAC<br>CTCT    | TTTTCACAATCAATGCC<br>CAA  | 59.8                             | 370                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13631062  | Ca4                                     | 13631062                      | GCC/GC                                                        | TTGGGCATTGATTGTG<br>AAAA   | TCGCAACTCGTATAGG<br>ACCA  | 59.9                             | 271                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13633364  | Ca4                                     | 13633364                      | TAAAAA/TAAAA                                                  | TGATTTACGAAATTGGT<br>TCTCC | TTTCAAATTCGCAGTT<br>GTGT  | 58.1                             | 812                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13633711  | Ca4                                     | 13633711                      | CTTATGTTAT/CTTAT                                              | TTCAATCATTTGTCCAA<br>TTTCC | CTCGCGGTAAAATTC<br>TGCT   | 58.8                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_13643836  | Ca4                                     | 13643836                      | ATTTTT/ATTTTTT                                                | ATAGTTGTTGAAGGGC<br>CACG    | GGGTGAAGAATGTATG<br>CCAAA | 60.0                             | 798                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13643938  | Ca4                                     | 13643938                      | AA/AATATA                                                     | GCTTCCGACAAAGGTC<br>AGAG    | GGGTGAAGAATGTATG<br>CCAAA | 60.0                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13643954  | Ca4                                     | 13643954                      | T/TA                                                          | GCTTCCGACAAAGGTC<br>AGAG    | GGGTGAAGAATGTATG<br>CCAAA | 60.0                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13649620  | Ca4                                     | 13649620                      | AG/A                                                          | TTGTCCCCTAACAAAT<br>GGA     | GACTTTCAAGCCCGAT<br>ACCA  | 60.2                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13650519  | Ca4                                     | 13650519                      | TTTATT/TTT                                                    | AGACAGTTGCTCAATG<br>CACG    | AATGCAGTGCTTTGCA<br>GTTG  | 60.1                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13651001  | Ca4                                     | 13651001                      | TC/T                                                          | AAGCAGCGAGTTGTTG<br>AGGT    | GGAAACTGCTTTTCGC<br>TTTG  | 60.1                             | 755                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13657394  | Ca4                                     | 13657394                      | CAAAAAA/CAAAAAAA                                              | TCGTTTTTCAACCATCA<br>GTCA   | TCTCCAATGTGATTG<br>CTCA   | 59.2                             | 823                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13658364  | Ca4                                     | 13658364                      | TTTTATTTATTT/TTTTATTTATTTATT<br>T                             | CATCAACTGACTAACG<br>ACATGGA | TGAAGATGGTGAATG<br>GGAT   | 60.0                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13659547  | Ca4                                     | 13659547                      | CCAAACAAAC/CCAAAC                                             | CCAAACTGGGGAGAA<br>ACAA     | AAAACGACGGTTATGA<br>ACGC  | 59.9                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13669625  | Ca4                                     | 13669625                      | TAAGAAG/TAAG                                                  | TCAAAACACAAACACAA<br>GCCA   | CCCTTTGTGGGTTCCC<br>TTAT  | 60.2                             | 800                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_13669889  | Ca4                                     | 13669889                      | TTTCTT/TTT                                                    | AACGTTATTTAAACGAG<br>GATTCA | CCCTTTGTGGGTTCCC<br>TTAT     | 58.3                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13671186  | Ca4                                     | 13671186                      | TCAA/T                                                        | CGTCCATTGTGGTTAT<br>GCTC    | TTCTAAAAAGTTAAAC<br>CGGCA    | 59.0                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13671252  | Ca4                                     | 13671252                      | ATTTTTTTT/ATTTTTTTTT                                          | CGTCCATTGTGGTTAT<br>GCTC    | TTCTAAAAAGTTAAAC<br>CGGCA    | 59.0                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13671299  | Ca4                                     | 13671299                      | ATTTTTTTT/AATTTTTTTTT                                         | CGTCCATTGTGGTTAT<br>GCTC    | TTCTAAAAAGTTAAAC<br>CGGCA    | 59.0                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13676197  | Ca4                                     | 13676197                      | AG/A                                                          | ACGTTTCCACGATTGG<br>TGAT    | GATGATCACGCTTCCA<br>CAAG     | 60.2                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13676268  | Ca4                                     | 13676268                      | AGTTT/AGTTTGTTT                                               | ACGTTTCCACGATTGG<br>TGAT    | GATGATCACGCTTCCA<br>CAAG     | 60.2                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13689699  | Ca4                                     | 13689699                      | CTAAAAATACAATAAAAAATACAATAA<br>/CTAAAAATACAATAA               | GTCGTGTTCCCGCTTA<br>AGAT    | GCAAATGGATAAAAAGT<br>CACATCA | 59.2                             | 684                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13712400  | Ca4                                     | 13712400                      | G/GC                                                          | TGGGGCTTATAGCCTC<br>CAAT    | AGGAAATGAAGGAAAC<br>GGGT     | 60.8                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13731926  | Ca4                                     | 13731926                      | ATTTT/ATTT                                                    | CAAGGGATTGTGAGTG<br>TTTGAA  | GTCCAAGTAATCTGGC<br>GCAT     | 60.0                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13732813  | Ca4                                     | 13732813                      | TCC/TC                                                        | TCCGCGAGCTTAGTTT<br>TGTT    | CACGGAGATGAGAAGA<br>GGGA     | 60.0                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_13739989  | Ca4                                     | 13739989                      | TA/T                                                          | TTTCTCCGTCTTAGTG<br>CGGT    | AAATGATCAAATCGAAA<br>AGAAAAA | 59.9                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13750785  | Ca4                                     | 13750785                      | ATTTTTTT/ATTTTTTTTT                                           | GAGCATGTTTGGATTT<br>ACTTTGC | TTTTTATGTAAAGGACG<br>AGGATGA | 60.0                             | 721                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13761691  | Ca4                                     | 13761691                      | ATTTT/ATTT                                                    | AAGGTGTGTGAAAGGA<br>TGCC    | TGCAAACAGCTCAATC<br>CTTG     | 60.0                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13770396  | Ca4                                     | 13770396                      | T/TG                                                          | AAGCACCCATCCTGAA<br>ATTG    | TTTCACCGCGATAAAAA<br>TCA     | 59.9                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13770434  | Ca4                                     | 13770434                      | AGTAC/AGTACGTAC                                               | AAGCACCCATCCTGAA<br>ATTG    | TTTCACCGCGATAAAAA<br>TCA     | 59.9                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13785898  | Ca4                                     | 13785898                      | CA/CACAA                                                      | CCGCCGGGAATAAAGT<br>AGTA    | TGAGTCTCACCTTGGG<br>CTCT     | 59.1                             | 442                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13793804  | Ca4                                     | 13793804                      | GTTATCAAAA/GTTATCAAACCAATT<br>ATCAAA                          | CACGAGGACAATGAAG<br>AGCA    | ATTGACGACGAAAATG<br>AGGC     | 60.0                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13795678  | Ca4                                     | 13795678                      | ATGTTGTTGTT/ATGTTGTTGTTGTT                                    | GCCGGAAATACACCGA<br>CTAA    | AAAGGGTAGGAACAAC<br>CGCT     | 60.0                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13807055  | Ca4                                     | 13807055                      | AT/ATCT                                                       | ATAGAATTCTGGGAGGG<br>GACA   | GGTGCCTGTGCTTTTC<br>TTGT     | 60.7                             | 248                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13808690  | Ca4                                     | 13808690                      | TA/TAGAAA                                                     | ATTCCACGTTCACTTCT<br>CCG    | CGCCACTCTTCTACGG<br>TTCT     | 60.1                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_13809545  | Ca4                                     | 13809545                      | ATT/ATTT                                                      | AAAAGGGGATGAGTTT<br>TTCT  | TCGTAATTAATCCACAT<br>GAATCTGA | 58.1                             | 923                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13813294  | Ca4                                     | 13813294                      | TG/T                                                          | TTTTTGCCCGTTAGAC<br>GATT  | TGGGTGAATTGGGTAG<br>GAGA      | 59.6                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13826117  | Ca4                                     | 13826117                      | ATTTTT/ATTTTTT                                                | AGGTGGTTGTTGCACT<br>TTGA  | CAAATTTGTTCCGCTTC<br>ACA      | 59.2                             | 474                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13828147  | Ca4                                     | 13828147                      | G/GA                                                          | GTAATTGCCGGGTCC<br>TTAT   | CAATAGTGTTCACG<br>TGGG        | 60.0                             | 430                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13829467  | Ca4                                     | 13829467                      | AT/ATT                                                        | TGAGAATTTGCATGCC<br>TCAC  | AGCGAAGTGCTAGCAA<br>CACA      | 59.8                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13830179  | Ca4                                     | 13830179                      | AT/ATATTT                                                     | TGTGTTGCTAGCACTT<br>CGCT  | GTGGTTGCACACATTT<br>CGAC      | 59.8                             | 922                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13831456  | Ca4                                     | 13831456                      | GATATAT/GAT                                                   | GATATTTTGTGTTGCC<br>CCCT  | GCAGGAAATGTGTTGT<br>GGTG      | 60.0                             | 154                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13835215  | Ca4                                     | 13835215                      | AT/A                                                          | GAGACGGCATCTAATT<br>GGGA  | ACCCCCATTACCATCTT<br>GTG      | 60.0                             | 647                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13847680  | Ca4                                     | 13847680                      | CTTTTTTT/CTTTTTTTTT                                           | TGTTCGAAGTTCCAT<br>CGAG   | CCTCCTCTTCTCCCCAT<br>CTC      | 58.8                             | 756                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13850847  | Ca4                                     | 13850847                      | TAACAA/TAACAACAACAA                                           | CCAAATTTTGGAGGA<br>CATAAA | TGAAAGTGGAGAATTC<br>AAAGC     | 58.0                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                 |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_13852149  | Ca4                                     | 13852149                      | ACTACCAACGGAGTTAAATCTA/ACT<br>A                                 | CATTGAATATGCAACC<br>CACG   | TCGATGCGTCCAATGA<br>TAAA   | 59.8                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13853238  | Ca4                                     | 13853238                      | TTTT/TTTTACTTT                                                  | TGGAGAATTCGTATGA<br>AAGGG  | AACGTGCATGAATCCA<br>AAAA   | 59.0                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13853568  | Ca4                                     | 13853568                      | TGG/TG                                                          | TTCCACAATGTTGAG<br>TTTCA   | TGCATATAATGGTCAGT<br>GATCG | 59.0                             | 315                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13854087  | Ca4                                     | 13854087                      | TAAAAAAAA/TAAAAAAAA                                             | CGATCACTGACCATT<br>TATGCAC | CCTTCTTTCCACAATG<br>TTGA   | 59.4                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13856503  | Ca4                                     | 13856503                      | A/AT                                                            | TCCTGATAACATTCCTT<br>TCACC | GGGTTCGAAATTGGTG<br>TGTT   | 58.0                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13908536  | Ca4                                     | 13908536                      | TC/T                                                            | CTCCTCCGATGTCTGG<br>AAAA   | CGCGGTTGCTTCAATT<br>CTAT   | 60.2                             | 232                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_13909254  | Ca4                                     | 13909254                      | CA/CAA                                                          | CATCACGATTGACGA<br>GTTGA   | AAAAACATGACTCCAAA<br>CACCA | 59.7                             | 636                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1395408   | Ca4                                     | 1395408                       | TAAATA/T                                                        | TAATCGACATCAGCTT<br>GCGT   | TGCTGCGACTAGCTGA<br>AAAA   | 59.4                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_14011652  | Ca4                                     | 14011652                      | TAATAATAA/TAATAATAACAATAATA<br>A                                | GCACCGACTTGCTGAT<br>GTAA   | GCCTCATGCTCCAATT<br>TGT    | 59.9                             | 755                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_14187232  | Ca4                                     | 14187232                      | TTATATATATATATATATATATATATA<br>T/TTATATATATATATATATATATATA<br>T | GACTCACGTCTGAATC<br>GCAA   | GCACAAGGAACCTCGAG<br>AACA  | 60.0                             | 865                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                         | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                       |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_14280638  | Ca4                                     | 14280638                      | T/TATATATATA                                                                                          | GTCTAAGGCTTGCTAC<br>CCCC    | AGAGGCTTCTCGTTGG<br>GTTT   | 60.1                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_14355071  | Ca4                                     | 14355071                      | AT/ATGGT                                                                                              | ACCTGCAATTTTGGCT<br>ATGG    | TGTGACGATCTCTTATG<br>GCG   | 60.0                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_14392979  | Ca4                                     | 14392979                      | G/GA                                                                                                  | ATTGAACTTGTGCGCA<br>GCCT    | GCAAGTTTTCGTTTTGT<br>TCG   | 59.9                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_14396557  | Ca4                                     | 14396557                      | TTAGTAGT/TTAGT                                                                                        | AGTCAGACGCTACTCG<br>GCAT    | GTGTGTGTGTGTGTGT<br>GTGTGT | 60.0                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_14397300  | Ca4                                     | 14397300                      | GATATATATATATATATATGTATA<br>TATATATATA/GATATATATATATATA<br>TATATATATATGTATATATATATATA                 | TAAATGCATGCTCCCC<br>TGAT    | AACACATCCGGGATCC<br>ATTA   | 60.4                             | 273                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_14416755  | Ca4                                     | 14416755                      | TTATATATATATA/TTATATATATATA<br>TA                                                                     | TCATTTCAAACCCTTAA<br>ACTCCA | TTGCGGTCAATTGTAT<br>GAAGAC | 59.9                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1463289   | Ca4                                     | 1463289                       | TAAAAAAAAA/TAAAAAAAAA                                                                                 | CCCCTTTTACGGAAG<br>ACGA     | CCCCAACCACTTCCTC<br>ACTA   | 60.1                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_14677950  | Ca4                                     | 14677950                      | CAAAAAA/CAAAAAA                                                                                       | TGTTGGGCAAAATAAA<br>TTGAGA  | CAAACCTTACCACCGT<br>CTTG   | 59.5                             | 424                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_14800285  | Ca4                                     | 14800285                      | CAAAA/CAA                                                                                             | TTGTACACGTAGTAGC<br>GCCG    | AAGATGGAATTCAAGG<br>GGCT   | 60.0                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_14999642  | Ca4                                     | 14999642                      | CATATATATATATATATATATATA<br>TATATATATATAT/CATACATATATAT<br>ATATATATATATATATATATATATA<br>TATATATATATAT | ACTATAGTACCCACCC<br>CGCC    | GGAGGATCCGAAAATT<br>ATGAAA | 60.1                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                         | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                       |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_15005039  | Ca4                                     | 15005039                      | AACA/AA                                                                                                               | TTCCAACGGTCATAAA<br>AGGC  | CCCAAAGATGGCTACT<br>TCCA     | 59.9                             | 395                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15048181  | Ca4                                     | 15048181                      | TA/TAA                                                                                                                | CAAAGCTGTAACACC<br>CCGT   | AATCGATTGATTCAGC<br>CCAG     | 60.0                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15081049  | Ca4                                     | 15081049                      | ATTT/ATTTT                                                                                                            | TTTGCAACTCCATTCTT<br>CCC  | GATTCCCCATTCTTAAC<br>GCC     | 60.1                             | 688                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15111382  | Ca4                                     | 15111382                      | CATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAA/CATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAA                    | TTGCACTTTTGAGAAG<br>TCACG | GGCACTTGAGTAGATG<br>TAGCAAAA | 59.1                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15465052  | Ca4                                     | 15465052                      | T/TG                                                                                                                  | GCAACTCATTCGTCCTC<br>ATTT | GGAAACGAAAAATTTG<br>CAGC     | 59.9                             | 712                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15488514  | Ca4                                     | 15488514                      | GTATATATATATATATATATATAT<br>ATAT/GTATATATATATATATATAT<br>ATATATATAT                                                   | CATGTTTCTCATCGTTC<br>CAAA | TGAAGATATTTTCGCT<br>GTTTTT   | 58.6                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1550381   | Ca4                                     | 1550381                       | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATATA<br>TATAT                                                       | CTTCCTCATCAATTTTG<br>GCA  | CAAAGTGTCGACAGGC<br>TCTCT    | 58.7                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15621540  | Ca4                                     | 15621540                      | AATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATATA<br>TAT                                                       | CGACGGAAGTTGTTTC<br>GAGT  | AATTGTGGGAAATCT<br>GTGC      | 60.3                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15676203  | Ca4                                     | 15676203                      | ATTTTTTTTT/ATTTTTTTTT                                                                                                 | ACAAAACGGTGAAGTT<br>TCCG  | TTGCAACGCGTTTGAA<br>AGTG     | 60.0                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15681893  | Ca4                                     | 15681893                      | CAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAATA<br>AA/CAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAA | AAAAAGCGAGGTTTCGG<br>ATTA | AAAGGGGAAATCCAAT<br>TTCTAA   | 58.8                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                  |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_15764982  | Ca4                                     | 15764982                      | AATATATATATATATATATATATATATATATAT/AATATATATATATATATATATATATAT    | GGGGCTAAGGAGTTTT<br>GTGA | CGTCGCTGTGGCATT<br>AATA   | 59.2                             | 250                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1592013   | Ca4                                     | 1592013                       | GATATATATATATATATA/GATATATA<br>TATATATATATA                      | CCCTAATGGGTGAGCA<br>GTTC | GTTGGTCAATCCACTC<br>GGTC  | 59.6                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15937811  | Ca4                                     | 15937811                      | TC/T                                                             | TCAGTTGATGTTCTGC<br>CGAC | AACTATGTGCACCTAC<br>CGCC  | 59.8                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15939075  | Ca4                                     | 15939075                      | AT/ATT                                                           | GTGCACCGGTAACGAA<br>GTTT | TTCGTTGGAGGTTTGG<br>ATTCT | 60.0                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15952606  | Ca4                                     | 15952606                      | AATTTATTTA/AATTTATTTATTTA                                        | ATTTCAACGTCAATCAC<br>GCA | CCCATGTTAGACACGC<br>ATGA  | 60.1                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15960155  | Ca4                                     | 15960155                      | AGG/AG                                                           | ACGATTTTCATCCAAG<br>CCAC | CGAGCAAAAGGTAAAA<br>CCCA  | 59.9                             | 882                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15960864  | Ca4                                     | 15960864                      | TAGAGA/TAGA                                                      | TGGGTTTTACCTTTTG<br>CTCG | ATTCCGTGAGGCCAAT<br>TACA  | 60.1                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15962571  | Ca4                                     | 15962571                      | ACTT/ACTTCTCTT                                                   | CAGGAAATTGTGCATC<br>ATGG | TGGTGCACTGACTGAAT<br>GGTT | 59.9                             | 723                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15981160  | Ca4                                     | 15981160                      | AGAGAG/AGAGAGGGAGAG                                              | TGGCCCTCTATTCGTG<br>ATTC | ATTGTTGCTTTGGCTCA<br>CCT  | 60.0                             | 807                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15988053  | Ca4                                     | 15988053                      | ATTATTTATTTATTTATTTTATT/ATT<br>ATTTATTTTATTTATTTTATTTTATT<br>ATT | TTCCGGTGGTTTTAGT<br>CCAG | GTTTCAATGAGGTTGG<br>CACC  | 60.0                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_15990734  | Ca4                                     | 15990734                      | ATTTTTTTT/ATTTTTTTTTTTT                                       | TGGCAAAACGGACTAC<br>CATT     | TGCACTTACATGTATCC<br>AATATTCC | 60.4                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_15990786  | Ca4                                     | 15990786                      | AA/AACTGTGA                                                   | TGGCAAAACGGACTAC<br>CATT     | TGCACTTACATGTATCC<br>AATATTCC | 60.4                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16015560  | Ca4                                     | 16015560                      | ACTCT/ACT                                                     | GGTGGAGAATGAAACG<br>GAGA     | TTTGGGCTGAAGCCAT<br>AAAC      | 60.1                             | 402                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16028033  | Ca4                                     | 16028033                      | CT/C                                                          | ATGCAACCTCCATTAG<br>CCTG     | TTGGTTTCTAACCCAAC<br>TCATATTC | 60.1                             | 322                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16028817  | Ca4                                     | 16028817                      | CGTGTGT/CGTGTGTGT                                             | TGATTTTACACAAGGG<br>TAATTTTG | CGCCGCATACTGTAAT<br>GGTA      | 57.3                             | 951                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16035272  | Ca4                                     | 16035272                      | GTT/GTTT                                                      | TTCATCCTTGTTGGCAT<br>GTG     | GGAATCCCTTGTGTGT<br>GGA       | 60.5                             | 879                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16056793  | Ca4                                     | 16056793                      | TAAAAAA/TAAAAAAA                                              | CTGCAATGCAACAACC<br>AATC     | TCAAAAAGAATCCCGA<br>CCTG      | 60.1                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16057308  | Ca4                                     | 16057308                      | CG/C                                                          | CAGGTCGGGATTCTTT<br>TTGA     | CATACTTACCCGTGCA<br>GCAA      | 60.0                             | 705                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16064554  | Ca4                                     | 16064554                      | T/TTA                                                         | TTGCAAGTAGCTTCCC<br>CATT     | AGGTGAGGTGAGGTGA<br>TTGA      | 59.7                             | 820                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16066119  | Ca4                                     | 16066119                      | GTTGAAATTGAAATT/GTTGAAATTG<br>AAATTGAAATT                     | GATGAAGCAGGGTTT<br>GCAT      | TCCAATGCACTTCAATC<br>GAG      | 60.1                             | 211                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)      | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                    |                             |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_16067505  | Ca4                                     | 16067505                      | CAAAAAAAAA/CAAAAAAAAA                                              | GGCTAAATTAAATCACT<br>GGTCCC | TACATCTGCGGCCCTT<br>TAAC     | 60.1                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16080244  | Ca4                                     | 16080244                      | GTTTTTTT/GTTTTTTT                                                  | TTCTCACGTGATCCC<br>TTTC     | TTCCATCTCCAATAAC<br>ATCAAA   | 60.1                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16080441  | Ca4                                     | 16080441                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                      | TTCTCACGTGATCCC<br>TTTC     | ACAATTGCTCCAACGG<br>TCAT     | 60.1                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16086000  | Ca4                                     | 16086000                      | CAAAA/CAAAAA                                                       | TGAACACGAGTCCTTC<br>CCTT    | TCCTCCAACCTCAAACA<br>ACC     | 59.7                             | 423                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16088405  | Ca4                                     | 16088405                      | ATTTATTTT/ATTTATTTTCTTTATT<br>TT                                   | AGCGTTGATTAAGTGC<br>GTGA    | TCCGAAAAGCAGCAAT<br>TCTC     | 59.5                             | 860                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16088431  | Ca4                                     | 16088431                      | GAT/GATCAT                                                         | AGCGTTGATTAAGTGC<br>GTGA    | CCCTCACTCACGATCT<br>TTCC     | 59.5                             | 906                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16101561  | Ca4                                     | 16101561                      | GT/G                                                               | CATCCACTCCATTGTC<br>ATGC    | ACCTTCAAATCACGCG<br>AAAC     | 59.9                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16120236  | Ca4                                     | 16120236                      | AATATATATATATATATATA/AATATA<br>TATATATATATA                        | TCGAAAGCATTCTTCTC<br>CAAA   | TGGTTTGACCTATTTAT<br>GGTTGG  | 59.9                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16129990  | Ca4                                     | 16129990                      | TTATATATATATATATAT/TTATAT<br>ATATATATATAT                          | AGCTCTAACAAGCGGG<br>AACA    | GAGGTGTCAAATAATA<br>AAGAGGAA | 60.0                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16138106  | Ca4                                     | 16138106                      | TTTATTATTATTATTATTATTATT<br>ATT/TTTATTATTATTATTATTAT<br>TATTATTATT | CAATGACATTACTTGG<br>GCCTT   | GGGAGAAGAAAAGAAT<br>GGGAA    | 59.0                             | 391                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                              | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                            |                             |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_16175560  | Ca4                                     | 16175560                      | CATATATATATATA/CATATATATATA                                                                | TGTTTGCTTGCTTTTGA<br>TGC    | GGTGTGTGTAGGGAA<br>GGAA      | 60.0                             | 269                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16227307  | Ca4                                     | 16227307                      | CTTTTTTTTT/CTTTTTTTTT                                                                      | TGAGGCTAAATAGAAC<br>CTGGTCA | TTTGGCTAACTAATATC<br>GCAGTTC | 60.1                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16238878  | Ca4                                     | 16238878                      | TTATATATATATATATATATATATAT<br>TATATATATATATATATATATA                                       | TGTTGTTGCGTTATTC<br>CAGC    | CACCCATCGTTTCCT<br>CTTA      | 59.7                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16257918  | Ca4                                     | 16257918                      | ACATCAAAT/ACATCAAATTCATA<br>AT                                                             | CATCGATGCATTTATG<br>CCAG    | CGAACATCGCAGCAAG<br>ATAA     | 60.1                             | 891                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16289827  | Ca4                                     | 16289827                      | TAAAAAAAA/TAAAAAAAA                                                                        | GGCCGATGGGTAAC<br>AGTA      | TTTCGCACTCAAGAT<br>CGTA      | 60.0                             | 625                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16481759  | Ca4                                     | 16481759                      | CA/CAAA                                                                                    | TCGAGACACCAACAC<br>GTAA     | AATTCGTCAAACCCACA<br>ACC     | 60.2                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16494222  | Ca4                                     | 16494222                      | AATTATTATTATTATTATTATTAT<br>TATTATTATTATTAT/AATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTAT   | CTCCCCAGTATTAGCC<br>CCTC    | TTAATTAATCGCAAATT<br>GTCCA   | 59.9                             | 766                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16785536  | Ca4                                     | 16785536                      | CATATATATATATATATATATATA<br>TA/CATATATATATATATATATA                                        | AATATGGGCCCACTAA<br>ACCC    | TTTTGGCCTAACTGGC<br>CTAC     | 59.9                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16793556  | Ca4                                     | 16793556                      | AG/AGG                                                                                     | ACACTTGCTATGAAAC<br>GGGG    | ACGCTTTGCAAGGTCT<br>GAAT     | 60.0                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16803738  | Ca4                                     | 16803738                      | CATATATATATATATATATATATA<br>TATATATATATATA/CATATATATATA<br>TATATATATATATATATATATATA<br>ATA | CTACCGGAAATGTTGG<br>CAAT    | AGTGGCAGGTGGATAC<br>TTCC     | 59.8                             | 869                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_16824557  | Ca4                                     | 16824557                      | TCCCC/TCCC                                                    | GCGTAGAGGAATGGAA<br>TGGA    | GCGACCATCTGTTGCA<br>GTTA | 60.0                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16862465  | Ca4                                     | 16862465                      | ATTTTTTTTTTT/ATTTTTTTTTT                                      | AACCAACCAACATTT<br>GTCG     | CTCGGTCATTGTGTT<br>GACA  | 59.8                             | 898                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16922622  | Ca4                                     | 16922622                      | TAA/TAAA                                                      | GAAACTTTGTCCAAGC<br>TGGC    | AATCTGGGATGCGACT<br>TGTT | 59.9                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_16943222  | Ca4                                     | 16943222                      | TATGAATGAAT/TATGAATGAATGAA<br>T                               | CTCAAGCTCAGTCCCA<br>GTCC    | TGCGTTTTGTTGGTG<br>TAGC  | 60.0                             | 668                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17001198  | Ca4                                     | 17001198                      | TAAAAAAA/TAAAAA                                               | CGATGGTGGTTGTGAA<br>AGTG    | TTGGGAAGAGAAAAGC<br>CAAA | 60.0                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17001569  | Ca4                                     | 17001569                      | ATTTTT/ATTTTTT                                                | TTGGCTTTTCTCTTCC<br>CAA     | AAAAATGGTTCGAAGG<br>GGAG | 59.8                             | 217                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17001899  | Ca4                                     | 17001899                      | TAAAAAAAAA/TAAAAAAAAA                                         | CCCCTTCGAACCATTTT<br>TCT    | TTCCCCGAGTTTCTAA<br>CCA  | 60.3                             | 696                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17015655  | Ca4                                     | 17015655                      | GTCT/GT                                                       | CCACGCTTTTACCTCT<br>CTGC    | TTCAATTCTTGCCTTG<br>GCT  | 60.0                             | 768                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17015921  | Ca4                                     | 17015921                      | TAAA/TAAAA                                                    | GGTTGCTTTTAATTCAA<br>CAGTGG | GCATCACCAGGTCTGG<br>ATTT | 59.9                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17019455  | Ca4                                     | 17019455                      | CTT/CTTT                                                      | GAAACCGTCCAAAAC<br>GCAT     | AGTGAGTGATTGTGGG<br>CACT | 60.0                             | 115                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                              |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_17023946  | Ca4                                     | 17023946                      | ATGATTAATTG/ATGATTAATTGATT<br>AATTG                           | TCGAAGGATGTCTCAA<br>GGCT      | TCGGAGTTGATCAAAC<br>GAATC    | 60.0                             | 462                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_17041835  | Ca4                                     | 17041835                      | TAAAAAAAAA/TAAAAAAAAA                                         | AACGTTTGGGTCTCTC<br>GTTG      | TCAATCATTATTA AAC<br>TGCCGAA | 60.1                             | 491                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_17071722  | Ca4                                     | 17071722                      | ATTTTTTTTT/ATTTTTTTTT                                         | GGGCTGCTACATAAAC<br>CGAA      | TCCGACATGCCATTTT<br>GTTA     | 60.1                             | 189                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_17095718  | Ca4                                     | 17095718                      | TAAAAAA/TAAAAA                                                | CGGTCATCATTGAGG<br>CTAT       | TCCATATGTGCCATT<br>GCTA      | 59.9                             | 694                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_17096036  | Ca4                                     | 17096036                      | CTTTCAA/CTTTCAAGTTTCAA                                        | CTGCAATTGTCAAGCT<br>CCAA      | TCCATATGTGCCATT<br>GCTA      | 60.0                             | 276                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_17157304  | Ca4                                     | 17157304                      | CAAAAAAAAA/CAAAAAAAAAA                                        | ATCTCCATCTCTGGAC<br>CGTG      | ACGACGCATAGCAAGG<br>TTCT     | 60.1                             | 691                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_17168334  | Ca4                                     | 17168334                      | GTA/GTATATGATATAATA                                           | CTCTACCTTGAGAGT<br>GTGTGG     | TGGACGGAGTATGCAT<br>TATTGA   | 58.9                             | 581                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_17171401  | Ca4                                     | 17171401                      | AGTGTGT/AGTGTGTGT                                             | GATGGAGGGCAGTAAC<br>GTGT      | GTGCTCTCAAAGTCGC<br>ACAA     | 60.0                             | 465                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_17186848  | Ca4                                     | 17186848                      | TC/T                                                          | CCGGCATCACTCGTTA<br>AGAT      | TGATTTGATCAGAGGT<br>ATGTGTCA | 60.1                             | 549                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_17186998  | Ca4                                     | 17186998                      | AAATTA/AA                                                     | TTTGACACATACCTCTG<br>ATCAAATC | TCATCCCCTTAAGATTC<br>CGA     | 59.4                             | 521                                           | INTERGENIC                                           | --                                  | --                    | --  |





| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_17251218  | Ca4                                     | 17251218                      | TTTT/TTTTACATCTCGATT                                          | GAGAGGAAAGGAATCC<br>AACG | CAAATTGTCGAACCAT<br>GTCG | 58.7                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17251690  | Ca4                                     | 17251690                      | TAAT/TAATCAAT                                                 | GCTCGATAAAGCAGTC<br>GTCC | GCCAAATCGAACCAAC<br>TTTT | 60.0                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17252021  | Ca4                                     | 17252021                      | ATTT/ATT                                                      | GCTCGATAAAGCAGTC<br>GTCC | CAACGTAACACGCCTC<br>TTGA | 60.0                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17254750  | Ca4                                     | 17254750                      | GTAATAA/GTAA                                                  | CAAATATTGTGCCAGC<br>CAAA | TCTTAATCTTGACCAGC<br>CCG | 59.6                             | 898                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17257974  | Ca4                                     | 17257974                      | AATA/AATATA                                                   | ACATGGCAGGTTGGAT<br>TCAT | TCATGGGTACCCAC<br>TTAG   | 60.2                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17258294  | Ca4                                     | 17258294                      | ATTTTT/ATTTTTTT                                               | ACATGGCAGGTTGGAT<br>TCAT | ATTGGTAGGCATGGCA<br>AGAC | 60.2                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17259048  | Ca4                                     | 17259048                      | CATATATATATATATAT/CATATAT<br>ATATATATAT                       | GCAAACTTTTTCACITG<br>CCC | TTCTGAAACAAATGCAC<br>CCA | 59.7                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17259358  | Ca4                                     | 17259358                      | TAAA/TAAAA                                                    | ATGGGTGCATTGTTT<br>CAGA  | GCCTGAGTTTGGCATA<br>CGAT | 59.0                             | 338                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17290057  | Ca4                                     | 17290057                      | TAAAAA/TAAAAAA                                                | ATGCAGTATCCCATC<br>AGCC  | TGTTTCATTGACCCAT<br>CCAA | 59.9                             | 843                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17290739  | Ca4                                     | 17290739                      | A/AC                                                          | TGAAAGCCAAGAATGG<br>CATA | CGTCACGCGATAATTTT<br>GTG | 59.3                             | 163                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_17313148  | Ca4                                     | 17313148                      | TC/T                                                          | AGAGGATGCAGCTATG<br>CGTT | CAACATTTTGGGAGGG<br>AAGA  | 60.0                             | 170                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17313521  | Ca4                                     | 17313521                      | TAAA/TAA                                                      | GCTAGACAGGTTTGCC<br>TTCG | AAGGCTCCTGCAAGCA<br>TTTA  | 60.0                             | 966                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17321954  | Ca4                                     | 17321954                      | TA/TATATATATATAA                                              | CTGCCGACCTGAATAC<br>CAAT | TGCCTTTAATGAAACAC<br>ACCA | 60.0                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17323828  | Ca4                                     | 17323828                      | CATATA/CATA                                                   | CTTGGTACAGTTTGG<br>CGAT  | TCTTGTGGTTGTGGT<br>TTCA   | 60.0                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17324366  | Ca4                                     | 17324366                      | TAAAA/TAAA                                                    | TGAAACCCACAACCAC<br>AAGA | CCCGACTCTTTCTCA<br>GCAC   | 60.0                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17327959  | Ca4                                     | 17327959                      | CATGTTTTTAAAATGTTTTTAA/CAT<br>GTTTTTAAA                       | GGTGTTACTGTTGAAG<br>CGGG | ATATTGCACGTGTCGC<br>ACTC  | 60.6                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17328665  | Ca4                                     | 17328665                      | GAA/GAAAA                                                     | ACACGTGCAATATCGG<br>TGAA | TCCTCCCTCTTTATCAT<br>GCC  | 60.0                             | 750                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17328879  | Ca4                                     | 17328879                      | GTTTTTT/GTTTTTTT                                              | CGTGATAAAACGTGCA<br>TCAA | TCCTCCCTCTTTATCAT<br>GCC  | 58.2                             | 244                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17329310  | Ca4                                     | 17329310                      | AC/A                                                          | GGCATGATAAAGAGGG<br>AGGA | TAACCTCTCACGTGCA<br>ATCG  | 59.1                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17332259  | Ca4                                     | 17332259                      | GAAAAAAAAAAAA/GAAAAAAAAA                                      | CGGCAAAATTACATCT<br>GTGG | GCGCATTGTCTAGCAT<br>TGAA  | 59.0                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_17332738  | Ca4                                     | 17332738                      | TAATAAAATAATAA/TAATAATAAA<br>TAAATAAA                         | GATGCAACTTCTTGGG<br>CAAT  | TTGTCACCGAACTGCA<br>TCAT   | 60.1                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17339892  | Ca4                                     | 17339892                      | ATTT/ATT                                                      | TTTTGGGGAACACAAC<br>CTTT  | GACATTTCTCATAGGG<br>GCGA   | 59.3                             | 297                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17348770  | Ca4                                     | 17348770                      | TCCATATATTGAATC/T                                             | TGGATTTCACAACTTTG<br>CCA  | ATTTGGACCATTGGCT<br>GAAC   | 60.1                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17367149  | Ca4                                     | 17367149                      | AATAT/AAT                                                     | GCAGCTAAAGGAGAGT<br>GCCA  | AGACAGTTCGCTCGCA<br>AATC   | 60.7                             | 506                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17367667  | Ca4                                     | 17367667                      | AC/ACC                                                        | TAAATGTGATTTGCGA<br>GCGA  | ATGCATGGAGGTGATG<br>ATGA   | 60.4                             | 284                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17367739  | Ca4                                     | 17367739                      | A/AAAAATGTAA                                                  | TAAATGTGATTTGCGA<br>GCGA  | ATGCATGGAGGTGATG<br>ATGA   | 60.4                             | 284                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17421137  | Ca4                                     | 17421137                      | GT/GTT                                                        | CCCGTGAGTTGTTGGA<br>AGTT  | ATGCCCTCATTGGAAC<br>TTGA   | 60.0                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17421248  | Ca4                                     | 17421248                      | G/GTTTAA                                                      | CCCGTGAGTTGTTGGA<br>AGTT  | TCGATAATTTGAAACCG<br>CCT   | 60.0                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17424073  | Ca4                                     | 17424073                      | CATATATAT/CATATATATAT                                         | GAGTGAGTGATGAGGG<br>ATGGA | GGGGACAAAGACATAA<br>TGGAGA | 60.1                             | 321                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17445543  | Ca4                                     | 17445543                      | GTTTTTTTTTTTT/GTTTTTTTTTT                                     | CCCCTTTCAACATTCCT<br>CAA  | CCAGAACATGCCTTCG<br>ATT    | 59.9                             | 891                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_17460394  | Ca4                                     | 17460394                      | TAAA/TAA                                                      | TGAAGGGCCATATTTG<br>ACAAT     | GAACGTATGGACCACC<br>GATT  | 59.3                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17463034  | Ca4                                     | 17463034                      | A/AT                                                          | AGAAATAAAATCACGA<br>GTAACCAAA | TTGCGGATTCCCAGTT<br>ACTC  | 57.6                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17475440  | Ca4                                     | 17475440                      | GT/GTTGTTATT                                                  | CGGGCAGTAGCATTAG<br>ATGG      | GGATGAATGGGAGGTG<br>GTTA  | 60.6                             | 210                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17532051  | Ca4                                     | 17532051                      | AT/A                                                          | ACTGGACTGGTCATCG<br>AACC      | GTCGCAGTTGCACCCT<br>TTAT  | 60.0                             | 114                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17532611  | Ca4                                     | 17532611                      | ATAAGTAAG/ATAAG                                               | CCGATGGAGGTGAAAG<br>AGAG      | GCACGGTACAACCTCAC<br>CAGA | 59.8                             | 691                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17533077  | Ca4                                     | 17533077                      | CAGTG/CAGTGCATAAGTG                                           | TGGTGAGTTGTACCGT<br>GCTC      | AAATGGCACCAGCAA<br>AAAG   | 59.8                             | 358                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17533461  | Ca4                                     | 17533461                      | AA/AATTA                                                      | CTTTTTGCTGGTGCCA<br>TTTT      | TGCAAGAAGAAGGAAG<br>CCAT  | 60.1                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17533529  | Ca4                                     | 17533529                      | GT/G                                                          | CTTTTTGCTGGTGCCA<br>TTTT      | TGCAAGAAGAAGGAAG<br>CCAT  | 60.1                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17533740  | Ca4                                     | 17533740                      | TAAAAAAA/TAAAAAAA                                             | TGTCCATAATAAATATC<br>GCATTTCA | TGCAAGAAGAAGGAAG<br>CCAT  | 59.6                             | 377                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17534710  | Ca4                                     | 17534710                      | ATATT/AT                                                      | CTGGATCCCCTCGGAA<br>GTAT      | AGAAACCGCACACACA<br>CAAA  | 60.3                             | 316                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                  |                              |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_17534970  | Ca4                                     | 17534970                      | AAAA/AAAAACATATTTCAAA                                            | TTTTGTGTGTGTGCG<br>GTTT      | TGTGTCAAAGATGGTA<br>TTTCAATG | 60.1                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17545144  | Ca4                                     | 17545144                      | TATTAATAATAATTA/TATTAATAA<br>AATAATTAATAATAATTA                  | ATCCAAAAGGTCGTCC<br>ACAG     | AAATCGGTTTCCCAG<br>TACC      | 60.0                             | 652                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17588721  | Ca4                                     | 17588721                      | CTTT/CTT                                                         | TAACGATGATGACACG<br>CTCC     | TCACATTTGTACCTC<br>CGA       | 59.7                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17600797  | Ca4                                     | 17600797                      | TC/T                                                             | AAGGGTGATGGACGAA<br>AAAC     | TTAAATGGTCGCATAG<br>AGCAA    | 58.9                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17600811  | Ca4                                     | 17600811                      | TAAAAA/TAAAAAA                                                   | AAGGGTGATGGACGAA<br>AAAC     | TCCAACAACATCAAAT<br>CATCC    | 58.9                             | 951                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17601611  | Ca4                                     | 17601611                      | AATTAATTAATACTATTAATTAATTA<br>ATTAATTAATACTATTAATTAATTA<br>CTATT | ACACAATCACCCCTTGT<br>CCC     | CCGTGTCTATCCCAT<br>TTTG      | 59.7                             | 211                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17601888  | Ca4                                     | 17601888                      | TAAA/TAAAA                                                       | CAAAATGGGGATAGAC<br>ACGG     | TTTCAAATGAACGTTTG<br>CTACA   | 60.2                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17602358  | Ca4                                     | 17602358                      | GT/GTT                                                           | TTTGAATGTGATTGTA<br>GCAAACG  | CCTATTCTCGAGAGCA<br>ACCG     | 59.2                             | 322                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17628350  | Ca4                                     | 17628350                      | CATATATATATATA/CATATATATA                                        | GCAGACCACTTCATGC<br>AAAA     | TGGATCACCGATTGCT<br>TGTA     | 59.8                             | 250                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1763098   | Ca4                                     | 1763098                       | ATTTTTTT/ATTTTTTTTTT                                             | TGATAAGGGTATGTGA<br>TTTTGGTT | ACATTTTGAAGGGCA<br>TCTG      | 58.7                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_1764559   | Ca4                                     | 1764559                       | TAAAAAAAAA/TAAAAAAAAA                                         | GCCAACTCATGTCTTT<br>GTCG  | ATTCTCGTGAGTGGGG<br>TTTG  | 59.3                             | 758                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17650207  | Ca4                                     | 17650207                      | AAGA/AA                                                       | CCAAGAGTTCAATACG<br>AGCCA | TGCGGTTCTATAAAAT<br>GGG   | 60.3                             | 251                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17650571  | Ca4                                     | 17650571                      | TTATATATATAT/TTATATATATATAT<br>AT                             | CCCATTTTATAGGAAC<br>CGCA  | TTGGTTTTTGAACAAC<br>GTG   | 59.8                             | 355                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17650657  | Ca4                                     | 17650657                      | GAA/GAAA                                                      | CCCATTTTATAGGAAC<br>CGCA  | TGCTCCAGAAAACGAA<br>CTCA  | 59.8                             | 809                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17675509  | Ca4                                     | 17675509                      | AAATAATAATAATA/AAATAATAA<br>TAATA                             | AACTTGCCATGTGGT<br>TGGT   | CTAGCACATGATCCCC<br>TCAA  | 60.3                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17677705  | Ca4                                     | 17677705                      | AT/A                                                          | GGGGGCCAAAAATTAA<br>GAGA  | ATATTGGGGATGATGT<br>GGGA  | 60.3                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17713411  | Ca4                                     | 17713411                      | TAA/TA                                                        | TCCGTCGTTTATTCTTT<br>GGC  | TGAATCGTTTTGGAAAA<br>TTCG | 60.1                             | 673                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17715354  | Ca4                                     | 17715354                      | AATAA/AATAACAATATTCCATAA                                      | TCAATTTGGAGGGTGA<br>CTCC  | TACCAGCTTTGGTTTCT<br>GCC  | 59.9                             | 250                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17716045  | Ca4                                     | 17716045                      | ACT/ACTCT                                                     | TTTAGTGTGACGGGAT<br>GGTG  | GGTTTGAGAAACAAA<br>ACTTGG | 59.4                             | 624                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17717044  | Ca4                                     | 17717044                      | TGG/TG                                                        | TCTGTCAAAGTCGGTG<br>CAAG  | ATAATGGCGCCACAGA<br>AAAG  | 60.0                             | 821                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_17734744  | Ca4                                     | 17734744                      | ATTTAAAAAAATT/AT                                              | AACAAAAATCGCAATC<br>CACC     | GAAGTTAACTCCAATC<br>GGGC      | 59.8                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17735574  | Ca4                                     | 17735574                      | T/TA                                                          | TCACGATCGAAAAACC<br>TATTTG   | AAACATGACAAAAGTTG<br>ATGTTGAA | 59.1                             | 916                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17735792  | Ca4                                     | 17735792                      | TC/TCC                                                        | AAGAATTTTGATGACGT<br>GACAATC | TGGGAGTGCATAATGT<br>TTGA      | 59.4                             | 787                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17738882  | Ca4                                     | 17738882                      | AC/A                                                          | TTCTTTCTTTGGTGT<br>GCG       | TTGCTGTATCAAGTGG<br>CAAAA     | 59.0                             | 745                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17739507  | Ca4                                     | 17739507                      | CAAAAAA/CAAAAA                                                | TCGGGATAGTGGATGA<br>GGTAA    | CGCTTGACCTCTAATC<br>AGGC      | 59.4                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1774381   | Ca4                                     | 1774381                       | CCTTCTT/CCTTCTTCTT                                            | CACACGAGTGTGCCT<br>AAGA      | TGGTATCCAGAGCCAT<br>CACA      | 60.0                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17744056  | Ca4                                     | 17744056                      | TAATAAATAAATAAA/TAATAAATAAA                                   | TGCGAGTCTAACATTA<br>AAACCTC  | GCGGAGACTTTGACCT<br>TTTG      | 57.7                             | 745                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17753614  | Ca4                                     | 17753614                      | CTTTTTTT/CTTTTTTTT                                            | TGGACGGACAATGCAA<br>TAGA     | TTTCAAAATGTTGCTTT<br>AAAAATCT | 60.1                             | 751                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17778807  | Ca4                                     | 17778807                      | TG/T                                                          | TGATTGGGAACCTGGT<br>GAAT     | CATGCCAAAATCAACA<br>GCAC      | 60.2                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17786473  | Ca4                                     | 17786473                      | TTTTTGT/TT                                                    | CGCGCCAACTTTACTT<br>CTTC     | TCCAAAATTTAGTGGCA<br>GCA      | 60.0                             | 621                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_1780181   | Ca4                                     | 1780181                       | GAAAAA/GAAAA                                                  | AATTCAGAAGACTGG<br>GGGAA     | TTTTTGCCGGTTGAAC<br>TGA   | 59.9                             | 444                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17821086  | Ca4                                     | 17821086                      | AGGGGG/AGGGG                                                  | GGAAGTGTCTGATTGT<br>TCCCA    | AGATGTGGGCATGTGT<br>TTCA  | 59.8                             | 805                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17823516  | Ca4                                     | 17823516                      | TTTCTT/TTT                                                    | ATATGCCCTGACGAA<br>CAAC      | TGAATGGTTTAAATTCT<br>GCCA | 59.8                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17823791  | Ca4                                     | 17823791                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                 | TCTCATGTCTTGCAAAA<br>TTCTTCT | TTTGTGATTGATATTG<br>CCGTT | 59.4                             | 354                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17825306  | Ca4                                     | 17825306                      | TAAAA/TAAA                                                    | AATCCATCAAACCTCG<br>TTGC     | TGCTATTTGGTTGGCC<br>TTTT  | 59.9                             | 301                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17825457  | Ca4                                     | 17825457                      | CGTTATGA/CGTTATGAGTTATGA                                      | AATCCATCAAACCTCG<br>TTGC     | GGGCCCCGTAAGTATT<br>CAGT  | 59.9                             | 679                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17825598  | Ca4                                     | 17825598                      | ACC/ACCC                                                      | AATCCATCAAACCTCG<br>TTGC     | GGGCCCCGTAAGTATT<br>CAGT  | 59.9                             | 679                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17825906  | Ca4                                     | 17825906                      | ATTTTTTT/ATTTTTTT                                             | AAAAGGCCAACCAAA<br>TATG      | CCTCAATTCTCGATTTC<br>CCA  | 59.6                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17825981  | Ca4                                     | 17825981                      | ATTTTTTTT/ATTTTTTTTT                                          | GGGGCCCCATAATCAT<br>ATTT     | CCTCAATTCTCGATTTC<br>CCA  | 59.7                             | 164                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17843324  | Ca4                                     | 17843324                      | TA/T                                                          | GGGGGAGACCTACCG<br>TATCT     | AGAAACGGGTTGTGCC<br>TATG  | 59.3                             | 224                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_17853769  | Ca4                                     | 17853769                      | CAAAAAAAAA/CAAAAAAAAA                                         | AATGGACAACATTCAT<br>CCCA | GAAACCCTAAACCCCTT<br>CGC    | 58.6                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17865327  | Ca4                                     | 17865327                      | TTAAGAGTA/TTA                                                 | ATATGGAAAGTCGCCG<br>TTTG | CCGAGGCAATAAAACA<br>CCTC    | 60.0                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17865546  | Ca4                                     | 17865546                      | TAAAAA/TAAAAAA                                                | GAGGTGTTTTATTGCC<br>TCGG | TGTTAATCCCAATTCAA<br>TATCCC | 59.6                             | 133                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17873043  | Ca4                                     | 17873043                      | TAAA/TA                                                       | CATTGAAATGCATGGA<br>CCAA | TTTTCTCCATGCACCCT<br>ACC    | 60.3                             | 885                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17942733  | Ca4                                     | 17942733                      | CTATATATATATATAT/CTATATATAT<br>ATATATAT                       | CATCGTCAGCACATCA<br>CAAA | CTTAGGAGGTCTTGCC<br>CCTC    | 59.2                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_17959700  | Ca4                                     | 17959700                      | C/CATTCCCTT                                                   | AGTGGCATGTGGGGAT<br>TAAA | TTTGGTGAAATGGCA<br>TGTA     | 60.2                             | 168                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_18005269  | Ca4                                     | 18005269                      | TA/TAACGAA                                                    | CAACGTTGCTACGAGG<br>ACAA | CATTCTGTCCTCAGAG<br>TGTG    | 59.9                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_18041622  | Ca4                                     | 18041622                      | CTTTTTTT/CTTTTTTTT                                            | CCTGTTTTCTCCACC<br>CTTT  | ATGGGGACTTGGGGAG<br>TAAC    | 60.3                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_18061059  | Ca4                                     | 18061059                      | TATAATAATAATAATAATAATAA/<br>TATAATAATAATAATAATAATAA<br>TAATAA | GAAGCGACCACCTGAA<br>GAAC | CAGAACAAATGACGTG<br>TCCC    | 59.9                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_18091373  | Ca4                                     | 18091373                      | TCATCAC/T                                                     | CCACGGATGTGATTTA<br>GCCT | GAAGCACCCTTCCTTC<br>TTGA    | 60.0                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_18110946  | Ca4                                     | 18110946                      | ATTTTTTTTT/ATTTTTTTTT                                         | TTCTTTGGAGACTGAG<br>TTGGTTC | GACTCGATGAAAATGA<br>TGGTGA | 59.8                             | 377                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_18152849  | Ca4                                     | 18152849                      | CTTTTTTTT/CTTTTTTTTT                                          | GTGAGCAGCATTGTGC<br>AGTT    | CTCGAGCTTGGTACGA<br>GAGG   | 60.1                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1818935   | Ca4                                     | 1818935                       | GAAAAAA/GAAAAAAA                                              | TTGCACTGTTTGGTGA<br>AAGG    | TTGTGGCAATTGAAAA<br>GGAC   | 59.7                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1819613   | Ca4                                     | 1819613                       | ATATTA/ATA                                                    | TCCTTTTCAATTGCCAA<br>CAAC   | ATTGCATTTGGAACCCT<br>GAC   | 60.0                             | 808                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_18196212  | Ca4                                     | 18196212                      | ATTT/ATTTAATCTTTTT                                            | GTGGTCCAGATTCTCC<br>CAAA    | TGTCGCTTCAGAAAA<br>AGAA    | 59.9                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1819707   | Ca4                                     | 1819707                       | ATTTTTTTT/ATTTTTTT                                            | CAATTGCCAACAACAA<br>AATCC   | ATTGCATTTGGAACCCT<br>GAC   | 60.2                             | 801                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1820022   | Ca4                                     | 1820022                       | CAAA/CAAAA                                                    | AAAGTCAGGGTTCCAA<br>ATGC    | CGATTCCCAATCGCTA<br>TCTT   | 59.0                             | 131                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1825344   | Ca4                                     | 1825344                       | TAAAAAA/TAAAAAA                                               | ATTTGTACGGTTTTGG<br>CTCG    | TTTTGGCCCTCGTAAG<br>TTTTT  | 60.0                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1825724   | Ca4                                     | 1825724                       | ATTTTTTTT/ATTTTTTTTT                                          | AATGAAATCAGTCGAC<br>CCCA    | TGTTGCAATGTTGGTT<br>CTTCA  | 60.3                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_18265518  | Ca4                                     | 18265518                      | CTTTTTTTTT/CTTTTTTTTTT                                        | TTCAAACCAATATCAA<br>AACGC   | TTGATTGAAACATTGAT<br>TTCCG | 59.0                             | 318                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                     |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_1826824   | Ca4                                     | 1826824                       | TTTTAACAGTTTA/TTTTA                                                 | AAAGACCGCATATGTA<br>ATTAGCC | GGAGAGATATGCGGGT<br>TGAA  | 59.8                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1827077   | Ca4                                     | 1827077                       | ATTTTTTTT/ATTTTTTT                                                  | AAAGACCGCATATGTA<br>ATTAGCC | GGAGAGATATGCGGGT<br>TGAA  | 59.8                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1827115   | Ca4                                     | 1827115                       | TA/TAA                                                              | AAAGACCGCATATGTA<br>ATTAGCC | GGAGAGATATGCGGGT<br>TGAA  | 59.8                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_18388650  | Ca4                                     | 18388650                      | ATATTA/ATA                                                          | AGTTATCGATCACGGA<br>TGCC    | CGTGTATATTCGCGCA<br>CTCA  | 59.9                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_18462391  | Ca4                                     | 18462391                      | GTTTTTTTTTT/GTTTTTTTTT                                              | AGGAAGGTGGATGCAG<br>ATTG    | TGGAAGAAAAGGAATC<br>CGAA  | 60.1                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1848187   | Ca4                                     | 1848187                       | TATAATAATAA/TATAATAATAATA                                           | AGAAGCAAAAGAGCCC<br>TTCC    | ATAGGAATATAGGCGC<br>GGGT  | 60.0                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_18515805  | Ca4                                     | 18515805                      | TATAAATAAATAAATAAATAA<br>T/TATAAATAAATAAATAAATAA<br>ATAAAT          | TTTTTGAGATTGGTAC<br>GGGA    | TCAGCGTTTGTGTGTG<br>ACTT  | 58.1                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_18530309  | Ca4                                     | 18530309                      | TTAATAATAATAATAAAT/TTAATA<br>ATAATAATAATAATAATAAT                   | TGCGTTGATAATCCAG<br>AGGA    | AGGTAACAAGGGCAAT<br>GACG  | 59.2                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_18554841  | Ca4                                     | 18554841                      | TTATATATATATATATATATATATA<br>TATAT/TTATATATATATATATATA<br>TATATATAT | TGGACCATATGTGTTG<br>GGTC    | CCCGGATAATTGTTCA<br>CTTTG | 59.1                             | 809                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1858416   | Ca4                                     | 1858416                       | GAAAAA/GAAAA                                                        | ATGGTGCACACAAAAC<br>AGGA    | AAACCGATATGCCCTTT<br>GAA  | 60.0                             | 788                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_1861853   | Ca4                                     | 1861853                       | AT/ATGAACCT                                                   | TGAGGACAAAAGATCC<br>CCTG      | AGGGTCCACAGAAAAT<br>CGTG  | 60.0                             | 870                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1861881   | Ca4                                     | 1861881                       | GTTTATTTATTTATTTATTTATT/GTT<br>TATTTATTTATTTATTTATTTATT       | TGAGGACAAAAGATCC<br>CCTG      | AGGGTCCACAGAAAAT<br>CGTG  | 60.0                             | 870                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1863218   | Ca4                                     | 1863218                       | TAAAAAAAAA/TAAAAAAAAA                                         | CCCGGGTTTAACTACC<br>CATT      | CAGCTACTCGCTGCAC<br>ACTC  | 59.9                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_18651098  | Ca4                                     | 18651098                      | AATATATATATATATATAT/AAAT<br>ATATATATATATATATAT                | TGCTTTCTTTGATGTG<br>CTGG      | TTCCCCCAACATCATT<br>TAGTT | 60.0                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_18703975  | Ca4                                     | 18703975                      | GACACA/GACA                                                   | CCACATTGACATAAACA<br>TCTTCTCA | TCAACAACGTTGCTCTT<br>TTTG | 60.3                             | 173                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_18705110  | Ca4                                     | 18705110                      | AAT/AATTAT                                                    | TTGTGCATTGACAAC<br>ATCC       | ATGCACAATCAAAAACA<br>GCG  | 60.5                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_19010119  | Ca4                                     | 19010119                      | ATTTTTTTTTT/ATTTTTTTTTTTT                                     | TGTCAAGTACCAAGCA<br>AGACCT    | CAATCGGATCAATGGC<br>TACC  | 58.9                             | 134                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_19045820  | Ca4                                     | 19045820                      | A/AT                                                          | GGGCTTGCTTGGTTTG<br>AATA      | TCAACTGCACGTGTTA<br>AATGC | 60.1                             | 825                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1907150   | Ca4                                     | 1907150                       | TATAAAAAATAAAAA/TATAAAAAATA<br>AAAAATAAAAA                    | AAAGAGTTTAAAGGCG<br>GGGA      | GCGGTCAATTCCGAA<br>TGAA   | 60.1                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_19081618  | Ca4                                     | 19081618                      | CAATAATAATAATAATAATAA/CA<br>ATAATAATAATAATAATAATAA            | CGACACTTCAACACAA<br>AATTCA    | TGTTGAAAAACATGT<br>TCCC   | 58.7                             | 893                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                         | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                                       |                           |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_19082750  | Ca4                                     | 19082750                      | AGG/AG                                                                                                                                                                | GCCTTAACGTTCACTC<br>CTGC  | TAAGCCATAAGCGGAG<br>AACG      | 59.9                             | 134                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_19147123  | Ca4                                     | 19147123                      | AT/ATACATCT                                                                                                                                                           | TTTCAACACTCCCCCT<br>CAAG  | GCTGAAGCTGAATACA<br>GGGC      | 60.1                             | 352                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1928030   | Ca4                                     | 1928030                       | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATAT<br>ATATATATA                                                                                                   | CAATTCCTTCATCGATC<br>CACT | ACAACCCATTCACTCCT<br>GGTA     | 59.0                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_19342121  | Ca4                                     | 19342121                      | TAAAAAAAA/TAAAAAAAAA                                                                                                                                                  | TTCCGAAAATTCATG<br>CAC    | GAATTTGGATTATTGCA<br>TTCTCTGA | 59.5                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_19369951  | Ca4                                     | 19369951                      | CAAAAA/CAAAAA                                                                                                                                                         | CCCATGTTTAAGGGTG<br>GTTG  | AATTTTTCACGACCTTC<br>TTCAA    | 60.1                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_19396924  | Ca4                                     | 19396924                      | TGAAGAAGAAGAAGAAGAAGAAGA<br>AGAAGAAGAAGAAGAAGAAGAAGA<br>AGAAGAAGAAGAAG/TGAAGAAGAA<br>GAAGAAGAAGAAGAAGAAGAAGAA<br>GAAGAAGAAGAAGAAGAAGAAGAA<br>GAAGAAGAAGAAGAAGAAGAAGAA | TTTGAGACCAATGGT<br>GACA   | TTGATTGAAACCAAGAC<br>CAGC     | 59.9                             | 938                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_19397426  | Ca4                                     | 19397426                      | GAAAA/GAAA                                                                                                                                                            | GCCAAACATATGCTTGA<br>TGGA | TTGAACTTTCTCCGTTT<br>GGG      | 59.5                             | 667                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_19415220  | Ca4                                     | 19415220                      | TAAAA/TAA                                                                                                                                                             | TCATCAAATCCGTAAC<br>GCAA  | TCTTAACATGCGGTC<br>CTCG       | 60.1                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_19445900  | Ca4                                     | 19445900                      | GA/GAA                                                                                                                                                                | ACAGATTCGTGGAGGT<br>GGAG  | ATGCCAAGCGTTTCAC<br>TTTT      | 60.1                             | 429                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_1958352   | Ca4                                     | 1958352                       | TAAAAA/TAAAAA                                                                                                                                                         | AACAAGCCCAATTTTG<br>CAGT  | TGGAGATTGTTACCC<br>ATCA       | 59.6                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                    | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                  |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_19643688  | Ca4                                     | 19643688                      | CTTTTT/CTTTTT                                                                                                                    | GGTGCAGTTGTTGAT<br>GCAC  | ATGCGATTACATGGTT<br>GGC   | 60.2                             | 255                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_19678061  | Ca4                                     | 19678061                      | C/CGGCTGGTACAA                                                                                                                   | ATTTTGGCAACGGCTG<br>ATAC | CCACAATCCTCCGTTG<br>TCTT  | 60.0                             | 492                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_19789343  | Ca4                                     | 19789343                      | A/AG                                                                                                                             | CTAGGGGATTGCATTC<br>CAAA | TTTTCCTGCCAAACACC<br>TTC  | 59.9                             | 177                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_19886492  | Ca4                                     | 19886492                      | CATTCTTATTTCTT/CATTCTT                                                                                                           | GACCCCTGACAAAGA<br>CAGA  | AGAGGGTTGTGCACTT<br>GAGC  | 60.1                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_19958903  | Ca4                                     | 19958903                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAA/AAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAA | GGCAAACCTAGGAATC<br>ACCA | TGTGGTTTGGTTTAGAT<br>TCCG | 59.9                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_20051846  | Ca4                                     | 20051846                      | GTAT/GTATGTGATTAGTGACTAT                                                                                                         | CACGAAGCGTATTGAC<br>TCCA | AAATTTGAAGGCGCTTT<br>TTG  | 59.9                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_20068492  | Ca4                                     | 20068492                      | TAAAA/TAAA                                                                                                                       | AACTGGATGCCCGACA<br>TAAG | CCGATTGGATTGTCAG<br>GACT  | 60.0                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_20108947  | Ca4                                     | 20108947                      | TTATATATATA/TTATATATA                                                                                                            | GGCTAACATATGGACT<br>CGCC | TGGTCATTTTGACCTCC<br>ACA  | 59.6                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_20170219  | Ca4                                     | 20170219                      | GTTTATTTATTTATTTATTTATTT<br>TATTTATTTATTTATTTATTTAT<br>T/GTTTATTTATTTATTTATTTA<br>TTTATTTATTTATTTATTTAT                          | AAAAGGCGTCTCCTCT<br>CTCC | TCGCACATGAAACAG<br>AAAT   | 60.0                             | 233                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_20186435  | Ca4                                     | 20186435                      | AT/A                                                                                                                             | GAGCTGTCTCGGTACG<br>GAGT | CAATCCACAGGTAC<br>GCTT    | 59.6                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                 | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_2022623   | Ca4                                     | 2022623                       | AAATAATAATAATAATAATAATA<br>ATAATAATAA/AAATAATAATAAT<br>AATAATAATAATAATAA                      | AACGTGTTTGAGTGCG<br>AAAA   | TCGAGATGCGATTATG<br>TGGA   | 59.4                             | 819                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_2030157   | Ca4                                     | 2030157                       | GAAAAAAAA/GAAAAAAAA                                                                           | TGAAAGTGCCAGAAAA<br>CCCT   | CGAATGTTTATGGTTG<br>GGGT   | 59.7                             | 354                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_20327473  | Ca4                                     | 20327473                      | CATATATATATATATATATATATA<br>TATATATATATATATA/CATATATA<br>TATATATATATATATATATATATAT<br>ATATATA | TAAGGTCATGAGGGAT<br>TGCC   | CACCCCCTTTCCTTTTA<br>TGC   | 59.9                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_20346298  | Ca4                                     | 20346298                      | ATTATTTATTTATTTATTTATTT<br>ATTTATTTATTTAT/ATTATTTATTTA<br>TTTATTTATTTATTTATTTATTTAT           | TGTTTTGTTCCATGCAT<br>TTCTT | GATGCTCATCCCTCCA<br>AAAA   | 59.5                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_20421380  | Ca4                                     | 20421380                      | TAAAAAAAAAAAA/TAAAAAAAAAA                                                                     | TTCGAACTAAAACTTG<br>GGCA   | CCTCTTGAGAAATGTTG<br>GGGA  | 59.7                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_20496333  | Ca4                                     | 20496333                      | CTTTTTTTTTTT/CTTTTTTTTTTT                                                                     | TGAGGACCAAACGTAA<br>CCCT   | GAGACGTTTTTCAGAAA<br>CCCC  | 59.4                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_20500766  | Ca4                                     | 20500766                      | GAAAAAAAAAAAA/GAAAAAAAAAA                                                                     | TCGTAAATTTGAGAAC<br>GTGAGG | AACCCAACCCATTATAG<br>GGC   | 59.3                             | 347                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_2052943   | Ca4                                     | 2052943                       | GATATATATATATATATATATATA<br>T/GATATATATATATATATATATAT<br>ATATAT                               | ACAAATGGTCAGTGG<br>TGCC    | TCAAATTTGTGAGCATC<br>AAACA | 60.8                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_20615648  | Ca4                                     | 20615648                      | ATTTTTTTTTTTTT/ATTTTTTTTTT<br>TT                                                              | CCATTGCGTTGTGTT<br>TTGC    | TGAATAATCTGCACGT<br>CCCA   | 60.0                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_20709240  | Ca4                                     | 20709240                      | ATTTTTTT/ATTTTTTTTT                                                                           | ACTTTGCCCATCAGTTT<br>TGC   | TCCGTTGGTGAAAGTT<br>TGAA   | 60.1                             | 251                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                                     | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                                                   |                            |                               |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_20738577  | Ca4                                     | 20738577                      | GGCTTATG/GG                                                                                                                                                                       | CTCCCTCCATGAGGT<br>TACA    | ACGCCACAAGGATTAA<br>CAGC      | 59.9                             | 818                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_20798832  | Ca4                                     | 20798832                      | TTTTATTATTTATTATT/TTTTATT<br>ATTTATT                                                                                                                                              | TAGTGCTTTTGCATGC<br>CTCA   | TTTGTCTGGGAAAAT<br>GCTC       | 60.5                             | 316                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_20919644  | Ca4                                     | 20919644                      | ATTTTTTTTT/ATTTTTTTTT                                                                                                                                                             | TCAGAAATTTGTCATT<br>GTCCA  | TCGTTGAAATCGGTTA<br>TTGA      | 58.1                             | 719                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_20954508  | Ca4                                     | 20954508                      | CTATTATTATTATTATTATCATT<br>TTATTATCATTAAATTATTATTATTA<br>TTATTATTATTATGATTATTATTATTA<br>TTATTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTATTA | TGAGAAAATGTTCCCT<br>CTGATT | TCGTTTATGTTAAATTA<br>CACCATGC | 59.6                             | 248                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_20955373  | Ca4                                     | 20955373                      | CTATATATATATATATATATAT/CT<br>ATATATATATATATATATATATAT                                                                                                                             | AGGCTTTATGCAAGGG<br>GTTT   | TCACAATTGGTGGTAC<br>CGTG      | 60.0                             | 191                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_2102792   | Ca4                                     | 2102792                       | ATAATGT/ATAATGTAATGT                                                                                                                                                              | AATGCATTATTGGTGG<br>GTCAA  | TTCTGTTCTCTCCACC<br>AAAGA     | 60.1                             | 582                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_21082826  | Ca4                                     | 21082826                      | AAATAATAATAATAATAATAAA/AA<br>ATAATAATAATAATAATAAA                                                                                                                                 | GTGCGTGCTTTGGGAT<br>TTTA   | CGAACTGAAGAACGAT<br>TAGGTG    | 61.0                             | 332                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_21226050  | Ca4                                     | 21226050                      | AT/AAAGGAACT                                                                                                                                                                      | CACGGCTCTACGAAGG<br>AAAG   | TGAACACCCCAAGGT<br>TAAG       | 60.0                             | 287                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_21248655  | Ca4                                     | 21248655                      | TAAAAAAAAA/TAAAAAAAAA                                                                                                                                                             | CAGGTTTAATTGTGGA<br>GGTGC  | TGCATTGCAGTGTGAA<br>ACG       | 59.5                             | 102                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_21261688  | Ca4                                     | 21261688                      | AATATATATATATATATATATATAT<br>ATATATATAAATATATATATATATAT<br>ATATATATATATATATATATATATA<br>TA                                                                                        | GAAAAATTTGCTGAGC<br>TGGTG  | TGCGACAGAATCTTAAT<br>GTGC     | 59.9                             | 485                                           | INTERGENIC                                           | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_2140233   | Ca4                                     | 2140233                       | AATATATATATATATATATAT/AA<br>TATATATATATATATATATAT             | AACGTATTGGAAATTG<br>AATGG | TAGTACTCGTACCGT<br>GCCC   | 57.9                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_2141158   | Ca4                                     | 2141158                       | T/TATTACCGACACGG                                              | CTATAGTACTCGCCCC<br>GCAC  | TGCGATTGAGCTGGTA<br>CTTG  | 59.8                             | 956                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_21529168  | Ca4                                     | 21529168                      | CAAAA/CAA                                                     | TGGGGGATTGTATTCC<br>AAAA  | TATGGAATGGACCTCC<br>TGCT  | 60.0                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_21529316  | Ca4                                     | 21529316                      | T/TA                                                          | TGGGGGATTGTATTCC<br>AAAA  | TGAAATCGTCACCGTC<br>TCAA  | 60.0                             | 886                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_21622605  | Ca4                                     | 21622605                      | TAATGTTAAAA/TAATGTTAAAAAAT<br>GTTAAAA                         | CGTGTATATACGCACA<br>CCCAA | GTTTTGGCGTTGGTT<br>CACT   | 59.4                             | 805                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_21640123  | Ca4                                     | 21640123                      | GT/GTGTCTTTCCCT                                               | TTTGGTATTGCATCCC<br>CTTC  | AGCCCATCAACGTCTT<br>TGTC  | 59.8                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_21657242  | Ca4                                     | 21657242                      | GTGAAAGAAAAT/GT                                               | CGAGAGCTTTGAAGAC<br>TTTGC | CGGAGTTCCAATCTCA<br>CAGA  | 59.4                             | 211                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_21726235  | Ca4                                     | 21726235                      | TAAAAAA/TAAAAAAA                                              | CGACATTCATTGTTACC<br>CCA  | TGGAGGAAGAACCGTT<br>ATCAA | 59.2                             | 739                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_21728459  | Ca4                                     | 21728459                      | TAA/TAATAATAATAAAAA                                           | CCATTCGTTGCTCCA<br>TCTT   | TGGTTTTTGTGTTTGG<br>TTTCT | 60.1                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_21804779  | Ca4                                     | 21804779                      | CTGT/CTGTTATGT                                                | CCGCATCATAAACAGC<br>CTTT  | CTAAAGCTGGTGCTTTT<br>GGC  | 60.1                             | 159                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_21838798  | Ca4                                     | 21838798                      | ATTTTTTT/ATTTTTTTT                                            | CCGTCTCGTGTCTGT<br>GCTA   | CGTGACGACTTCCAAG<br>ATGA    | 60.0                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_21849002  | Ca4                                     | 21849002                      | CAAAAA/CAAAAAA                                                | AAGAGAGGTCACCTTG<br>GCGA  | TGGAGAATTTCAAGCT<br>GCTT    | 60.0                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_21928505  | Ca4                                     | 21928505                      | CTTTT/CTTTT                                                   | ACCAGGAAAAGAAGAA<br>GGGC  | AAGCGCTGTAAAAGGC<br>GTTA    | 59.7                             | 900                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_21984745  | Ca4                                     | 21984745                      | ATATATTTATAT/ATATAT                                           | AATAAAGGCGCATGG<br>AAAA   | TCAAAAGTTTGGTGCG<br>ATGA    | 59.6                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22052600  | Ca4                                     | 22052600                      | AATTATTATTATTATTATTA/AATTAT<br>TATTATTATTA                    | GGATGCGACCTGCTAC<br>TGAT  | GGATGCGACCTCCTAC<br>TAGC    | 60.2                             | 801                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22062454  | Ca4                                     | 22062454                      | CT/CTT                                                        | TGCAACAGAACACGAC<br>AAAA  | AGTCTACGGTCGGTGT<br>AGCG    | 58.9                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22327879  | Ca4                                     | 22327879                      | TAAAAAAAAA/TAAAAAAAAA                                         | ACCGGAAATTCACGC<br>CTTA   | GATTGGCGAGATTGAC<br>GAAT    | 61.7                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_2233798   | Ca4                                     | 2233798                       | CT/C                                                          | TTCAATTCGGGGAAC<br>TAGC   | TTGTTATTTAGTCTTGC<br>TTGCCA | 59.3                             | 264                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22441886  | Ca4                                     | 22441886                      | CTA/CTATA                                                     | TCCAATGGTGAAAAAT<br>AAACG | TCAATCACAAATTTCAA<br>GGAGG  | 59.7                             | 848                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22460898  | Ca4                                     | 22460898                      | GTT/GTTT                                                      | TTAATGCCCTCGTCAT<br>GTTT  | TAATTTCCGCTGTGCA<br>CTTG    | 58.1                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                      | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                    |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_22535036  | Ca4                                     | 22535036                      | ATTTT/ATTTT                                                                        | TTTGAGTGTGCGCATCC<br>CATA | TCACGGCTTCATGGAT<br>GTTA    | 60.1                             | 722                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22546535  | Ca4                                     | 22546535                      | AATATATATATATA/AATATATATATA<br>TATA                                                | CATTTTGGTTTCAAAGC<br>CGT  | CCAGGGGATGAGATCA<br>TAGG    | 60.0                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22601946  | Ca4                                     | 22601946                      | AAATAATAATAATAATAATAATA<br>ATAATAATA/AAATAATAATAATAATA<br>ATAATAATAATAATAATAATAATA | TCGCGTCTTCCATTCA<br>TTTC  | CGATTTTCATGAATTGCA<br>AATGT | 61.1                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22622741  | Ca4                                     | 22622741                      | ACA/ACATGTGAATCCA                                                                  | ACTTGTGGCCCTGTTTT<br>TGG  | ATGCACTGTGTGTTTG<br>GGAA    | 60.0                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22649924  | Ca4                                     | 22649924                      | A/AT                                                                               | CCGTCCAAATCAAATG<br>AAAAC | CATTACCATGTGCTTT<br>TTATGC  | 59.3                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22650061  | Ca4                                     | 22650061                      | TAAAA/TAAAA                                                                        | TGATGCATAAAAAGCA<br>CATGG | TCACTTTAAATTACGC<br>TGCA    | 59.6                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22663072  | Ca4                                     | 22663072                      | CCTTCTT/CCTT                                                                       | ACCCCTCTTCTCGTG<br>TTTT   | AGGCTCAGGCAACTAG<br>GGAT    | 60.0                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22664879  | Ca4                                     | 22664879                      | AA/AAGA                                                                            | TCGCGTTCGATTTGTT<br>CATA  | GGTCATTCTTATTGATT<br>GACCCA | 60.2                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22668695  | Ca4                                     | 22668695                      | TGG/TG                                                                             | GTTTCCCGTCCTTTTCAT<br>TCA | CAGTGACAAAAGGCCA<br>ATCA    | 59.9                             | 712                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22677817  | Ca4                                     | 22677817                      | AC/ACC                                                                             | TCTCCCCCTTTTGATG<br>ATG   | TCCTAAGGCTGAACCC<br>TCAA    | 59.9                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_22706706  | Ca4                                     | 22706706                      | TCC/TC                                                        | CCAACAAATTGGGTGG<br>AAAA    | TCGCTGCAACCAATAA<br>ATGA  | 60.6                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22719475  | Ca4                                     | 22719475                      | A/AT                                                          | ACACGTCATTGTGTTTG<br>GCA    | TGTTGCAATAGAAGGT<br>CGCA  | 60.0                             | 390                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22720347  | Ca4                                     | 22720347                      | GAAAAAAAA/GAAAAAAAAA                                          | ATGCCAAACAAATGA<br>CTGTT    | TGTTGGTTTTGATTGC<br>GAA   | 57.1                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22728327  | Ca4                                     | 22728327                      | ATTTTTTTTT/ATTTTTTTT                                          | GCAAAAACGTTTGTC<br>CTTG     | CCATCGTAGTTGACAA<br>ATGGC | 60.5                             | 315                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22728505  | Ca4                                     | 22728505                      | GTTG/GTTGTTTTG                                                | GCAAAAACGTTTGTC<br>CTTG     | TCAGTGTTGTTGAGCA<br>CGTT  | 60.5                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22744609  | Ca4                                     | 22744609                      | ACCC/ACC                                                      | GCCATCTCGAGTCAAC<br>AACA    | CATTGGTGGCTAGCAT<br>GAGA  | 59.8                             | 343                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22755158  | Ca4                                     | 22755158                      | ATTTTTTT/ATTTTTTTT                                            | CTATGTGCGTCGTCAG<br>GAAA    | CCAAAAACGGTTTCAC<br>CAGT  | 59.9                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22774524  | Ca4                                     | 22774524                      | TTCTCTCTC/TTCTCTCTCTC                                         | CATCATCATCACGCCT<br>CATC    | AATCGGTGTAGAGGCA<br>ATGG  | 60.0                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22774585  | Ca4                                     | 22774585                      | TTTCTT/TTT                                                    | CATCATCATCACGCCT<br>CATC    | AATCGGTGTAGAGGCA<br>ATGG  | 60.0                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22780799  | Ca4                                     | 22780799                      | TTAAAAATAAAATAAAATA/TTAAAAATAA<br>AAATA                       | TCTATTTTTGATGATGT<br>TGCGTT | TCCACACCGTTTTTGAT<br>ATTG | 58.7                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_22782656  | Ca4                                     | 22782656                      | TTATAAATATACAT/TTATAAATATAC<br>ATATAAATATACAT                 | AAGAGCAGGACAAATT<br>AATGAGA  | TTTGGCATTGATGAATT<br>GGA    | 57.2                             | 733                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22794336  | Ca4                                     | 22794336                      | CAA/C                                                         | TGACGAGTGGCAGAAC<br>TTCA     | TATGGACTAGAGCAAC<br>CCGC    | 60.6                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22796646  | Ca4                                     | 22796646                      | TGGG/TGGGG                                                    | ATTGCGATGGAGGAAT<br>TGAG     | GCGCCAAATATCTTGG<br>AAAA    | 60.0                             | 805                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22799910  | Ca4                                     | 22799910                      | AAAA/AAAAAATTAAA                                              | TCGGTGTGATTGTGT<br>GTGA      | GTGCAATCATGCAATC<br>AAGG    | 59.5                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22800253  | Ca4                                     | 22800253                      | CTAAACTCAAT/C                                                 | CCTTGATTGCATGATT<br>GCAC     | CCTAAATTTTAAAGGC<br>TAAATGG | 60.1                             | 165                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22801771  | Ca4                                     | 22801771                      | GATCA/GA                                                      | GCATACCTCAATTCCC<br>TACCA    | ACACAAGTGGGGGAGA<br>CAAC    | 58.9                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22818473  | Ca4                                     | 22818473                      | GTATATATATAT/GTATATATATATAT                                   | CAATTGCATGTTGAAAT<br>GGTG    | TGGCCATATTGTTTTG<br>CAT     | 59.8                             | 821                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22824281  | Ca4                                     | 22824281                      | AAA/AAAGTAA                                                   | ACATGCACCAGAGTTA<br>ATGTTTT  | GCTTCAACACCGGGAA<br>TAGA    | 57.8                             | 167                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22825336  | Ca4                                     | 22825336                      | TTT/TTTGTT                                                    | TGGCTTCCATAGTAAG<br>AGAGTGAA | AAATAACGTGTACGG<br>GGAT     | 59.5                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22848738  | Ca4                                     | 22848738                      | AATACATATA/AATA                                               | AGTATTGAAATTGCC<br>GCGT      | ACGACTGGCTAAGGTG<br>CTGT    | 59.6                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_22853847  | Ca4                                     | 22853847                      | ATTTTTTTTT/ATTTTTTTTT                                         | TCAAAACACATTGGAG<br>GCAC       | AAGCGTAAATGGCAGA<br>TGTGT   | 59.5                             | 344                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22854290  | Ca4                                     | 22854290                      | GAAAAAAAA/GAAAAAAAA                                           | CACATCTGCCATTAC<br>GCTT        | AAATGGCACAAGGCA<br>AACT     | 58.8                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22855998  | Ca4                                     | 22855998                      | TATCCGAT/TAT                                                  | CCTGTCAACTCCAAGA<br>ATCTCC     | AAAGCCATATTTTAACC<br>CAAAAA | 60.1                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22856126  | Ca4                                     | 22856126                      | GTTTATTT/GTTT                                                 | CCTGTCAACTCCAAGA<br>ATCTCC     | AAAGCCATATTTTAACC<br>CAAAAA | 60.1                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22856342  | Ca4                                     | 22856342                      | CTTTTTTTTT/CTTTTTTT                                           | TTTTGTACTTCTCGTG<br>TTAAGAGTTT | AAAAATGGAATTACGTC<br>CAATGA | 58.3                             | 701                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22867161  | Ca4                                     | 22867161                      | ATTTT/ATTTT                                                   | TCACCACTGACCAACC<br>CTTT       | CACCACCACCACAAAA<br>CACT    | 60.4                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22867292  | Ca4                                     | 22867292                      | TAAAAAAAA/TAAAAAAAA                                           | TCACCACTGACCAACC<br>CTTT       | CACCACCACCACAAAA<br>CACT    | 60.4                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22867454  | Ca4                                     | 22867454                      | GAAAAAAAA/GAAAAAAAA                                           | GATCTTCATCCCCTGC<br>AGAC       | CACCACCACCACAAAA<br>CACT    | 59.6                             | 292                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22869907  | Ca4                                     | 22869907                      | TAAAAAAAA/TAAAAA                                              | GAGAAGGGGCAAGAG<br>AGTGA       | TTTGGTTTTTACCGAT<br>TCC     | 59.5                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22869940  | Ca4                                     | 22869940                      | TAAAAAAAA/TAAAAA                                              | GAGAAGGGGCAAGAG<br>AGTGA       | TTTGGTTTTTACCGAT<br>TCC     | 59.5                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_22879215  | Ca4                                     | 22879215                      | A/AAT                                                         | TCATCTGCGTTTTCTG<br>CAC    | ACCAATCCGAAGACGA<br>TCAC | 60.0                             | 828                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22889580  | Ca4                                     | 22889580                      | AC/A                                                          | GGGTCAGGATACTTAC<br>AACCCA | TCCACCCCCAAATTTTA<br>TCA | 60.1                             | 717                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22890323  | Ca4                                     | 22890323                      | GG/GGAGTCCATTATG                                              | TGATAAAATTTGGGG<br>TGGA    | AGGTAGGAGCAAATC<br>GCAA  | 60.0                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22890495  | Ca4                                     | 22890495                      | GAAAAAAAAA/GAAAAAAAAA                                         | TCATGGTCCCCCAAT<br>TTTA    | AGGTAGGAGCAAATC<br>GCAA  | 60.0                             | 443                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22890677  | Ca4                                     | 22890677                      | AG/A                                                          | TTGCGATTTTGCTCCTA<br>CCT   | AGGCGCAACTTGCACT<br>TACT | 59.8                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22895304  | Ca4                                     | 22895304                      | ATTTTTTT/ATTTTTTTT                                            | TGGTATCAAATAAGTTT<br>CCGGT | GTTGGGTTGAGCCTGT<br>TTGT | 57.6                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22902727  | Ca4                                     | 22902727                      | ATT/ATTT                                                      | CACTATGCAAAATGGC<br>CTCA   | TCTCTTATGTGGGGTG<br>CCTC | 59.7                             | 186                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22906009  | Ca4                                     | 22906009                      | ATTT/ATTTT                                                    | TGTTGAAGCGAACTGC<br>ACAT   | GGGGAACAAAAACCC<br>AGAT  | 60.5                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22922451  | Ca4                                     | 22922451                      | GA/GAA                                                        | CACCGTCCGAATACCA<br>AAAC   | AGTCATTGCAATGTGG<br>GACA | 60.2                             | 391                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_2293129   | Ca4                                     | 2293129                       | ATGT/A                                                        | CGGTCATCAATCCGAC<br>TAGG   | AATGATTTATTGCGGC<br>GAAG | 60.5                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_22974622  | Ca4                                     | 22974622                      | TGG/TGGG                                                      | ATTTTGGGCGAAATCC<br>TTTT   | GAACCACTCATCCTCC<br>CAAA     | 59.8                             | 442                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22985821  | Ca4                                     | 22985821                      | TTTA/TTTAGTTA                                                 | ATAAGCCTTGCCATCTT<br>CCA   | CTTAGATGGGCCACCC<br>AATA     | 59.7                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_22988357  | Ca4                                     | 22988357                      | AG/A                                                          | CTCCAAAGGACGCATC<br>TCAT   | TGGGGTTTAGGGTGTC<br>ACAT     | 60.2                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23002548  | Ca4                                     | 23002548                      | ATTATTTATTTTATTTTATT/ATTATT<br>TTATTTTATTTTATTTTATT           | TCGATCGCTGATGTCA<br>AACT   | TGGGCTTGACCTATGT<br>GTGT     | 59.4                             | 147                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23002623  | Ca4                                     | 23002623                      | TTTACTATTACTATT/TTTACTATTAC<br>TATTACTATT                     | TTTATGGCGGCTGGTT<br>TTAC   | ACGATGCATTTGATTGA<br>TGTT    | 60.0                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23013499  | Ca4                                     | 23013499                      | CTA/CTATA                                                     | TCGGTTGGTACACACC<br>AATTT  | AATTGGAGATAGCATC<br>CCCTC    | 60.1                             | 506                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23014862  | Ca4                                     | 23014862                      | CATATATA/CATATATATA                                           | GAACATGTGCGTGCTA<br>CGTT   | GCTGTTCAAAGGGCTA<br>GACG     | 59.8                             | 756                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23018298  | Ca4                                     | 23018298                      | AAAT/A                                                        | ATTCGTTTGTCTTC<br>GAG      | TTTTAAAAAGATTACA<br>TGCACTAA | 59.2                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23018550  | Ca4                                     | 23018550                      | GAAAAAA/GAAAAAAA                                              | TCAGAGAGAATGCACG<br>ACATTT | GGCCTGACGACACAGC<br>TAAT     | 59.9                             | 774                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23019641  | Ca4                                     | 23019641                      | G/GT                                                          | CCAATTGGCCCTCATT<br>AGAC   | GGAACCGTTGTTTCTT<br>GGTC     | 59.4                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_23037799  | Ca4                                     | 23037799                      | AC/ACC                                                        | TCGACAAAAGCAAAGC<br>AATG     | CGCTTCTTGGTTTTC<br>AGTC    | 60.0                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23039824  | Ca4                                     | 23039824                      | CAAAAA/CAAAAAA                                                | TAACACGAGGGCAAAC<br>TTCC     | CGAGCCATAACATTGA<br>AGAGG  | 60.1                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23048460  | Ca4                                     | 23048460                      | ATTTTTTTTTTT/ATTTTTTTTTT                                      | TAAGGAGCCCACAAC<br>AAGG      | TGGTTGCTCTTCTCGC<br>CTAT   | 60.1                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23058519  | Ca4                                     | 23058519                      | ATCT/AT                                                       | CGGATATGAGTTTTAT<br>GGACGA   | CTCCCTTTTGCACAC<br>ACA     | 59.0                             | 434                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23060171  | Ca4                                     | 23060171                      | AATG/AATGCATG                                                 | TGCATTTGGCAATTTG<br>AAGA     | TCAACGCATGTGACTG<br>CATA   | 60.2                             | 254                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23076109  | Ca4                                     | 23076109                      | CTTT/CTTTT                                                    | TGGCATTGCAAGAAGA<br>AACA     | CCTCTTTCAACACCTTT<br>GGC   | 60.4                             | 760                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23077647  | Ca4                                     | 23077647                      | ATT/AT                                                        | AAGAAAAGGGTTGCGT<br>TTGA     | TGAATTCATGTGTATTG<br>TCGGA | 59.7                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23078135  | Ca4                                     | 23078135                      | ATTTTTTTT/ATTTTTTTTTT                                         | TTTGAAGAACCAGAGT<br>TTGAAGAA | TTCAATGCCCATAATCG<br>TGA   | 59.5                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23078167  | Ca4                                     | 23078167                      | TC/T                                                          | TTTGAAGAACCAGAGT<br>TTGAAGAA | TTCAATGCCCATAATCG<br>TGA   | 59.5                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23078243  | Ca4                                     | 23078243                      | TAAAA/TAAA                                                    | AAAAATCCGACAATAC<br>ACATGAA  | GAATGCGTACACCTTG<br>ACGA   | 59.7                             | 897                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_23079294  | Ca4                                     | 23079294                      | ATCTTCTT/ATCTT                                                | TAAATAGCATTTCGCTCC        | TTTTTCTTCGATTGCTCC         | 59.9                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23079344  | Ca4                                     | 23079344                      | TCC/TCCC                                                      | AATTGCAAGTGGACTG<br>GACC  | CCGAGCCAAAATCCAA<br>AATA   | 60.0                             | 787                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23100528  | Ca4                                     | 23100528                      | AT/ATT                                                        | GTTGCTCGTGTGCCCC<br>TTAT  | TGCAAAAGTGTTTAA<br>GCTACC  | 60.1                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23134800  | Ca4                                     | 23134800                      | TG/T                                                          | ATGCTGCGAAATTGTT<br>GAAA  | CGGACCTCTCATTGCT<br>GAAT   | 59.3                             | 739                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23145296  | Ca4                                     | 23145296                      | TAAAAAAA/TAAAAAAA                                             | TGCATGTTTCATGGTG<br>ATCC  | CACCAATTACAGTGGC<br>ATCAA  | 60.3                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23145659  | Ca4                                     | 23145659                      | ATTTTTTT/ATTTTTTT                                             | TGGGAAGTTAGGATTC<br>CGTTC | CAAAATTTGAATCCGCCT<br>ACTG | 60.3                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23145891  | Ca4                                     | 23145891                      | ATTTTTTTTT/ATTTTTTTTT                                         | GCTTGAGGATTCAGTA<br>GGCG  | GAGTGGAGGACCACAT<br>GTCA   | 60.0                             | 408                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23192116  | Ca4                                     | 23192116                      | CTA/CTATA                                                     | TTCGAACAAAATGATTC<br>CCA  | TAAACCAATGCCACACA<br>TGG   | 58.9                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23217567  | Ca4                                     | 23217567                      | AATATATATATATATAT/AATATAT<br>ATATATATATATATATAT               | CTCTAGGGAAGCGACC<br>TCCT  | CCAACAACCATTTGTGG<br>GAGT  | 60.0                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23220387  | Ca4                                     | 23220387                      | ATTT/ATT                                                      | GCCGCCACAAAATATT<br>CACT  | ATGCCTATACCGGCCT<br>CTTT   | 60.0                             | 357                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                       | Forward primers (5'-3')     | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------|-----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                     |                             |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_23272983  | Ca4                                     | 23272983                      | ATTTTTTTTT/ATTTTTTTT                                                                                | ACCACATCGGAAGAAA<br>CGAC    | GGACGAAGTAGAACGG<br>ACCA       | 60.0                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23408499  | Ca4                                     | 23408499                      | TAAAAAAA/TAAAAAAA                                                                                   | ACCAAAACGGTTGATA<br>CCCA    | ACTACCGTCAATCGTG<br>CTCC       | 60.1                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23453202  | Ca4                                     | 23453202                      | AATATATATATATATATATATATAT<br>ATATA/AATATATATATATATATAT<br>ATATATATATATA                             | GCTTCCCCAGTCACAC<br>TCAT    | TCACTGAATTGACACAT<br>AATAAATCA | 60.1                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23500297  | Ca4                                     | 23500297                      | AG/A                                                                                                | GAACCCCAAGCAAGAA<br>TCAA    | TGCACAAAAGCACTTCT<br>GAAA      | 60.1                             | 379                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23517542  | Ca4                                     | 23517542                      | GAAAAAAAAA/GAAAAAAAAA                                                                               | ATTGGATCTCGCTGAA<br>TCGT    | GAAGGTAAAAATGGTGG<br>GGGT      | 59.7                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23575550  | Ca4                                     | 23575550                      | TAAAAAAAAAAAAA/TAAAAAAAAAA<br>A                                                                     | CATTGGTAAAAGTGAA<br>AAATCCG | AACCGAAACAAATCGC<br>ACAT       | 59.8                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23721197  | Ca4                                     | 23721197                      | TAAACA/TAAACAAAAACA                                                                                 | ATTTGTGTGCATTGCT<br>CTGA    | TGGGCAATCGACTGAC<br>TAAA       | 60.1                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23756363  | Ca4                                     | 23756363                      | TTATATATATATATATATA/TTATATA<br>TATATATATATATA                                                       | TTGGAACGTAATTGAT<br>GCG     | CCCGTTGCTTCTGTAT<br>GCTT       | 59.6                             | 872                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23760339  | Ca4                                     | 23760339                      | CATATATATATATATATATATATATA<br>TATATATATATATATATATATATA/CA<br>TATATATATATATATATATATATAT<br>ATATATATA | GGATGGGTGCTACCCC<br>TAAT    | AACTCGTGCCTTCGAC<br>AAAT       | 60.0                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_23762953  | Ca4                                     | 23762953                      | GAAAAAAAAAAAAA/GAAAAAAAAAA<br>AA                                                                    | GATCATCCAGCAACAG<br>CAGA    | GGCCTTATTTTCGACTC<br>AATG      | 60.0                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)  | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                |                          |                              |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_23824374  | Ca4                                     | 23824374                      | CATATATATATATATATATATATA/<br>CATATATATATATATATATATATA<br>TA    | TCATTCAAAACAACCC<br>CCT  | TGCTATTAGAATGCTTA<br>TCGCTTA | 60.2                             | 551                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_23864193  | Ca4                                     | 23864193                      | CTTTTTTTTT/CTTTTTTTTT                                          | GCAATGTTCAATTGGT<br>GTGC | ACCATGCTTAGGGGGA<br>AGAG     | 60.0                             | 248                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_23891239  | Ca4                                     | 23891239                      | CATATATATATATATATATAT/CATAT<br>ATATATATATAT                    | TGTCGTCGAATTGGTC<br>TTGA | TGTGTGGTTGTTATTGA<br>ACGC    | 60.1                             | 469                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_2390421   | Ca4                                     | 2390421                       | ATTTTT/ATTTTT                                                  | GCACTTTTGGTCCCC<br>TATT  | TATTCCAGTATGCGT<br>CTGC      | 60.2                             | 168                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_24140557  | Ca4                                     | 24140557                      | CATTATTATTATTATTATTATTA/CAT<br>TATTATTATTATTATTATTATTA         | TTATTTCAACGTCGTGT<br>CCA | TTGTGTGTTGGCCGAT<br>TTTA     | 60.0                             | 234                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_24147426  | Ca4                                     | 24147426                      | AAATAATAATAATAATAATAATA<br>AT/AAATAATAATAATAATAATAA<br>TAATAAT | GGAAAACGACTTACAC<br>CCGA | TTCTCGGCTTTCTTTG<br>CTA      | 60.0                             | 654                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_24228039  | Ca4                                     | 24228039                      | AATATTGATATATTG/AATATTGATAT<br>ATTGATATATTG                    | TGATCCTCCCATCCTA<br>CCAA | TTGCGTCTTCTGTTTGA<br>TGC     | 60.3                             | 560                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_24269057  | Ca4                                     | 24269057                      | CTTTT/CTTTT                                                    | CGTTGCACGGAATACT<br>CACT | TCCTGCATGCAATCTG<br>CTTA     | 58.8                             | 490                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_24273906  | Ca4                                     | 24273906                      | TTATATATATATATATATATATATA<br>TA/TTATATATATATATATATATAT<br>ATA  | GGGGGAGTTGTTATTC<br>GGTT | GAAAAGTGTGTCGTG<br>TGTGC     | 60.1                             | 646                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_24356217  | Ca4                                     | 24356217                      | TCCC/TCC                                                       | CGCTTTGTTCTTTACC<br>GCAT | CATGGAACAACCTGCAC<br>CATAA   | 60.3                             | 350                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_24359275  | Ca4                                     | 24359275                      | TAAAAAAAA/TAAAAAAAA                                           | GGGAGGGTGGGAGTA<br>AATGT | TGTGGCTTTCCAATGTA<br>CGA | 60.1                             | 571                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24362931  | Ca4                                     | 24362931                      | TAA/TA                                                        | GGTTTAGATGGGGGAT<br>CGTT | CCCCGAGTTGGTCCTT<br>TATT | 60.0                             | 947                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24425317  | Ca4                                     | 24425317                      | GTTT/GTTTT                                                    | TGGGGTGTTTCATAGC<br>ATCA | ACCGTTTAATTGGCGA<br>ACAG | 59.9                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24427573  | Ca4                                     | 24427573                      | GTT/GTTT                                                      | CTGGAAATCCTCCTC<br>CTCC  | TTCGTCTCAACAATCTC<br>CCC | 60.0                             | 346                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_2445427   | Ca4                                     | 2445427                       | TATAATA/TATA                                                  | GGAGGTCACAACCACT<br>CCAA | ATTTGTGACGTTCCCCT<br>CAA | 61.0                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24478956  | Ca4                                     | 24478956                      | CAA/CAAA                                                      | CGGTTCTACACAAGTT<br>GCGA | TCGATTATGCGTAGGG<br>AAGG | 59.9                             | 746                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24479035  | Ca4                                     | 24479035                      | ATTTTTTT/ATTTTTTTTTT                                          | CGGTTCTACACAAGTT<br>GCGA | TCGATTATGCGTAGGG<br>AAGG | 59.9                             | 746                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24488859  | Ca4                                     | 24488859                      | TAAA/TAAAA                                                    | TTGGAACATGCAAA<br>TGGA   | CGATACTACCCCCTCG<br>TTGT | 60.0                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24553735  | Ca4                                     | 24553735                      | GATTAT/GAT                                                    | TGGTGCGATTGTGGAA<br>AATA | GAGTAGATGTGCCAAC<br>AGCG | 59.9                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24554220  | Ca4                                     | 24554220                      | T/TA                                                          | GTGCGGATTATGTCGG<br>GTAT | ACTAGATGGTCGCATC<br>CTGG | 59.7                             | 751                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_24608449  | Ca4                                     | 24608449                      | GTTTT/GTT                                                     | GGAATGAGGAGAGTGA<br>AGCG    | CTAAATGCGACCCATC<br>CACT      | 60.0                             | 684                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24628360  | Ca4                                     | 24628360                      | AT/ATATATATGTGT                                               | TATTTTGGATTTTGGCT<br>CGG    | AGGAAGAGTGGAGTTG<br>CGAA      | 59.9                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24677817  | Ca4                                     | 24677817                      | ATTTTTTTTT/ATTTTTTTTT                                         | CACGAAAACCTTAAAC<br>CCCA    | TCTTAAAAGCGATGTAA<br>AGGGC    | 59.8                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_2470923   | Ca4                                     | 2470923                       | TTATATATATATATATATAT/TTAT<br>ATATATATATATATAT                 | CGGCCCTGATTTAGT<br>TGAA     | TCGCTGCCACCTCTAA<br>ATCT      | 60.1                             | 298                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24737329  | Ca4                                     | 24737329                      | AATTATTATTA/AATTATTATTATTAT<br>TATTATTA                       | CCCCTAGTTCTACGTT<br>GGCA    | AGGAAAGTTGGGTGTA<br>TGCG      | 60.1                             | 798                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24748886  | Ca4                                     | 24748886                      | GAAAAAAAA/GAAAAAAAA                                           | CACGACCACATCTGTG<br>AGAAA   | TTCCAAAATTTCTTCAA<br>CACTCAA  | 59.7                             | 629                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24824930  | Ca4                                     | 24824930                      | CTTTTTTT/CTTTTTTT                                             | TGAATCTTCGAGAAGC<br>CTAACC  | CCTTTTTAACGTCGTCC<br>CAA      | 59.9                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24828297  | Ca4                                     | 24828297                      | ATTTTTTTTT/ATTTTTTTTT                                         | TGGAATTCAGACTGC<br>CTTG     | GGGCACGAAGAAGCAC<br>TATC      | 58.8                             | 716                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24919292  | Ca4                                     | 24919292                      | TAAA/TAAAA                                                    | GGAACCTTCGAAAATC<br>CCTC    | CTATGGCTTTGTGAGA<br>CGCA      | 59.9                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_24925584  | Ca4                                     | 24925584                      | CAAAAAAAAA/CAAAAAAAAA                                         | TCGATTCTTTGAACCAT<br>CTCTTC | GACCATTTGAAAATAAA<br>GTTAGGCA | 59.7                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_24956663  | Ca4                                     | 24956663                      | GAAAAAAAAA/GAAAAAAAAA                                         | AAATTGGTGCTATTGC<br>TGGG | GATTCTAACCGTCGTT<br>CCG  | 60.0                             | 159                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25011504  | Ca4                                     | 25011504                      | GA/GAAGAAGAAAGAGAAAA                                          | TCCTCGTCAAATTGCT<br>TCC  | CATGTTGGAGTTGTTG<br>GCTG | 60.2                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25034090  | Ca4                                     | 25034090                      | GAAAAAA/GAAAAAA                                               | GTTGGTCATGCAGAAA<br>GCAA | GCAGACGTTATTGGGA<br>AGGA | 59.8                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25036917  | Ca4                                     | 25036917                      | T/TA                                                          | ATCCAAGTTGAGCAAG<br>CATT | CATTGAGACTTTGCCA<br>CGAA | 57.4                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25046968  | Ca4                                     | 25046968                      | TGCTGAGCTGA/TGCTGA                                            | ATGTTTCGTGCAATGG<br>TCAA | AAGGTCAAGGGCCAAA<br>AACT | 60.0                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25053641  | Ca4                                     | 25053641                      | TAAAAAAA/TAAAAAAA                                             | CTGAGGCTTATGATTC<br>CCCA | CGATAAGGGTGTCGAG<br>GAAA | 60.0                             | 154                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25061838  | Ca4                                     | 25061838                      | GTTTTTTTT/GTTTTTTTT                                           | GGTAACCAATCCGAAG<br>ACGA | TCGATTATGCGTAGGG<br>AAGG | 59.9                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25063885  | Ca4                                     | 25063885                      | AAA/AAATAA                                                    | CCCCAACGATTACACT<br>TGCT | ACCGTTTTGGTGTTTCT<br>TGC | 60.0                             | 899                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25064267  | Ca4                                     | 25064267                      | AATATATATATATATA/AATATATA<br>TATATATATATA                     | AATTCATCCCCTCTCA<br>ACC  | ACCGTTTTGGTGTTTCT<br>TGC | 60.1                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25071336  | Ca4                                     | 25071336                      | CA/C                                                          | TGAGACTGCTTGGCTA<br>CCCT | ATCTGAATCATCCCAAG<br>CCA | 60.0                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_25088043  | Ca4                                     | 25088043                      | CCT/CCTCCTTCTCT                                               | AACCTTCGCAAGAACC<br>CTTC   | ATCAATCTCGTTTCTC<br>GGG      | 60.6                             | 219                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25139153  | Ca4                                     | 25139153                      | TCC/TC                                                        | TTGTGTTGCAATAGTG<br>CTTGC  | TGCTCCACATAAAGCG<br>AAGA     | 59.9                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25146347  | Ca4                                     | 25146347                      | GAAAAAAA/GAAAAAAA                                             | TCATCCTTGCCTCGAT<br>TAGG   | GGAAATGCAATCAAAA<br>CCAA     | 60.2                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25159546  | Ca4                                     | 25159546                      | TTGATG/TTG                                                    | TTTATACGGTGGGGGA<br>ATGA   | TCCAAATCCACATACA<br>CACA     | 60.0                             | 406                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25168771  | Ca4                                     | 25168771                      | AA/AATA                                                       | GACCAAGGCAAGCAAG<br>AAAG   | GTGGAAGTTGAAACGA<br>CGGT     | 60.0                             | 178                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25193095  | Ca4                                     | 25193095                      | GAAAAAAAAA/GAAAAAAAAA                                         | CATCACCCACCATTGA<br>CAAG   | CATCCACGAAACACTC<br>ATGG     | 59.8                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25205443  | Ca4                                     | 25205443                      | TAGATTTGGCACAAAAGATTGG/TA<br>GATTTGG                          | GATGGAGGATCAGCCA<br>CATT   | ATGGTGGAATGCCTCA<br>AAAG     | 59.9                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25213751  | Ca4                                     | 25213751                      | GAG/GAGATCATAG                                                | TCATTCAACGTCATCGT<br>ATCAA | TGTGTTTGTATCAATAT<br>CGAAGGC | 59.0                             | 562                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25235982  | Ca4                                     | 25235982                      | ATTTTTTTTTTT/ATTTTTTTTTT                                      | TTTCAAATTCTCATCGG<br>GGA   | GGTTGCATGCATATT<br>GAG       | 60.4                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25243065  | Ca4                                     | 25243065                      | A/AC                                                          | AATCCCCTTGATTGAC<br>AACG   | TGAGACTCGTGTCTCTC<br>CACA    | 59.8                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_25246291  | Ca4                                     | 25246291                      | ATTTTT/ATTTTTTT                                               | GAAAGCGCCTAAGGTA<br>AGGG  | ATTAAACCAGCCACACA<br>GGC   | 60.2                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25258427  | Ca4                                     | 25258427                      | GAAAAAAAA/GAAAAAAAAA                                          | TTTGTGCGCAACAAC<br>AGA    | TGTGGGGAGCAAAAGT<br>GTTT   | 60.0                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25280052  | Ca4                                     | 25280052                      | CTTT/CTT                                                      | CTCACTTTTGTTCCCA<br>CAAA  | TGGTGCAAGGTCTAAA<br>GGAGA  | 59.9                             | 292                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25303619  | Ca4                                     | 25303619                      | GTTTTT/GTTTTTT                                                | TTGAGGCAGGAACCTC<br>AACT  | CATTTCTTAAGCCCA<br>TGA     | 59.8                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25348827  | Ca4                                     | 25348827                      | AGGGGGG/AGGGGG                                                | GGCAAATGCTAACCCA<br>TGTT  | TTGCTTACAATCCGAG<br>ACGA   | 59.8                             | 224                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25352441  | Ca4                                     | 25352441                      | AAATAATAAT/AAATAATAAT                                         | CACTGCTATAAGCCGC<br>ACAA  | AGCCTTACGCATGTATT<br>GCC   | 60.0                             | 906                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25352610  | Ca4                                     | 25352610                      | T/TA                                                          | GGAAATGGTTCTTTGA<br>AAGCC | AGCCTTACGCATGTATT<br>GCC   | 59.9                             | 719                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25357817  | Ca4                                     | 25357817                      | ATTTTTTTT/AATTTTTTTT                                          | AAAATTCTGTTTGGGG<br>GACC  | ACATGCATGCAATTCAA<br>TAGAG | 60.0                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25358106  | Ca4                                     | 25358106                      | TTAAATAAATAAATAAATAA/TT<br>AAATAAATAAATAAATAA                 | GGGACTACTTTCGCGA<br>TTCA  | ATTACACGCTTGCGA<br>CGAA    | 60.2                             | 842                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25359522  | Ca4                                     | 25359522                      | GATATAT/GATATATATAT                                           | CGACAAAGCCTCACGA<br>GTTA  | GGAGCCACAAACGATT<br>GACT   | 59.1                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_25365837  | Ca4                                     | 25365837                      | GTTTTTTT/GTTTTTTT                                             | AATTTTGTGCCCTC<br>CAAT        | TGCTATGGCACAAGTC<br>TCCA     | 60.5                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25365904  | Ca4                                     | 25365904                      | TTTTTT/TTTTTTTTTTATTTTT                                       | AATTTTGTGCCCTC<br>CAAT        | TGCTATGGCACAAGTC<br>TCCA     | 60.5                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25366618  | Ca4                                     | 25366618                      | AAATCCACTAAGGAAT/AAAT                                         | TCTTGGAAGACGCGT<br>GTAA       | CACCTTGAATCCAACCT<br>TGA     | 59.5                             | 227                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25399861  | Ca4                                     | 25399861                      | TA/TAAA                                                       | TTTAAATGGAATGGG<br>CTGTG      | TTTCCGTGTGTCTCGT<br>ATGC     | 59.8                             | 322                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25439114  | Ca4                                     | 25439114                      | TAA/TA                                                        | GAGGTGGAGAATGATT<br>GGTCA     | TCGAGACTTGGCTCAT<br>GTTG     | 59.9                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25466708  | Ca4                                     | 25466708                      | CATATATATATATAT/CATATATATAT<br>AT                             | TATAGGGAGCGGAACA<br>CACC      | GCTTCACACAAGTCAC<br>TTCCA    | 60.0                             | 367                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25467890  | Ca4                                     | 25467890                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                     | TTGGGAATTAACATGA<br>GAGCAA    | TGTGTTGATAAAACAA<br>GATTTCAA | 59.6                             | 802                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25468010  | Ca4                                     | 25468010                      | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATATATA<br>T   | TTCAAAATACAAATGTG<br>ATGGAAAA | TTTTTGTTCCTTATTG<br>TTTGACA  | 59.7                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25478172  | Ca4                                     | 25478172                      | TAAAA/TAAAAA                                                  | TGTGATGCAGTTGCTC<br>CATT      | GACCTTGCTCTCTTGAT<br>GGG     | 60.3                             | 703                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25519864  | Ca4                                     | 25519864                      | GAAAAAAA/GAAAAAAA                                             | GGGTCCTCGATCAAG<br>AGGT       | TGTCAGTTGAGCTCCT<br>GTCG     | 60.5                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                 |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_25524341  | Ca4                                     | 25524341                      | CAAAA/CAA                                                       | CTTTGGACGAGGCCA<br>AAAC   | TTGGAAGGAATTTGAAT<br>GGC | 59.9                             | 764                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25535456  | Ca4                                     | 25535456                      | ACACCTTGAGTTTGGTCCA/ACACC<br>TTGAGTTTGGTCCACCTTGAGTTTG<br>GTCCA | TGTGGGATGCATGTCC<br>TTTA  | TTGAAATTGAACCAATC<br>CGA | 59.9                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25543812  | Ca4                                     | 25543812                      | TTTTCTTCTTCTTCTTTC/TTTTCTT<br>CTTTC                             | AGGACTTTCGACCACC<br>ACAC  | TACCTTTGCTAGCCC<br>CTTT  | 60.0                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25589839  | Ca4                                     | 25589839                      | ATTTTTTTTT/ATTTTTTTT                                            | AATTACGCCAAAGGAT<br>GCAC  | CCCTGTGACGAACTGG<br>AGAT | 60.0                             | 789                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25596032  | Ca4                                     | 25596032                      | TTAT/TTATAT                                                     | AGTGATGTGGGCAACA<br>ATGA  | TGCATTTTACAGCGCTT<br>TTG | 60.0                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25630012  | Ca4                                     | 25630012                      | TG/T                                                            | AGTAGACTTGCCCTCCC<br>GGTT | CCTTGTTGTGGAGTGT<br>GGTG | 60.1                             | 788                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25642263  | Ca4                                     | 25642263                      | CAAAAA/CAAAAA                                                   | TTTGTGTGGTGTCTT<br>GGGA   | TACAACCAAACCCCTT<br>GAGC | 60.0                             | 318                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25671434  | Ca4                                     | 25671434                      | CAAGAAG/CAAG                                                    | CTCCGACAGGCTACTT<br>CCAG  | TGAGATGAAGCAAATG<br>CTCG | 60.0                             | 347                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25694964  | Ca4                                     | 25694964                      | CAAAAAAAAA/CAAAAAAAAAAAAA                                       | CCACTTCGCTTAGGGA<br>TCAA  | TATGGGCATTCTTCTTT<br>GGG | 60.2                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25720958  | Ca4                                     | 25720958                      | AAAGAAAGAGATA/AA                                                | ACCACGCCATTCAAAA<br>TAGG  | AGGACTTGACGTAACC<br>CACG | 59.8                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_25754372  | Ca4                                     | 25754372                      | AAAAATAAAATAAAATAAA/AAAAATA<br>AAATAAA                        | AATGGGCGCTGTAAATGTC     | TCATTTAAACCACTGCGTCAA   | 60.0                             | 750                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25758155  | Ca4                                     | 25758155                      | CAAGTAAGT/CAAGT                                               | TTGGTCCTCGTCATTTCTC     | TCCAAACTTCCATGTGATTCC   | 60.1                             | 422                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25760041  | Ca4                                     | 25760041                      | ATTTTTTT/ATTTTTT                                              | CACAACGGAATTTGGGTTTC    | TTGAGCTTGCAACTTGATCACT  | 60.2                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25760083  | Ca4                                     | 25760083                      | ATTTTTTT/ATTTTTTT                                             | CGGATTTTGTGTGTCATCCCT   | TTGAGCTTGCAACTTGATCACT  | 59.8                             | 181                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25761284  | Ca4                                     | 25761284                      | ATTTTTTTTT/ATTTTTTTTTT                                        | TTGTTGTGTGCAAGAGGATTG   | GGAGATCATGGACGAAGGTG    | 59.7                             | 366                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25763103  | Ca4                                     | 25763103                      | CTT/CT                                                        | ATCCTTGCGGGGATTTAGAG    | ATTGCCTCATCCAAACGAAC    | 60.4                             | 295                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25774052  | Ca4                                     | 25774052                      | TAAAAAAAAAAAA/TAAAAAAAAAAAA                                   | TGTCAAATCCAACGCAAGA     | TGCGAACCAACAAAGCATA     | 60.2                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25776089  | Ca4                                     | 25776089                      | G/GAC                                                         | TGGAATGAGAGGGGAAGATG    | TCCGAGACAGGTATTTTGGC    | 60.0                             | 366                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25790471  | Ca4                                     | 25790471                      | CAAAACGAAACGAAACGAAAC/CAAA<br>CGAAAC                          | CCTCAAATCCAATTGTGCC     | TCATCCTCACCCCAGTTAG     | 60.3                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25822369  | Ca4                                     | 25822369                      | CAAAAAA/CAAAAAA                                               | TGTTTGAACCCGAGACTTAC    | CGTGGCATTTGAAAAAGCAT    | 60.1                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_25830993  | Ca4                                     | 25830993                      | CTTTTTTTTTTT/CTTTTTTTTTT                                      | CCCAGAAGGAGCAATT<br>TGAA  | TTGCGGTTTCCTTAATG<br>GTC  | 60.2                             | 315                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25834950  | Ca4                                     | 25834950                      | AAGACGTTCCGTA/AA                                              | TCGCTGCTTATTCATGT<br>TCA  | ACCACCAGTGAGGATT<br>TTGC  | 58.0                             | 336                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25847698  | Ca4                                     | 25847698                      | T/TG                                                          | CATGCTACCAAAGCGA<br>TTGA  | ATCGATTTCGCGAGTC<br>TTGT  | 59.8                             | 370                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25848017  | Ca4                                     | 25848017                      | AA/AAGA                                                       | CATGCTACCAAAGCGA<br>TTGA  | CCCAAGAAAGTAGCCA<br>CCAG  | 59.8                             | 806                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25860833  | Ca4                                     | 25860833                      | GAAAAAAAAA/GAAAAAAAAA                                         | CAGCTCGCATAAACCA<br>ATCA  | AAAGCATTGTCGTAGG<br>TGCC  | 59.8                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25869082  | Ca4                                     | 25869082                      | ATTTTT/ATTTT                                                  | TATTTGTCGATTTCGCT<br>GGA  | TTATAAGTGCGGTTAG<br>CGGG  | 60.1                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25925060  | Ca4                                     | 25925060                      | GTTTTTTT/GTTTTTTT                                             | TTTCGCACAGCATAGG<br>ACAG  | CAACGGCGCTGAGATT<br>TATT  | 60.0                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25933731  | Ca4                                     | 25933731                      | ACGCGCGCGCG/ACGCGCGCGCG<br>G                                  | TGGCATTGATGATGGC<br>TTTA  | ACCTTGTTGGATGGCAG<br>TTTC | 60.0                             | 340                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25933783  | Ca4                                     | 25933783                      | CTCGGTTTCGGTTCGG/CTCGGTTTCG<br>GTTTCGGTTCGG                   | TGGCATTGATGATGGC<br>TTTA  | ACCTTGTTGGATGGCAG<br>TTTC | 60.0                             | 340                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25936338  | Ca4                                     | 25936338                      | GTTTTTTTTT/GTTTTTTTTT                                         | GAGGTTTCGATTCTCTC<br>CACA | AAATTGCAATAGGTCG<br>TCCG  | 60.1                             | 705                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_25936921  | Ca4                                     | 25936921                      | CTTTTTTTTTTT/CTTTTTTTTTTT                                     | AGGTGCGAATATCCAC<br>CTTG    | AAATGGACAACGTCGA<br>AAGG    | 60.0                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25937535  | Ca4                                     | 25937535                      | GC/GCTTTTGCTC                                                 | TCGACGTTGTCCATTT<br>GTGT    | ACACGAGCGTTTGAGC<br>TTTT    | 60.0                             | 621                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25941584  | Ca4                                     | 25941584                      | A/AG                                                          | CGATCGTTGTTGGTAT<br>GTCG    | AGCTGACCAATGCGT<br>AAGG     | 60.0                             | 244                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25941878  | Ca4                                     | 25941878                      | CAA/CAAAA                                                     | CGATCGTTGTTGGTAT<br>GTCG    | CCGTTTTTCTTGCGATT<br>CTC    | 60.0                             | 899                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25949029  | Ca4                                     | 25949029                      | CTTTTT/CTTTTTT                                                | TTCATTGAGATTGATTA<br>TGCTCG | GCTAAACACATGGAGA<br>TCAAACA | 59.2                             | 754                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25950770  | Ca4                                     | 25950770                      | CAAAAAAAAAAAAA/CAAAAAAAAA<br>AAAA                             | GATCTTTGCTTAAGCG<br>CTGG    | TTTCCAATCAAAATGGC<br>ACA    | 60.1                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25958010  | Ca4                                     | 25958010                      | TTATATATATAT/TTATATATATATAT                                   | TCGGGGAAATCAATTC<br>GTTA    | TGGAAGTCATCGACCC<br>ATT     | 60.3                             | 673                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25959074  | Ca4                                     | 25959074                      | GCC/GC                                                        | TGAAGATGAAGAAGAG<br>GGCAA   | TGTGGCATAAGGAGGA<br>GTTTC   | 59.9                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25966069  | Ca4                                     | 25966069                      | ATTT/ATTTT                                                    | GGCATGGACAACCTCA<br>CCTT    | CGAAATCCTCAAAATC<br>GGAA    | 60.0                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25967972  | Ca4                                     | 25967972                      | ATTTTTTTT/ATTTTTTTTTT                                         | TTGTACCCTTGTCGA<br>CCAA     | TGGTTGGATACTTGCA<br>ATGG    | 60.0                             | 180                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_25968820  | Ca4                                     | 25968820                      | GTTT/GTTTT                                                    | TTCTTCTGCCAAAAAT<br>GCT   | CCTCAAGCAGACCTTT<br>GGAG | 59.8                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25969511  | Ca4                                     | 25969511                      | ACC/AC                                                        | TCCCTTGCCCTCTAGCC<br>AGTA | GCAGATGTTCTCAACA<br>GCCA | 60.0                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25970159  | Ca4                                     | 25970159                      | AC/A                                                          | TGGTTGGGTCTTGTT<br>TGTT   | CACCTGCTATGGATGC<br>AATG | 60.2                             | 709                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25971278  | Ca4                                     | 25971278                      | GATTGAAGAA/GA                                                 | GCTTCGCCAAGCTTAC<br>AATC  | CCAACGATCATCAAAG<br>GGAT | 60.0                             | 268                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25976449  | Ca4                                     | 25976449                      | CTTTTT/CTTTTT                                                 | CCCCTTTTTGCACATG<br>ATCT  | GGGAATCCTATCCAC<br>CCAT  | 59.9                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25978445  | Ca4                                     | 25978445                      | CT/CTTT                                                       | TGCCTCAAAGGCTTCA<br>TCTT  | AGCACTCATCCTCGGG<br>TAGA | 60.0                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25979689  | Ca4                                     | 25979689                      | TG/TGG                                                        | GTCCTCGTCAGGAGGT<br>TGAG  | CCACTGTTGCTGGCAG<br>ATAA | 59.8                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25982514  | Ca4                                     | 25982514                      | CAATAATA/CAATAATAATA                                          | GCGCAAAACAAGAAG<br>GAAG   | GGTCCAGGTTGTTGG<br>AGAA  | 60.0                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25984201  | Ca4                                     | 25984201                      | AG/A                                                          | CGATTTTAAACAGCGT<br>GGGT  | TTTGGGCTTTGCTCTC<br>AAAT | 60.0                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25984442  | Ca4                                     | 25984442                      | TGAGAG/TGAGAGAG                                               | AGATCCTGTTGACACG<br>GCTT  | CGGTTGTTGTTGTGAT<br>TTGC | 59.7                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_25987622  | Ca4                                     | 25987622                      | TCC/TC                                                        | TTCAACTGGGGTAAAT<br>GCCT     | TGTTCTAGTCCAGATCA<br>AAACGA | 59.4                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25987851  | Ca4                                     | 25987851                      | CTTT/CT                                                       | TTCCTTCCTAATGTTCTG<br>TTTTGA | CGTGTCTCATCTTTGT<br>GCTTT   | 60.0                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25988978  | Ca4                                     | 25988978                      | AAAGAAGAAGAAG/AAAGAAGAAG                                      | AAGCTGGATGTGGACT<br>TTGC     | AGTTCCAATTGGCCTC<br>CTTT    | 60.3                             | 404                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25989281  | Ca4                                     | 25989281                      | TCCCC/TCCC                                                    | AAGCTGGATGTGGACT<br>TTGC     | AGTTCCAATTGGCCTC<br>CTTT    | 60.3                             | 404                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25989322  | Ca4                                     | 25989322                      | GTTTT/GTTTTT                                                  | GTACGCGATCTAGTCC<br>CCAA     | CCGGGGAGAAAGTTCT<br>AGTG    | 60.1                             | 168                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25994447  | Ca4                                     | 25994447                      | G/GT                                                          | ATCCACAACCGAGTTA<br>GCGT     | TACCACACCCCTCAA<br>TCTT     | 59.6                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25994543  | Ca4                                     | 25994543                      | GTTTTT/GTTTTTT                                                | TTAAGATTGAGGGGTG<br>TGGG     | CACCACTTCATTCGGG<br>ACTT    | 59.8                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25994721  | Ca4                                     | 25994721                      | AC/A                                                          | TTAAGATTGAGGGGTG<br>TGGG     | CACCACTTCATTCGGG<br>ACTT    | 59.8                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_25995802  | Ca4                                     | 25995802                      | ATTTT/ATTT                                                    | CCCTAAATCAAAGCAG<br>CGTC     | TGCACTGTTGTTGTTG<br>CTGA    | 59.8                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26009737  | Ca4                                     | 26009737                      | TC/T                                                          | GGAACCTCTCTTGTCG<br>CAGC     | ACCCTTTGCATCCCTTT<br>CTT    | 60.0                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_26018351  | Ca4                                     | 26018351                      | TAAAAAAAA/TAAAAAAAA                                           | AGAACATGGTGGATGC<br>ACAG    | TCCAAGAGCTTGGTCT<br>GACA      | 59.6                             | 373                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26020559  | Ca4                                     | 26020559                      | CTTTTTTTTT/CTTTTTTTTT                                         | CGTTTGCAATTTCTTT<br>GGG     | TGTTCCAGTTCCACGT<br>CAGA      | 60.5                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26058753  | Ca4                                     | 26058753                      | TAAA/TAAAA                                                    | AGGAACCAATCCTACC<br>AGCC    | TCTGGTCATGCATCCTT<br>TGA      | 60.3                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26071794  | Ca4                                     | 26071794                      | CCACA/CCA                                                     | ATCGAGTGGCCAATTG<br>AAAG    | ACAGAAACCACATTG<br>CACA       | 60.1                             | 729                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26073975  | Ca4                                     | 26073975                      | TAAAAAAAAA/TAAAAAAAAA                                         | GCTAAATAGCACTCAC<br>GATCCC  | TTTGCTTGCTGAGTGA<br>TTGG      | 60.1                             | 873                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26074517  | Ca4                                     | 26074517                      | GTTTA/GTTTAAATAAAATATTTTA                                     | CCAATCACTCAGCAAG<br>CAAA    | CGAAGCATCCTGCATT<br>TAAG      | 60.0                             | 354                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26075846  | Ca4                                     | 26075846                      | TAAAAA/TAAAAA                                                 | TTTAACAAAATCAACA<br>AACAGGA | AAGTGAAAAATATGTGT<br>CCCGTACT | 57.9                             | 220                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26082693  | Ca4                                     | 26082693                      | TG/T                                                          | TTGATGGCTACATGGG<br>ATGA    | TTTGGTTTGGTTCTGG<br>TTTG      | 59.9                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26108429  | Ca4                                     | 26108429                      | GAAAAA/GAAAAA                                                 | TTTGC GTTACGAAATT<br>GGTG   | TGCACTGCTAATTGCC<br>TCTG      | 59.6                             | 328                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26110333  | Ca4                                     | 26110333                      | TCCC/TCCCC                                                    | CCAACAATCTCCCCCT<br>TTTT    | GCATCTGGTTGCAGTT<br>CTCA      | 60.2                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_26110396  | Ca4                                     | 26110396                      | CTTTTTTTTT/CTTTTTTTTTT                                        | CCAACAATCTCCCTT<br>TTTT    | GCATCTGGTTGCAGTT<br>CTCA    | 60.2                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26121192  | Ca4                                     | 26121192                      | CTTTTTTTTT/CTTTTTTTTTT                                        | GCTGGTTTTTGGCATG<br>ATTT   | GAGGCATGCATTTGTC<br>TCATT   | 59.9                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26123152  | Ca4                                     | 26123152                      | CTTTTTTTTT/CTTTTTTTTTT                                        | CAAGCATGCAAATAAG<br>CGAA   | GCAGCAAGATGCAACT<br>CTCA    | 60.0                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26136319  | Ca4                                     | 26136319                      | TTTTATTT/TTTT                                                 | TTTGACGCATTTTGTT<br>ACAT   | TGCTCTCTCTCCCTCA<br>CCAT    | 59.1                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26140041  | Ca4                                     | 26140041                      | TAAAAAAA/TAAAAAAA                                             | GAAGCCAACATGGCTC<br>AAAT   | AGCAGGGATTTTGGC<br>TTTT     | 60.1                             | 754                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26166307  | Ca4                                     | 26166307                      | TAAAAAAAAAAAAA/TAAAAAAAAA<br>A                                | GCATGCCATGAATCAC<br>ACTT   | GCACGTGGGTACAGTG<br>ATTG    | 59.5                             | 803                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26199834  | Ca4                                     | 26199834                      | A/AT                                                          | GGGCAAGGTGAACACA<br>AGAT   | GCATCGTCCTTCCATG<br>ATTT    | 60.0                             | 383                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26205632  | Ca4                                     | 26205632                      | TAAAAAAAAAAAAA/TAAAAAAAAA<br>A                                | TGTGTCATGAAAATT<br>AAGGGTT | TTTTCACTTAGGTCCT<br>TGATTTT | 58.9                             | 876                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26236698  | Ca4                                     | 26236698                      | TGGGGG/TGGGG                                                  | GTTACGATTGTGTTCC<br>GCCT   | TAATCTCACTGCGCAC<br>CTTG    | 60.0                             | 368                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26259040  | Ca4                                     | 26259040                      | ATTTTTTTTT/ATTTTTTTTT                                         | TTCTCGAATCAATTCCG<br>TCC   | CTCAGAGCCGACCTA<br>TACA     | 60.0                             | 888                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_26301785  | Ca4                                     | 26301785                      | GAAAAAAAA/GAAAAAAAAA                                          | ACCACTACGCCACACA<br>TCAA | GTGACAGTACTGGGG<br>AAGC   | 60.0                             | 428                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26313553  | Ca4                                     | 26313553                      | TAAAAAAAAA/TAAAAAAAAA                                         | TGAGGTATGCCCAAAG<br>AAGG | TTTGAAACATGAATTT<br>CGGA  | 60.1                             | 319                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26313656  | Ca4                                     | 26313656                      | ATTTTTTTTT/ATTTTTTTTT                                         | TGAGGTATGCCCAAAG<br>AAGG | TTAGGCCGTAGTCAGG<br>CTGT  | 60.1                             | 837                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26314670  | Ca4                                     | 26314670                      | TAAAAAAAAA/TAAAAAAAAA                                         | ATGTTGTGCACCGAA<br>AACT  | CCCAATATCCGAGTGT<br>GTTCT | 60.4                             | 362                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26339363  | Ca4                                     | 26339363                      | CAAGAAGAAGAAGAAGAAGAA/<br>CAAGAAGAAGAAGAAGAAGAA<br>GAAGAA     | TCAAGACGTTGATCTC<br>GTGC | CATCTTCATTGCCTCCC<br>ATT  | 60.0                             | 397                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26361460  | Ca4                                     | 26361460                      | CTTTTTTT/CTTTTTTT                                             | GAAACTCGCAGACTTC<br>GGAC | TATTGGGCGAATCAAG<br>GAAG  | 60.0                             | 520                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26363618  | Ca4                                     | 26363618                      | T/TTTAC                                                       | GCCAAAATTCCTTCGT<br>TGA  | ATTCCCCAAGAACATCA<br>CCA  | 60.1                             | 613                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26363648  | Ca4                                     | 26363648                      | CCTC/CCTCTC                                                   | GCCAAAATTCCTTCGT<br>TGA  | ATTCCCCAAGAACATCA<br>CCA  | 60.1                             | 613                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26389681  | Ca4                                     | 26389681                      | ATTTTTTTTT/ATTTTTTTTT                                         | CCGAGCCAAATCCAA<br>AATA  | AGGGGCCTATGACTTG<br>GTCT  | 59.9                             | 643                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26398945  | Ca4                                     | 26398945                      | AATTTAATTT/AATTTAATTTATCTAT<br>TTAATTT                        | GTGGCGAATTGATTTG<br>TCCT | CGACGTAATCTGGGTT<br>GGTT  | 59.9                             | 413                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_26411287  | Ca4                                     | 26411287                      | GTTT/GTTTT                                                    | TGTTCTGCTTAAGGGG<br>CCTA | GATCAAGAGGTCACCG<br>GTTC  | 59.8                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26456492  | Ca4                                     | 26456492                      | T/TG                                                          | GCGAGCATGAGAAGTT<br>GTTG | AATTCAATGGGAAAAAC<br>CACA | 59.6                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26459581  | Ca4                                     | 26459581                      | GTATTGATGTT/GT                                                | CCAACTTATGAGCCCC<br>TCAA | TAATTGAATCAGGGAA<br>GGCG  | 60.1                             | 597                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26488208  | Ca4                                     | 26488208                      | GAAACA/GA                                                     | AAATTGAACCGTCAAAT<br>CGG | TCCTCGACCGTGTAAT<br>TTCC  | 59.8                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26492251  | Ca4                                     | 26492251                      | ACTC/AC                                                       | CAATGCACATGAGAA<br>CCGT  | AATGATCCGGAACCAT<br>TTCA  | 59.6                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26495554  | Ca4                                     | 26495554                      | GAAAGTTGTTG/GAAAGTTGTTCAAA<br>GTTGTTT                         | AACGATTTATCCTGGT<br>CCCC | CCCGAATACAAACCCA<br>AGTC  | 60.0                             | 844                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26498057  | Ca4                                     | 26498057                      | GTTTTTTT/GTTTTT                                               | ATGCTCTTGTGTGGCT<br>AGGG | TGTTTGACGACAAGCA<br>AAGG  | 60.3                             | 850                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26514892  | Ca4                                     | 26514892                      | GAAAAAAA/GAAAAAAA                                             | TGCTCTTGGGGATGTC<br>AAAT | TGGTCCGGTCTAGAAG<br>CCTA  | 60.5                             | 687                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26525402  | Ca4                                     | 26525402                      | GTTTTTTTTT/GTTTTTTTTT                                         | TGTAGCTACCGCATTG<br>ATGG | GCTGCAAGGGATGATT<br>TGAT  | 59.7                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26526816  | Ca4                                     | 26526816                      | GTTTTTTT/GTTTTTTT                                             | TGGAATGGTTCAGGT<br>GTCA  | TTCATGAAAGGCCATT<br>CTCC  | 59.9                             | 255                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_26529457  | Ca4                                     | 26529457                      | ATCTCTCTCTCTCTC/ATCTCTCTCTCTCTCTC                             | ATAGCAGCAATTTCCATCCG    | GTCCCACGAAGTAAGTCCCA    | 60.1                             | 286                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26542242  | Ca4                                     | 26542242                      | TAAAAA/TAAAAA                                                 | GCACGGAAGAAGACGAGTTT    | GGCACACGTAAATGCACATC    | 59.5                             | 185                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26547528  | Ca4                                     | 26547528                      | AT/A                                                          | TCCAAAACCTTGATATCTCAAGC | TTTGCTCTTCTGCAACAAGG    | 58.8                             | 815                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26552272  | Ca4                                     | 26552272                      | TAAAAAA/TAAAAA                                                | TCCTGGTTCACTCAATGTGG    | CTCAAGTTGAAGGCCAAAG     | 59.5                             | 818                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26620833  | Ca4                                     | 26620833                      | GTT/GT                                                        | AAAGAAGGAAGGGTCTTGCC    | TCAAAATCGAACCAATCACA    | 59.7                             | 593                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26622922  | Ca4                                     | 26622922                      | GAAAAAAAA/GAAAAAAAA                                           | TGGCTGTTGTCCATTGTGT     | TCAGACACAGTTGGTCGGTT    | 60.0                             | 604                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26662668  | Ca4                                     | 26662668                      | ATTTTTTTTT/ATTTTTTTTT                                         | GTGACGTGGGGGAGTTAAGA    | CAACGACCTTAACATTTGGTG   | 60.0                             | 799                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26728004  | Ca4                                     | 26728004                      | TG/T                                                          | ATGGTCGTGTTCCCATTT      | TTGTTGATTAAAGTGGCCGA    | 60.1                             | 832                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26733428  | Ca4                                     | 26733428                      | TAAAAAAAA/TAAAAAAAA                                           | AGTACCATCCAAGTGGTCCG    | TCTTTTCACCATCCCGACT     | 60.0                             | 302                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_26739311  | Ca4                                     | 26739311                      | TAAAAAAAAA/TAAAAAAAAA                                         | TCCATGATTTGGTGGTTCCT    | TTCTTCAGCAATGGTCTCC     | 60.2                             | 492                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_26740657  | Ca4                                     | 26740657                      | TAAT/TAATCAAT                                                 | TTGACCACAGGTCCAC<br>AAGA  | TTTtagtgCGCATTTA<br>CCC     | 60.1                             | 250                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26750453  | Ca4                                     | 26750453                      | GTATA/GTATATA                                                 | AAAAAGCAAATGATCC<br>CATCC | TGGATCCTCTCAATTCA<br>AATCTC | 60.1                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26753796  | Ca4                                     | 26753796                      | G/GATTTA                                                      | AGAGCGGCAACTCAAA<br>CAAT  | TGCAGGGGACATCTCT<br>TACC    | 59.9                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26775300  | Ca4                                     | 26775300                      | TAAAAAAAAA/TAAAAAAAAA                                         | ACGGCGCTAAACCAAC<br>ATAG  | TTGTGTGCTTAACCTTT<br>GCG    | 60.2                             | 320                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26778486  | Ca4                                     | 26778486                      | GTTTTTTTT/GTTTTTTTT                                           | GCCCATCCAAGTGATG<br>AGAT  | TGAATCGCGAAAGTAG<br>TCCC    | 59.9                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26778550  | Ca4                                     | 26778550                      | CTTT/CTTTT                                                    | GCCCATCCAAGTGATG<br>AGAT  | TTCTTTTCGGCAAAAT<br>CAC     | 59.9                             | 811                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26792383  | Ca4                                     | 26792383                      | CTTTT/CTTTT                                                   | AAGGCAAATGAGGGTG<br>TTTG  | TTGGCGTATAGTGAT<br>GCAA     | 60.0                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26842237  | Ca4                                     | 26842237                      | GAAAAAAAAA/GAAAAAAAAA                                         | TAGCATGCCTCAATC<br>CCTC   | AGCAACACCGTATTGA<br>CATCC   | 60.2                             | 726                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26847079  | Ca4                                     | 26847079                      | AAAAATAAAATAAAATAAAATA/AAAA<br>ATAAAATAAAATAAAATAAAATA        | GGAGAACGTTAAGGCA<br>GCAG  | GTGGTGTAGGTTTCGA<br>TCCG    | 60.0                             | 689                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26847495  | Ca4                                     | 26847495                      | A/AC                                                          | AGCTTCAAGTCGGATC<br>GAAA  | AAAAATCTTGTGGAAT<br>AATTCAA | 60.0                             | 216                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_26850722  | Ca4                                     | 26850722                      | TAA/TAAA                                                      | GGAGAACGTTAAGGCA<br>GCAG    | GTGGTGTAGGTTTCGA<br>TCCG     | 60.0                             | 726                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26903304  | Ca4                                     | 26903304                      | T/TG                                                          | ACTCGATTGGTCCATG<br>CTTC    | ATGTTTTGGACGCACA<br>CAGA     | 60.1                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_2690387   | Ca4                                     | 2690387                       | ATTTTTTTTTTT/ATTTTTTTTTTT                                     | TCCTTTTAAAGTGTCGT<br>CTTCTG | TCAGACACAGATGCGA<br>GGTC     | 59.0                             | 728                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26936840  | Ca4                                     | 26936840                      | CAAAAAAAAA/CAAAAAAAAA                                         | TCAAGGCTTTAGGCGT<br>GAGT    | GTAAATGCGTTGTGCG<br>ATCA     | 60.0                             | 615                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26941918  | Ca4                                     | 26941918                      | ATTTTTTTTT/ATTTTTTTTT                                         | GAGGGTTTAGTTCGGA<br>AGGG    | CAAAAATTGCATAAAAT<br>GAAACAA | 59.9                             | 851                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26954877  | Ca4                                     | 26954877                      | GTTTTTTTTT/GTTTTTTTTTT                                        | TCAATTTTGATGATGTG<br>GCAA   | CGGTCAAACAATCAGC<br>TTCA     | 59.9                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26957417  | Ca4                                     | 26957417                      | GTTTTGATTTTTTTTT/GTTTTGATTT<br>TTTTTATTTTTGATTTTTTTTT         | GTTTGTCCTCCCAAGCAA<br>CAAT  | CTAGCCCATTTGAGCT<br>TTGC     | 59.8                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26959252  | Ca4                                     | 26959252                      | TAAA/TAAAA                                                    | ACCACCAGCACACGAC<br>ATTA    | GGGGTTAGGGGTTACT<br>TTGG     | 60.0                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26967509  | Ca4                                     | 26967509                      | TAAAAAAAA/TAAAAAAAAA                                          | TTGGTGCGTTGTGTGT<br>AATGA   | TGAATGGGAAATGGAG<br>GAAG     | 59.7                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_26992631  | Ca4                                     | 26992631                      | T/TTAA                                                        | CACATCATCCTGAAAC<br>AACTCA  | CAATTCAAAGGGGACT<br>CGAA     | 58.6                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_27017251  | Ca4                                     | 27017251                      | GTTTTTTTTT/GTTTTTTTTT                                         | CCTTTGCATCTCAGGG<br>ACAT    | TGAGACCGGTTTGAG<br>TACC   | 60.1                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27052671  | Ca4                                     | 27052671                      | ATTTTTTTTT/ATTTTTTTTT                                         | GGCATGGTTTAACTTG<br>ACACG   | TGAGAAAATCCAAATCT<br>TGCG | 60.4                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27067931  | Ca4                                     | 27067931                      | ATTTTTTTTT/ATTTTTTTTT                                         | AACCTCCATTAATTTT<br>GCCA    | CATTGCAATTCAAGC<br>GAAC   | 58.5                             | 438                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27074666  | Ca4                                     | 27074666                      | GAAAAAAAAA/GAAAAAAAAA                                         | ATTGGCATCAGAGCCA<br>GTCT    | TTTCCAAGAGAGCGC<br>ATTT   | 59.8                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27087434  | Ca4                                     | 27087434                      | TA/TAAAA                                                      | TTATTGCGATGCCGAC<br>TAGT    | AATGATGTGGCTGGGT<br>TAGC  | 59.7                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27096077  | Ca4                                     | 27096077                      | CTTTTT/CTTTTT                                                 | TGAAATTAAGTTAAGGA<br>ACCGCA | GCTCAGTCGCTCACCT<br>AACC  | 60.0                             | 429                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27096186  | Ca4                                     | 27096186                      | GAAAAAAAAA/GAAAAAAAAA                                         | GGTTAGGTGAGCGACT<br>GAGC    | GCTCTTTCTTTTCCC<br>GGT    | 60.0                             | 122                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27138934  | Ca4                                     | 27138934                      | GAAAAAAAAAAAAA/GAAAAAAAAA<br>A                                | GGAAGGCTTGTCGACT<br>TGAG    | AAGACGCATTGAGAAG<br>CGAT  | 60.0                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27152769  | Ca4                                     | 27152769                      | ATTTTTTTTT/ATTTTTTTTT                                         | TGTGCAGTTATGTCCC<br>TTCG    | GACAGGGATGGAGATG<br>GAAA  | 59.7                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27159634  | Ca4                                     | 27159634                      | ATTTTTTTTT/ATTTTTTTTT                                         | CGAACTTTGAACGAA<br>CGTG     | TCCACCTCAAAACACAC<br>GAA  | 59.4                             | 408                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_27165248  | Ca4                                     | 27165248                      | A/AG                                                          | AGGGGCAGAAATGACA<br>TGAA  | TTCAAAATCAGCATTAT<br>CCACG | 60.5                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27168549  | Ca4                                     | 27168549                      | CAAAAA/CAAAAA                                                 | AGGGCCAAGGGACAAT<br>AAGT  | TGGTTTGTGCAATGTC<br>CCTA   | 59.8                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27185776  | Ca4                                     | 27185776                      | TAAAAAAAA/TAAAAAAAAA                                          | GCCCAAAACGGGAATA<br>ATTT  | GGGCAAAAGATGGAAC<br>AAGA   | 60.0                             | 712                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27205960  | Ca4                                     | 27205960                      | TAAAA/TAAA                                                    | CGAGTTGATTGGTTC<br>GGTT   | AGCACAGCTGAATGAA<br>GTGC   | 60.0                             | 754                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27260077  | Ca4                                     | 27260077                      | GAAA/GAAAA                                                    | GCGTCCAAGTCTTTGA<br>GGAA  | TTTGGGGTGCATAATT<br>TGA    | 60.4                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27261340  | Ca4                                     | 27261340                      | CAAAAA/CAAAAAA                                                | ACTCCAACACACAACC<br>CCTC  | AATTGAGCCCAGAAAA<br>CCCT   | 59.9                             | 366                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27285679  | Ca4                                     | 27285679                      | G/GAA                                                         | TATTTGAGGGCGTAC<br>CAAC   | CCAGCCTACCCCTTTT<br>ATCTG  | 60.0                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27318870  | Ca4                                     | 27318870                      | TAAA/TAAAA                                                    | GACGAGCACCAATGGA<br>GTTT  | TGGTCTTCAAAAGTCA<br>CCCC   | 60.1                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27319031  | Ca4                                     | 27319031                      | TT/TTATAT                                                     | CAAAAAGGGGGAGATT<br>ATTGG | GCTTTAGCCATTCTG<br>GCTTT   | 59.7                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27326085  | Ca4                                     | 27326085                      | TTCT/TT                                                       | CAGAAAACAAAGAACG<br>CTCG  | TACAACCTCCAACGGA<br>CACA   | 58.7                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_27357106  | Ca4                                     | 27357106                      | TCC/TC                                                        | GAGCGAGAGGTGTTGT<br>GTGA    | AGTGCTTCACCCCAA<br>ATGA   | 60.0                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27364858  | Ca4                                     | 27364858                      | TAAAAAA/TAAAAA                                                | TTTTGGGGAGAAGCA<br>TGTC     | TAGCCATCTAACCATT<br>GGC   | 60.1                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27365149  | Ca4                                     | 27365149                      | AT/ATT                                                        | TTGCAATGGAAAAGGA<br>GCTT    | TAGCCATCTAACCATT<br>GGC   | 59.8                             | 138                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27366853  | Ca4                                     | 27366853                      | TG/T                                                          | TGAGACAATGAGGCTT<br>GTGG    | TGCACTTGGTCAATGT<br>GTGA  | 59.8                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27387851  | Ca4                                     | 27387851                      | CACAAAAACACAAAA/CACAAAA                                       | AACAACAATTCCAAC<br>CGC      | GTCGTTCAAGTGGCATA<br>GGGT | 59.8                             | 769                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27395838  | Ca4                                     | 27395838                      | TT/TTGT                                                       | AAGTTTTGGGTGCTC<br>ATGG     | TTGTCCCAAGCAACA<br>ATTA   | 60.0                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27400557  | Ca4                                     | 27400557                      | ACCCCC/ACCCC                                                  | AGCCTGATACTCAAGG<br>AGGG    | CATTTTCCTTCTCACCC<br>ATCA | 58.4                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27402844  | Ca4                                     | 27402844                      | TAAAAAAA/TAAAAAA                                              | CGAGTAGCGAATCGA<br>CCAT     | TATTTTGCTTCGTTGTT<br>GCG  | 60.2                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27403176  | Ca4                                     | 27403176                      | GTTTTTT/GTTTTTTT                                              | CGCAACAACGAAGCAA<br>AATA    | GCACGGTTGAGTGAAA<br>AAGG  | 59.9                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27405634  | Ca4                                     | 27405634                      | TTATATATATAT/TTATATATAT                                       | GAGTTGGTATTTCAATT<br>GTTCCG | GTGGTTAAGATGGACC<br>ACCG  | 59.8                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_27405693  | Ca4                                     | 27405693                      | TAAAA/TAAAAA                                                  | GAGTTGGTATTTTCATT<br>GTTCCG | GTGGTTAAGATGGACC<br>ACCG   | 59.8                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27406421  | Ca4                                     | 27406421                      | ACTCTC/ACTC                                                   | TTTGATGGTTCGAAAT<br>CGTT    | CGCAAAATAAGAGAAA<br>AGACGC | 58.1                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27406459  | Ca4                                     | 27406459                      | TTATATATATATAT/TTATATATATAT                                   | TTTGATGGTTCGAAAT<br>CGTT    | CGCAAAATAAGAGAAA<br>AGACGC | 58.1                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27424528  | Ca4                                     | 27424528                      | ATTTTTTTTT/ATTTTT                                             | CGAACCAAAAGTGGAT<br>TTGA    | AAAGTTTTGTGGCCGT<br>CTTT   | 58.6                             | 733                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27432873  | Ca4                                     | 27432873                      | ATTTT/ATTT                                                    | ACGACAAGAAAGGCAG<br>AGGA    | AGCTCGTGTTCTGCA<br>ATTT    | 60.0                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27435493  | Ca4                                     | 27435493                      | CAAAAAAAAAAAAA/CAAAAAAAAA<br>AA                               | GACACCAAGCCACAAA<br>CCTT    | GCATGTTGTTGAAGG<br>AGGT    | 60.0                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27484671  | Ca4                                     | 27484671                      | TG/T                                                          | ACACATGTTGGTGGCT<br>TTGA    | CCAATGCTTGAGTTAT<br>GCCA   | 60.0                             | 679                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27496407  | Ca4                                     | 27496407                      | CTG/CTGTG                                                     | TCGGAAACGAATTGGG<br>AATA    | GGAGTTTGAGAAAGGG<br>GTCC   | 60.3                             | 750                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27498412  | Ca4                                     | 27498412                      | GAAAA/GAAAAA                                                  | GACTCCATGGCAAAGA<br>GGAG    | CTTCAACAGCCATGCT<br>CAAA   | 59.8                             | 925                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27498504  | Ca4                                     | 27498504                      | CTCTTT/CT                                                     | AAGTTCGAATATTGACT<br>GGCA   | CTTCAACAGCCATGCT<br>CAAA   | 57.4                             | 739                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_27503266  | Ca4                                     | 27503266                      | AG/AGG                                                        | GGGGTTCTCCTTGAAC<br>CACT    | CCTGCCATTTTCTTCCA<br>AAA     | 60.3                             | 343                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27504292  | Ca4                                     | 27504292                      | AG/A                                                          | CATTCATGCCACAGGT<br>ATCG    | AACACCAACACACCAA<br>AGCA     | 59.9                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27506038  | Ca4                                     | 27506038                      | CAA/CAAA                                                      | GAGATCATTGCATCCC<br>AGGT    | CACCTGAAACCCCTTTT<br>GAA     | 59.9                             | 819                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27508639  | Ca4                                     | 27508639                      | T/TC                                                          | TCCAATGGAGATCAAT<br>GCAA    | AACATAATGCCATGCC<br>CAAT     | 60.0                             | 233                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27509778  | Ca4                                     | 27509778                      | TTAT/TT                                                       | AACATTCCTTCCATCCA<br>ACG    | CATGGTTTTTCCGTGG<br>TTTT     | 59.8                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27513599  | Ca4                                     | 27513599                      | ATTTTTTT/ATTTTTTTTT                                           | TGATGGGGTTTTGTGT<br>GAGA    | ATGCATTACACGACCG<br>CATA     | 59.9                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27514430  | Ca4                                     | 27514430                      | CTTTTTTTTT/CTTTTTTTTTT                                        | TGGTGCTCTCAACCAT<br>TGAA    | TTATCCATCGCCTAAGT<br>CGG     | 60.2                             | 754                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27537181  | Ca4                                     | 27537181                      | AGTGTGTGTGTGT/AGTGTGTGTGT<br>GTGT                             | TTTCATCCTCTCTCACG<br>GCT    | TCTTCATGGCAACACTT<br>CCA     | 60.0                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27539521  | Ca4                                     | 27539521                      | TAA/TAACATAGTGAA                                              | CTTGTGAAAGCCTCAA<br>AGCC    | TTGATTTCTGTGAGTTCA<br>TTTCAA | 60.0                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27539986  | Ca4                                     | 27539986                      | ATA/ATAGATTA                                                  | TTGAAATGAACTCACG<br>AAATCAA | CACCCTCGCTTAGAAA<br>AACG     | 59.6                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_27548804  | Ca4                                     | 27548804                      | TAAAA/TAA                                                     | TTCCCCATTCTTAACAC<br>CCA   | TTCGCAACTCCACTCTT<br>CCT  | 60.2                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27555037  | Ca4                                     | 27555037                      | GCTC/GCTCATCCTC                                               | CCAACAACACAGATGC<br>AACC   | TGCGCTTTCCTTTGTTA<br>TGA  | 60.0                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27636569  | Ca4                                     | 27636569                      | A/AAGGTAGAT                                                   | TGCCTCATAAATTGAC<br>CCCT   | TACAGGTGGACGCTTT<br>GTTG  | 59.4                             | 331                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27639256  | Ca4                                     | 27639256                      | GAAAAAAAA/GAAAAAAAA                                           | TACCACCAAGGTTTGG<br>CTTC   | CGTGGAATCACTTGC<br>AAAA   | 60.0                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27647713  | Ca4                                     | 27647713                      | TAAAAAAAA/TAAAAA                                              | TTGTCCACGATACATG<br>CGTT   | GCCACTCAATTCTCAAC<br>CGT  | 60.0                             | 261                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27682659  | Ca4                                     | 27682659                      | C/CCTTAAGA                                                    | AGACGGCGCAAGTAGA<br>GAAC   | TGTTTTCTTTGCGTTGC<br>TTG  | 59.6                             | 262                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27689404  | Ca4                                     | 27689404                      | GATAT/GAT                                                     | TGCGTCATAAAATGGC<br>TTGA   | GGATGAGCTGACCCCT<br>TACA  | 60.2                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27746278  | Ca4                                     | 27746278                      | CTTTTTTTTTT/CTTTTTTTT                                         | AGTTTTCTGTGGGTTT<br>ACCG   | TGCCACATCACCCCTAA<br>ATCA | 60.0                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27764770  | Ca4                                     | 27764770                      | T/TA                                                          | AACCTCAACGAAATCTT<br>TCCAA | GCGTGCGATAGGTTGG<br>TATT  | 60.0                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27767764  | Ca4                                     | 27767764                      | TA/TAGGGGTGA                                                  | CGAACGGGGATTGAGA<br>CTTA   | AAAACGGGAAAGTTTG<br>ACGA  | 60.1                             | 324                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_27929931  | Ca4                                     | 27929931                      | GTTTT/GTTTT                                                   | CCTTCTCATTGCGAAC<br>CCTA  | TGGTTGCACCACATTT<br>GACT  | 60.2                             | 427                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27956988  | Ca4                                     | 27956988                      | TCCCCCCC/TCCCCCCCC                                            | ACTCCACTTCAAACAAC<br>CGC  | TTTAAAGCCACACCACA<br>CCA  | 60.2                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_27998494  | Ca4                                     | 27998494                      | CTTTTTTTTT/CTTTTTTTT                                          | AAGGAGGAGGAGGTG<br>AAGGA  | GAAAAGGAGGCCACAA<br>ATGA  | 60.2                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28018591  | Ca4                                     | 28018591                      | A/ACTCACTGAACT                                                | CAAAGAGAGACGTGCA<br>ACCA  | TCCGATTCAAAAACGTT<br>GAAG | 60.0                             | 708                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28019655  | Ca4                                     | 28019655                      | CAAAAAAAAA/CAAAAAAAAA                                         | CGCATTAAAGTTGGATT<br>GGGT | TTGAGGTTGAACATGG<br>TTGG  | 59.8                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28020575  | Ca4                                     | 28020575                      | TG/T                                                          | GGGAGCAAAAGCTTTG<br>AATG  | AATGAGACCTACGTCA<br>CGGG  | 59.8                             | 427                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28023593  | Ca4                                     | 28023593                      | GAAAAAAAAA/GAAAAAAAAA                                         | CTCAAACCATTGAGGC<br>CAGT  | AATCTGCATCCCAAAT<br>TGC   | 60.1                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28026871  | Ca4                                     | 28026871                      | TAAGAA/TAAGAAGAA                                              | GACATCACCAATTC<br>GACG    | TTTTGAAGGAGATGGG<br>GTTG  | 60.0                             | 885                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28042758  | Ca4                                     | 28042758                      | TC/T                                                          | GTCCTTTTCCTTTGGC<br>CTTC  | CACCCTCCTCCATATC<br>CATT  | 60.1                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28058610  | Ca4                                     | 28058610                      | TAAAAAAAAA/TAAAAAAAAA                                         | CTACCAGTTGGAGCCA<br>CCAT  | CTTCGAGAGCCACAC<br>AACA   | 60.0                             | 250                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_28062048  | Ca4                                     | 28062048                      | GTTTTTTTT/GTTTTTTTT                                           | TCAACAATTGTAATTGA<br>CTATCAACG | TATAGGCCGATCAGTC<br>AGGC | 59.4                             | 771                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28086943  | Ca4                                     | 28086943                      | GTAGAA/GTAGAATAGAA                                            | TTTTGCATACGTCGGA<br>ATCA       | ACGACGTTGATTGATC<br>CAAA | 60.1                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28108572  | Ca4                                     | 28108572                      | TAAAAAAAA/TAAAAAAAA                                           | GCAATGTTGGCGAAG<br>TACA        | AGTGTGTGCTTGTGG<br>ATCA  | 59.7                             | 301                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28120280  | Ca4                                     | 28120280                      | TAAAAAAAA/TAAAAAAAA                                           | TAGGGTGAAGGAGAAC<br>GGTG       | TTTTGTGCGTTTGACT<br>GATG | 60.1                             | 822                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28120543  | Ca4                                     | 28120543                      | TAAAAA/TAAAAA                                                 | CCAACTCCCTCCCT<br>TTTA         | CAATACGAGCACCTGG<br>CTCT | 60.3                             | 994                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28121722  | Ca4                                     | 28121722                      | TAAAAAAAAAAAAAAAA/TAAAAAAAA<br>AAA                            | TGAACCTTTCTTGGG<br>TGGG        | ATACGCATAATCGACTC<br>CCG | 60.1                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28131693  | Ca4                                     | 28131693                      | TT/TTCGGTGGCT                                                 | TAGCAAGAACCACATC<br>GCAA       | TTAACCTCAATTGCC<br>GTTC  | 60.4                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28143040  | Ca4                                     | 28143040                      | ATTTTTTTTTTTTT/ATTTTTTTT<br>TTTT                              | TCAAACAATGCCAAGT<br>CCAA       | TGGATATTGTGTGGGA<br>ATGC | 60.1                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28148545  | Ca4                                     | 28148545                      | ATACTTACT/ATACT                                               | TGGTCATAATCGAGT<br>TGGA        | CTGCAAGCAGCAGAAG<br>AACA | 59.9                             | 956                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28150064  | Ca4                                     | 28150064                      | GTTTTTTTTTT/GTTTTTTTTT                                        | GCAGCCCTATGAGGTG<br>AAGA       | ATTCAAGATATGGGCG<br>CAAC | 60.4                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_28153242  | Ca4                                     | 28153242                      | CAA/C                                                                         | TTGGCAGTGGTTCATT<br>TTCA | AAAAGCTTGCGAACAT<br>CACC | 60.1                             | 365                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28159857  | Ca4                                     | 28159857                      | TAAAAAAAA/TAAAAAAAAA                                                          | TTTGGGGGTACAAGGG<br>AAAT | TGCAACCTCATACTGG<br>GAAA | 60.4                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28162271  | Ca4                                     | 28162271                      | TAAAAAAAA/TAAAAA                                                              | AAACAAGTGGTTCTGG<br>GCAC | CGAAACTTTGCATGCA<br>TCTC | 60.0                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28163369  | Ca4                                     | 28163369                      | TGTTTATTTATGTTTAAGTTTATTTA/<br>TGTTTATTTATGTTTAAGTTTATTTA<br>TGTTTAAGTTTATTTA | GAGGAGGTCCAGGAT<br>GATGA | AGCTGGTCTCTCTGTG<br>CCAT | 60.0                             | 731                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28169092  | Ca4                                     | 28169092                      | GC/G                                                                          | TTTTTGCCCATTCAAAC<br>ACA | AAATGCGTCAGCCAG<br>TAAG  | 59.9                             | 829                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28169343  | Ca4                                     | 28169343                      | TAAAAAAAA/TAAAAA                                                              | GGGGTGAGAAAAGAT<br>GTGG  | AAATGCGTCAGCCAG<br>TAAG  | 59.5                             | 180                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28177449  | Ca4                                     | 28177449                      | ATTTTTTTTT/ATTTTTTTTTT                                                        | TCATAAAATTGCATGG<br>CACA | TTCTATGGGACAGCCC<br>AATC | 58.6                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28180440  | Ca4                                     | 28180440                      | TAAAAAA/TAAAAA                                                                | GGAAGAGCGAGAAGG<br>GAGAT | ACCAATGTCCAACGGG<br>AATA | 59.9                             | 325                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28183509  | Ca4                                     | 28183509                      | GC/G                                                                          | ACTGGCAGCCATTAC<br>TCTT  | TGACAACCCCAAACTT<br>GTGA | 59.9                             | 745                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28184015  | Ca4                                     | 28184015                      | A/ACG                                                                         | TCACAAGTTTGGGGTT<br>GTCA | ACGCAAGGTCAACAAA<br>GGTC | 60.0                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_28205282  | Ca4                                     | 28205282                      | CAAAAAA/CAAAAAA                                               | GGCAACAATGTCTCAA<br>AGCA  | CACGTTGAATTCACCC<br>TTCA | 59.8                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28208528  | Ca4                                     | 28208528                      | TAAAATTAA/TAAAATTAAAAATTAA                                    | CGATAGCACGTTGGTG<br>AGAA  | TTCCCTCCAAAGTTGG<br>ACAC | 59.9                             | 242                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28209971  | Ca4                                     | 28209971                      | T/TA                                                          | ATTGATGGAGCGAATC<br>GAAC  | AATTCCTCTTTTGGTGG<br>GCT | 60.0                             | 891                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28213499  | Ca4                                     | 28213499                      | CTTTTTTT/CTTTTTTTTT                                           | ACTGACCTGACCTAGG<br>CGTG  | GTTGCAAAATTGGTGT<br>CTGC | 60.3                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28214353  | Ca4                                     | 28214353                      | GACAA/GACAACAA                                                | TCCGAGTCTAATCGGG<br>CTAA  | TGGAAAAGGGAGCCAA<br>TATG | 59.8                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28237092  | Ca4                                     | 28237092                      | C/CA                                                          | TCGGTTTTTGCCTCAC<br>TTTT  | GTGGAGGCTCAGTTGG<br>AGAG | 59.7                             | 758                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28237880  | Ca4                                     | 28237880                      | TG/T                                                          | CTCTCCAAGTGCCT<br>CCAC    | GCAGTTTCGTGCTAAG<br>GAGG | 60.0                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28254483  | Ca4                                     | 28254483                      | CAACAA/CAACAAGACAAACAA                                        | GGGGAAGTCTCAAGT<br>CACA   | CGTGGAACCAACCTT<br>GTCT  | 60.1                             | 703                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28275732  | Ca4                                     | 28275732                      | GAAAAAAAA/GAAAAAAAAA                                          | TTGGACGGTATCCTTT<br>TTGAA | TGCAAAACAACAGAGT<br>TGGC | 59.4                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28277078  | Ca4                                     | 28277078                      | AC/A                                                          | TCAACATTTTACCGTT<br>GAGC  | TCTCATTGTTGCGTGTA<br>GGC | 60.0                             | 348                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_28277405  | Ca4                                     | 28277405                      | GTTTTTTTTT/GTTTTTTTTTTT                                       | GCCTACACGCAACAAT<br>GAGA   | AAGTTTTTCTAAACCGC<br>AATTTTT | 59.9                             | 423                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28278132  | Ca4                                     | 28278132                      | GAAAAAAAA/GAAAAAAAAA                                          | AAAAGGAATTGAATG<br>ACCACAA | AAAGTGGAGTGCGACC<br>AAGT     | 59.7                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28290158  | Ca4                                     | 28290158                      | TAACAACAA/TAACAACAACAA                                        | ACCATTACACTACCGC<br>TGCC   | TTAATTAATATCCGCGC<br>AACG    | 60.0                             | 688                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28290227  | Ca4                                     | 28290227                      | A/AG                                                          | ACCATTACACTACCGC<br>TGCC   | TTAATTAATATCCGCGC<br>AACG    | 60.0                             | 688                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28293593  | Ca4                                     | 28293593                      | GTTTTTTTTT/GTTTTTTTTT                                         | TCATTACTCGCCATAA<br>GTGGAA | ACTCTCGATGCCACCT<br>CATC     | 59.6                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28296583  | Ca4                                     | 28296583                      | TCC/TCCC                                                      | TAGCTGCTCACACTGC<br>CAAC   | GGTTGTTGTGCCCAGA<br>GATT     | 60.2                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28305975  | Ca4                                     | 28305975                      | AGG/AG                                                        | TTTCCCCACATGTCTCA<br>CAA   | TTCTCGCAAAAGACAAA<br>CCC     | 59.9                             | 391                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28306538  | Ca4                                     | 28306538                      | CTTTTTTTT/CTTTTTTTTT                                          | GGGTTTGCTTTTTCG<br>AGAA    | AATTGTCCCATCCCTTA<br>CCC     | 60.2                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28320855  | Ca4                                     | 28320855                      | ATTTTTTTT/ATTTTTTTT                                           | TGAGAAACGGCAAAAC<br>ACAA   | AAATATTGGGCATGTG<br>AGCC     | 60.3                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28322339  | Ca4                                     | 28322339                      | A/ACCGT                                                       | TGCGTACACGAAAAAG<br>CAAC   | TGTTGTTGCCGACTGA<br>GAAG     | 59.9                             | 333                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_28322577  | Ca4                                     | 28322577                      | C/CCTTTTTTTTTT                                                | CTTCTCAGTCGGCAAC<br>AACA   | CTCCAGAGTAGCAAG<br>CAGG     | 60.0                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28331028  | Ca4                                     | 28331028                      | CAAAAAAAAA/CAAAAAAAAA                                         | CTTGAAGGGACGGCTA<br>GATG   | TTGCCATAATGTTGAGA<br>AGGG   | 59.8                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28333301  | Ca4                                     | 28333301                      | TAAAAAAAAA/TAAAAAAAAA                                         | CAGGTCTTCCCAACGT<br>TATCA  | TTTGTGATTGCTTGCTT<br>TAATTC | 60.0                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28336543  | Ca4                                     | 28336543                      | TAAAAAAAAA/TAAAAAAAAA                                         | CAAAGCAGGGAGTTTC<br>CATC   | TGGTTTAAGTCCTCGG<br>CTGT    | 59.7                             | 723                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28338388  | Ca4                                     | 28338388                      | TAAAAA/TAAAAA                                                 | TGACTCGGGCTGCAGA<br>TTAT   | CACCGTGGTCTTTCC<br>TTTA     | 60.8                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28338753  | Ca4                                     | 28338753                      | TGGGGCT/TGGGGCTTAAGAGAGG<br>GGGCT                             | AAGACCACCGGTGTTT<br>ATGG   | TCAATTTGACAAGCCC<br>CTTA    | 59.7                             | 724                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28338890  | Ca4                                     | 28338890                      | CAAAAAAAAA/CAAAAAAAAA                                         | TATTTATGGGGCTCA<br>AAGC    | TAACCGCCTATTTCTT<br>GCG     | 60.0                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28346696  | Ca4                                     | 28346696                      | A/AT                                                          | ACCACAGGTGAAAGAA<br>ACCG   | TTTTCAACTCTATCCGT<br>AGCCC  | 60.0                             | 340                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28349135  | Ca4                                     | 28349135                      | ACAT/ACATATCAT                                                | CTTTCGATCAAATGG<br>TCAA    | TCAAGCTCAAAACGTG<br>ATGC    | 59.7                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28352450  | Ca4                                     | 28352450                      | AAATGAA/AAA                                                   | TTTCTTCGGTTTTCAT<br>TTATGG | AAAACTCAAGGTTTC<br>CCAA     | 59.4                             | 636                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_28358208  | Ca4                                     | 28358208                      | GTTTTTTTTT/GTTTTTTTTT                                         | TGCGCTAAAATTTAACCTTC    | TCATGCACCAATCAGTTTCC    | 58.5                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28390462  | Ca4                                     | 28390462                      | TAA/TAAA                                                      | GTCATCAAAAGCCGACGAAT    | GGCCCAACAATTTTGAAAGAGA  | 60.1                             | 786                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28401988  | Ca4                                     | 28401988                      | TAATTAA/TAATTAATTAAATAAAATTAA                                 | ACTTGGATGAAGGGAAAGGG    | GCATTTGCGAAAAATTTGAA    | 60.3                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28403002  | Ca4                                     | 28403002                      | TTATATATAT/TTATATAT                                           | CATTCTTCTTCATTAAGTGGCA  | TTGACGTGTCAACCTTGCTC    | 60.5                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28407567  | Ca4                                     | 28407567                      | CAAAAAA/CAAAAAA                                               | TGGTCATAAAGGGAACAGG     | GGAGGGGGTGAATTAGGTGT    | 59.8                             | 146                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28407643  | Ca4                                     | 28407643                      | AA/AAGA                                                       | ACACCTAATTCACCCCTCC     | TCCCTTTTCCAACCACTTTG    | 60.1                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28410297  | Ca4                                     | 28410297                      | GAAAAA/GAAAA                                                  | TTTTGGGATCTCAAGGTGAAA   | ATCGTGGCAAAGATGACACA    | 59.5                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28414876  | Ca4                                     | 28414876                      | CAAT/CAATAAT                                                  | GCCCATGTTTGTGCTTAAT     | GGATTGAGCATCCGTCAGT     | 59.8                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28417839  | Ca4                                     | 28417839                      | CAA/CAATAGAA                                                  | TGCCTTGGAAGAGGCTTTTA    | TGAAAAATAGCCCAATGGTGA   | 60.0                             | 715                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28421576  | Ca4                                     | 28421576                      | TAAAAA/TAAAAA                                                 | CCAATCCATCGGTTTTTAC     | TGCATGGAAAGCTGTGTAG     | 60.2                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_28422388  | Ca4                                     | 28422388                      | TA/TAA                                                        | TGAAGGAACTTTGAT<br>GCCA     | TTGGGTGATGGTAGTT<br>TCAATG    | 59.2                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28457671  | Ca4                                     | 28457671                      | TCTCTA/TCTCTATTTAACTCTA                                       | TACAAAGCACCTGACC<br>CTCC    | CCCAATCAAAGCAAG<br>CAAT       | 60.1                             | 765                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28504169  | Ca4                                     | 28504169                      | CAA/CA                                                        | GCTGCGGGAATTAGT<br>ATGA     | GCTTCCCACTATCAC<br>TCCA       | 60.1                             | 132                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28513752  | Ca4                                     | 28513752                      | ATTTTT/ATTTTT                                                 | CTATTCCGTGAACAAC<br>CCGT    | TCATATGGTGTA AAC<br>AATTGGTAA | 59.9                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28519648  | Ca4                                     | 28519648                      | TAAAAAAAA/TAAAAAAAA                                           | GCCATGAAGTGGCCTA<br>ACAT    | TCACGGTTTTGTAGAG<br>CGGT      | 60.0                             | 620                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28519731  | Ca4                                     | 28519731                      | AA/AAGA                                                       | GCCATGAAGTGGCCTA<br>ACAT    | TCACGGTTTTGTAGAG<br>CGGT      | 60.0                             | 620                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28520308  | Ca4                                     | 28520308                      | TAAAAAAAA/TAAAAAAAA                                           | ACCGCTCTACAAAACC<br>GTGA    | AGCAGCTAACTTTTG<br>GGCA       | 60.7                             | 870                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28536428  | Ca4                                     | 28536428                      | ATTTTTTTTT/ATTTTTTTTTTTTT                                     | TTGTAACACCCGTTTT<br>TCG     | CCTCAGATGAGAGCCA<br>GGAC      | 60.8                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28541959  | Ca4                                     | 28541959                      | TAAAAAAAA/TAAAAAAAA                                           | TTGCATCGGCCTACTT<br>TCTT    | CGGATTCATCCAAGT<br>TTCAA      | 59.8                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28556813  | Ca4                                     | 28556813                      | TAAAAAAAA/TAAAAAAAA                                           | GCAAAAATTCATTCAAA<br>AATTCG | TGGTGGTGGGTGAAG<br>AAGT       | 59.9                             | 295                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_28558898  | Ca4                                     | 28558898                      | AAAGTAAG/AAAG                                                 | GGCAGGCAATGGTATT<br>GTTT  | GTGGTTGTTTGCTCCT<br>CGAT  | 59.8                             | 840                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28559061  | Ca4                                     | 28559061                      | GAAAAAAAAA/GAAAAAAAAA                                         | AGGTCCGTTTGGAGGA<br>TTTT  | GTGGTTGTTTGCTCCT<br>CGAT  | 59.8                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28581947  | Ca4                                     | 28581947                      | TAAAAAAAAA/TAAAAAAAAA                                         | CATTCCCCACACCAA<br>TTTC   | AAGGATGATGATTGTG<br>CATGT | 60.0                             | 379                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28583861  | Ca4                                     | 28583861                      | ATT/AT                                                        | AGAGGGAGGGACCAAA<br>ACTT  | CTGAGCAAGCTTTCC<br>AAAC   | 59.0                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28586798  | Ca4                                     | 28586798                      | ATTTTT/ATTTT                                                  | GCCCAAAGCATACGAG<br>ACAT  | TTGGGGGATAATTGT<br>TGGA   | 60.1                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28597058  | Ca4                                     | 28597058                      | GATATATATATATATAT/GATATAT<br>ATATAT                           | CGAATATCCGTGAATG<br>TTGAA | ATTTCTTTTGCCGTTT<br>CCA   | 58.5                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28622371  | Ca4                                     | 28622371                      | CAAAAAAAAA/CAAAAAAAAA                                         | TAAACATCGCAACAAAA<br>CGG  | GTGAGGTGATTCGGT<br>CCAT   | 59.6                             | 183                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28623236  | Ca4                                     | 28623236                      | ATTTTTTT/ATTTTTTT                                             | GAAATGTTGAATGTGT<br>GCCG  | TGTCCGAAACATTAAAC<br>CCA  | 60.0                             | 249                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28714992  | Ca4                                     | 28714992                      | GATAT/GAT                                                     | AGAGCCAACGCTCATA<br>GGAA  | TTAAATTCCCTCCTCG<br>GCT   | 60.0                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28783066  | Ca4                                     | 28783066                      | TAAA/TAA                                                      | AGGAGAGAAGTGTTT<br>GGCA   | ATGAAGGAGCAAGCTT<br>TCCA  | 59.8                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_28793395  | Ca4                                     | 28793395                      | TAA/TAAAAACAA                                                 | CCAAAATTACACCAAC<br>GGTTC    | TTGTTTCGATGCTCATT<br>CTC    | 59.2                             | 275                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28797185  | Ca4                                     | 28797185                      | AT/ATT                                                        | ATGGGGCTTAAGTAAT<br>GGGG     | TAAAGAAACGCTTCGT<br>GGG     | 60.0                             | 891                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28801392  | Ca4                                     | 28801392                      | ATTT/ATT                                                      | TGGCATAGAGCTTGGT<br>CTCA     | CCCCTCATTTCATGTTT<br>TCCA   | 59.5                             | 940                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28802275  | Ca4                                     | 28802275                      | AT/A                                                          | TTGTGGTTTGGACTGT<br>GGAA     | TTAGGTGCAAGTGTGG<br>ATGG    | 60.0                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28822156  | Ca4                                     | 28822156                      | TC/T                                                          | AAGCGCAAAAGTGCAT<br>GTTA     | AACACCATTTCGGAA<br>GAAG     | 59.5                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28822376  | Ca4                                     | 28822376                      | ATTTT/ATTT                                                    | CTTCTCCGCAAATGG<br>TGTT      | TGAATTGGAGAGTTCC<br>TTGAAG  | 60.1                             | 155                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28823023  | Ca4                                     | 28823023                      | ATTTTTTT/ATTTTTTTT                                            | AAGCCTCTTTTCAAATT<br>ACCAGA  | TTCTCAAGATGGTCAA<br>CAACTCA | 58.5                             | 907                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28823256  | Ca4                                     | 28823256                      | CAAAAA/CAAAAAA                                                | TGGTTTTAATGTGTGC<br>ATTTTATG | TTCTCAAGATGGTCAA<br>CAACTCA | 58.9                             | 266                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28823535  | Ca4                                     | 28823535                      | AAATAATAATAATAATAATA<br>ATA/AAATAATAATAATAATAATA              | TGAGTTGTTGACCATC<br>TTGAGAA  | ACCAAGGGCAGATCTT<br>AGGG    | 59.8                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28826108  | Ca4                                     | 28826108                      | CA/C                                                          | GCAGCAATTAGAACCG<br>TCGT     | TGGTCATGGAGCAACA<br>TCAT    | 60.3                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)            | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                          |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_28832888  | Ca4                                     | 28832888                      | TGGTGTATA/T                                                              | CAGTTGTGCACTTTGA<br>ATGTTG | AAAATCACATGGAGGA<br>ACAAAAA | 59.3                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28846796  | Ca4                                     | 28846796                      | ATTTTTTTTTTTTT/ATTTTTTTTTTT<br>TT                                        | CCAACATTCGGGGACT<br>TAAA   | TGGTGATCGGTAGACA<br>CGAA    | 59.8                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28848503  | Ca4                                     | 28848503                      | A/AG                                                                     | CGAAAAACCGTCTCT<br>TTCA    | CATTGTGGCATCATTT<br>CTCT    | 60.2                             | 151                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28850439  | Ca4                                     | 28850439                      | ATTATTTTTATTT/ATTATTTTTATT<br>TTATTTT                                    | GTCAGAGGCAGTGAGC<br>CTTC   | TTTTAGCTTTCCAACGC<br>CTG    | 60.1                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28854169  | Ca4                                     | 28854169                      | GGTTCAGTT/GGTTCAAGTCAGTT                                                 | CCGAAGTGAACCGGTT<br>TTTA   | ATACTCCTGCCGGATA<br>CACG    | 60.0                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28909527  | Ca4                                     | 28909527                      | ACC/ACCC                                                                 | TGAAAAATGTTTTTAAC<br>GCCA  | TCGTTTCCACAAATACC<br>AACA   | 58.3                             | 378                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28913802  | Ca4                                     | 28913802                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATT/TTTATTATTATTAT<br>TATTATTATTATT | AAATAGAAAGTCGCAT<br>CCCG   | CAACGTCCTCCCATTT<br>GTTT    | 59.2                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28915766  | Ca4                                     | 28915766                      | AATATATATATAT/AATATATATATAT<br>AT                                        | TTGGCAAAACGTTATTT<br>TTGG  | ATGTTGAAATGGTGC<br>CTCC     | 59.9                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28920238  | Ca4                                     | 28920238                      | GTTAGGACTTAGGACTTAGGACT/G<br>TTAGGACTTAGGACT                             | TCCCACGTCCTAATTTT<br>TGC   | ACTACATGCGACCGTT<br>CTCC    | 59.9                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28930811  | Ca4                                     | 28930811                      | CATTATTATTATTATT/CATTATTATT<br>ATTATTATTATTATT                           | CTCGTTCAAAGGGCTA<br>GACG   | TAATTTGAAATGGCGC<br>ACAA    | 60.0                             | 722                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_28933902  | Ca4                                     | 28933902                      | GTT/GT                                                        | GATGGACACTCATGTC<br>AATGAAG | TGGCCAAACTGATGAT<br>TCAA      | 59.5                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28938203  | Ca4                                     | 28938203                      | ACCCCC/ACCCC                                                  | CTGATTTCCAACACGA<br>GGGT    | CATTCTCCACCCAAAT<br>GCT       | 60.0                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_28989260  | Ca4                                     | 28989260                      | TAAAA/TAAAA                                                   | GAGGCAATTGACAACC<br>CAGT    | GTCCATTGTTGAGGT<br>CGTT       | 60.0                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29008246  | Ca4                                     | 29008246                      | GTTTT/GTTT                                                    | CCTACAATCCAAGAC<br>AAGGA    | ATTAATGCCCATGAAG<br>GCAC      | 59.0                             | 252                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29034169  | Ca4                                     | 29034169                      | TA/TAA                                                        | TGAATGGAAAGAACCT<br>GGACA   | TGTGAGCATCCACTCT<br>CAGG      | 60.5                             | 758                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29035883  | Ca4                                     | 29035883                      | ATTTTTTT/ATTTTTTTT                                            | TTGGACAGAGGCATGC<br>AATA    | GGACCAACTCTGGAAG<br>AAAAA     | 60.2                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29037899  | Ca4                                     | 29037899                      | TAA/TAAA                                                      | GAGCTGAAACATGCGA<br>ACAA    | TGATACCTTGCAATTGAA<br>CAAATTC | 60.0                             | 716                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29052614  | Ca4                                     | 29052614                      | CTTTTTTT/CTTTTTT                                              | GGTTCCAACACGTGTC<br>CTCT    | CAATCAACATTGCAACA<br>GGG      | 60.0                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29070111  | Ca4                                     | 29070111                      | TAA/TAAA                                                      | CGCGAGTCTGCTCTTG<br>AACT    | CCACCTATCGCGTCTG<br>GTAT      | 60.9                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29073548  | Ca4                                     | 29073548                      | ATTTTTTTTT/ATTTTTTTTTT                                        | TGCAAAATGAGGGT<br>GCAA      | CACCTATTTTGTGCC<br>CAAC       | 60.1                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)      | Forward primers (5'-3')        | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------|--------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                    |                                |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_29091211  | Ca4                                     | 29091211                      | T/TAA                                                              | TTTAAAATCTATCCAA<br>AATGAAAAGC | GCGTGTTATTTTGTGA<br>CGC    | 59.4                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29091323  | Ca4                                     | 29091323                      | TAAA/TAA                                                           | TTTAAAATCTATCCAA<br>AATGAAAAGC | GCGTGTTATTTTGTGA<br>CGC    | 59.4                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29100812  | Ca4                                     | 29100812                      | GGTAGTA/GGTA                                                       | TCAAGAAATAGTGGGG<br>GCAG       | TGGAGAACTCTTCGG<br>CTGT    | 60.1                             | 840                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29110502  | Ca4                                     | 29110502                      | ATTTTT/ATTTT                                                       | TGCAACATGGATGGG<br>AATA        | CACGGTTTCTAACACC<br>ATTTGA | 59.7                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29122319  | Ca4                                     | 29122319                      | TAAAAAAAA/TAAAAAAAAA                                               | TTGTGTGCCACATCAT<br>CACA       | TACCAGCGACATGCTT<br>TCAG   | 60.6                             | 832                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29158154  | Ca4                                     | 29158154                      | T/TG                                                               | TTGGGGGAGACTGAAG<br>ATGG       | GCTCACGTTTTTGTAA<br>GTCCA  | 60.0                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29160471  | Ca4                                     | 29160471                      | GATTATTATTATTATTATTAT<br>TAT/GATTATTATTATTATTATTA<br>TTATTATTATTAT | CAGTTTCAATTCATGCA<br>TTTCC     | GTTTGAAATCGCACCC<br>AAAT   | 59.5                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29161765  | Ca4                                     | 29161765                      | CTTTTTT/CTTTTTTTT                                                  | CACATACACATTGCTTT<br>CCGA      | TTGCAATCAGAAGTCC<br>CAAA   | 59.6                             | 256                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29162014  | Ca4                                     | 29162014                      | TCC/TC                                                             | CTTCCCGATTTCGTC<br>CTTT        | TGGACAAATCGTTTCTT<br>TTGTG | 60.4                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29162382  | Ca4                                     | 29162382                      | AATA/AA                                                            | CTTCCCGATTTCGTC<br>CTTT        | GGCCAGCGAAAATTAC<br>TACC   | 60.4                             | 804                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_29191237  | Ca4                                     | 29191237                      | CTTTTTTT/CTTTTTTTT                                            | CCAACTTGTTCCAAC<br>AATCT | GGAGAAAAGTTAGGGG<br>GTGC | 58.9                             | 119                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29208577  | Ca4                                     | 29208577                      | CAAAA/CAA                                                     | CGGTCAACCTAATCGG<br>AGAA | TTCTCTTGTTCACGTG<br>GCG  | 60.1                             | 760                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29209441  | Ca4                                     | 29209441                      | AATATATATATATATA/AATATATATA<br>TA                             | AGGTTGCTCGCAGTTG<br>AGAT | GCCGTCTCAACTCTCT<br>GTCC | 60.0                             | 689                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29220873  | Ca4                                     | 29220873                      | AACAGCGCTT/AACAGCGCTTTTTTC<br>ACAGCGCTT                       | GTAGATGGCCGCACAC<br>TACA | CTGAATTCACAAGGCA<br>CCCT | 59.7                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29221849  | Ca4                                     | 29221849                      | CTTTTTTT/CTTTTTT                                              | TTGTTCGTACATCCGG<br>GAAT | CGCACATAGAGAGGTG<br>CATT | 60.2                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29221975  | Ca4                                     | 29221975                      | ATTTTTTTTTTTTTT/ATTTTTTTTTT                                   | TTGTTCGTACATCCGG<br>GAAT | CGCACATAGAGAGGTG<br>CATT | 60.2                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29222326  | Ca4                                     | 29222326                      | ATTTTTTT/ATTTTTTTT                                            | TGCACCTCTCTATGTG<br>CGTG | TTCTTCCGGACAAAT<br>CTTC  | 61.0                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29228849  | Ca4                                     | 29228849                      | T/TG                                                          | CATTTATTTCTTCCCC<br>GGT  | CACGAAGACGTTGGAA<br>CAGA | 60.0                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29230365  | Ca4                                     | 29230365                      | TAAAAA/TAAAAA                                                 | TTGTCAACTTTGTTGG<br>GGAA | GTTTGTGTTTGGCAAGA<br>CCG | 59.0                             | 156                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29231627  | Ca4                                     | 29231627                      | TA/TAGGA                                                      | TTCTCCCATGAAACG<br>ATGT  | TCTGGGGACAAATGA<br>GGAG  | 60.3                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_29233852  | Ca4                                     | 29233852                      | A/AT                                                          | AGGAAAATGATGCAAG<br>GCTG  | TAGAAGCAAAGGCGGA<br>AAAA  | 60.2                             | 726                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29238831  | Ca4                                     | 29238831                      | A/AC                                                          | CCATGAGATCCACATA<br>ATCCG | TTGCAAGAATCCATCCA<br>TCA  | 60.2                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29243916  | Ca4                                     | 29243916                      | TAAAAAAAAAAAAAAAAA/TAAAAAAAAA                                 | ATTCTTGTGCGAGGT<br>CAAC   | TCACCTGCAAAGTCAG<br>CATC  | 60.1                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29245578  | Ca4                                     | 29245578                      | T/TA                                                          | TTACCAACCAAATTGCA<br>CCA  | CCCTAATGGGCCAAAT<br>TACA  | 59.8                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29262137  | Ca4                                     | 29262137                      | AAT/AATTAT                                                    | TTCAAAGGTGCATTGT<br>CGAT  | CACTGCGACGAACTT<br>ACCA   | 59.1                             | 619                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29280125  | Ca4                                     | 29280125                      | ATTTTTTTTTTTT/ATTTTTTTTTTT                                    | AGGTCGTCCAAATCA<br>AACG   | TTATCGCTCGCATTCA<br>TAC   | 60.0                             | 328                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29292512  | Ca4                                     | 29292512                      | TCC/TC                                                        | CACATGTTTCAACTTG<br>GTTGC | GATCCTCATGGGAACG<br>TGAT  | 59.1                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29310770  | Ca4                                     | 29310770                      | TAAAAAAAAA/TAAAAAAAAA                                         | GTGGTGTCCATCTCGG<br>TCTT  | TAAGCCAGCAACTCCA<br>GGAT  | 60.0                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29315886  | Ca4                                     | 29315886                      | CTTTTTTTTT/CTTTTTTTTT                                         | CGTGGCAACCCAAGAC<br>TTAT  | TCAATGTTCAAGAATCG<br>GTCC | 60.0                             | 733                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29320476  | Ca4                                     | 29320476                      | CTTTTTTTTT/CTTTTTTT                                           | TGGCTTTCAAGGAAGG<br>GTAA  | TTGGCAAACCTCGAAA<br>TAGG  | 59.7                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                             |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_29321184  | Ca4                                     | 29321184                      | ATTTTTTT/ATTTTTTTT                                                          | AACACATCAGCAAATG<br>GCAA   | TGGGTTTCGGGTACAAG<br>CTAC   | 60.1                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29331432  | Ca4                                     | 29331432                      | CAAAAAAAAAAAAA/CAAAAAAAAAA<br>A                                             | TGCCCTTAGTCAAACG<br>ATCA   | GCATTTGCTGTTGGAA<br>CCTT    | 59.3                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29350232  | Ca4                                     | 29350232                      | AC/A                                                                        | GTAAATTTGCTGGAG<br>CACG    | ACCAAGATTGGGCATC<br>TGAA    | 58.4                             | 160                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29358565  | Ca4                                     | 29358565                      | CAAAAAAAAA/CAAAAAAAAAA                                                      | AACCAATTCAATGCAAA<br>CCG   | ATGCGAACCATCATCA<br>GTCA    | 60.7                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29364474  | Ca4                                     | 29364474                      | CAAA/CAA                                                                    | GGGCATGAACTCCAAC<br>TTGT   | AACCTTGATCAATCGCT<br>GAGTGT | 60.0                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29369378  | Ca4                                     | 29369378                      | ACATCAAATCCATCAAAT/ACATCAA<br>AT                                            | TTTCCATCTCCAACAAC<br>AACA  | AACCACTTTGCAAGCA<br>GTTG    | 59.0                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29370210  | Ca4                                     | 29370210                      | ATTTTT/ATTTT                                                                | GCATGCCTGTTCTCTC<br>AACA   | AAAGGGCCATAGGAGA<br>GTCC    | 60.0                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29379238  | Ca4                                     | 29379238                      | CAAAAAA/CAAAAAA                                                             | ATGCAAGTGGGCCTAG<br>ACAG   | CACTTCGTTTTGGAATC<br>GGT    | 60.3                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29393253  | Ca4                                     | 29393253                      | ATTATTTATTTATTTATTTATTTATTT<br>ATTT/ATTATTTATTTATTTATTTATTT<br>ATTTATTTATTT | GCTTGCAGCTAGGAAG<br>CAGT   | TTTGTGATCTACGCAT<br>CGG     | 59.9                             | 404                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29415553  | Ca4                                     | 29415553                      | C/CCG                                                                       | AATATGCATAACTCGA<br>CGGAGA | ACAGGTGTCGAAGACC<br>GACT    | 58.7                             | 481                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_29418531  | Ca4                                     | 29418531                      | TT/TTAT                                                       | GGTGGTGTACGGTGG<br>AAGTT   | GTCAAGGCAGACCAGA<br>AAGC       | 59.7                             | 383                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29420218  | Ca4                                     | 29420218                      | ATTT/ATT                                                      | TCACAATGCAAGCTTAT<br>GCC   | TTGAAACAAAAACCACG<br>ATGA      | 59.8                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29420847  | Ca4                                     | 29420847                      | T/TA                                                          | CTTCGCCGTTGCTTTT<br>CTAC   | GGCTCAAATGAAAAAG<br>GCAT       | 60.0                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29422304  | Ca4                                     | 29422304                      | CA/CATA                                                       | ATGCGTTGCCAAATG<br>TATG    | TCCCTCACATGATGGT<br>AAAAAG     | 59.4                             | 766                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29428218  | Ca4                                     | 29428218                      | ATTTTTTTTT/ATTTTTTTTT                                         | TCCATCTTCTTCATTGA<br>TCACG | TGCCAAAAATACTCTTG<br>TAAACAAAT | 60.1                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29431394  | Ca4                                     | 29431394                      | TAAAAAAAAAAAAA/TAAAAAAAAA                                     | TCGACCTTGTTAGGAG<br>CGAT   | CCATAGCCAATGGTTC<br>CTTC       | 59.8                             | 629                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29442652  | Ca4                                     | 29442652                      | T/TG                                                          | CGTGACTGATCCTCCA<br>TCCT   | AAAGTTGGTTTGTGG<br>CAGG        | 60.1                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29443305  | Ca4                                     | 29443305                      | CTTTTTTTTT/CTTTTTTTTT                                         | CCTGCCAACAAACCAA<br>CTTT   | GGCTGGAGGAAAACAA<br>ACAA       | 60.0                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29498412  | Ca4                                     | 29498412                      | ATTTTTTTTT/ATTTTTTTTT                                         | TTGGATTGATTTTGGG<br>TTTGTC | AACTTGATTGAAATATT<br>GCCATTG   | 60.0                             | 779                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29501722  | Ca4                                     | 29501722                      | TGG/TGGG                                                      | ATGGAGGTGCAGGGAA<br>GAAT   | TGAGTGGAAAATGGCA<br>TCAA       | 60.9                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_29511821  | Ca4                                     | 29511821                      | CTTTTTTTTT/CTTTTTTTTT                                         | AAAGGGCTAAATAGCT<br>CCCG   | TCCCGATTTGGTCATT<br>GTT     | 59.7                             | 506                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29531556  | Ca4                                     | 29531556                      | G/GA                                                          | CAAGGTCGGGGATTG<br>ACTA    | GTTATGCGCAAAATAG<br>CGGT    | 59.9                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29532848  | Ca4                                     | 29532848                      | TAAAAAA/TAAAAAA                                               | TCCTTGCAAAGGACAT<br>TAAACA | TGCCAAGTCATGGATA<br>ATATGGT | 59.6                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29532946  | Ca4                                     | 29532946                      | TAAAAAAAAA/TAAAAAAAAA                                         | CCATATTATCCATGACT<br>TGGCA | CCGTTAGAAATCAAATG<br>GGC    | 59.7                             | 562                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29534339  | Ca4                                     | 29534339                      | CAAAAAA/CAAAAAA                                               | GGTCCGTCAAAAGAGT<br>GTGAG  | CCTCGAGCTATGCAAT<br>ATGATG  | 59.8                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29544316  | Ca4                                     | 29544316                      | GATAT/GAT                                                     | CCATCAAACCACAACA<br>AACA   | CCCAATTCCTTCGGTT<br>TTT     | 57.8                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29544653  | Ca4                                     | 29544653                      | ATTTTTTTTT/ATTTTTTTTT                                         | TTTCAAGTGCAACTAA<br>GGGCT  | CACCCAGCGTATCACG<br>TATG    | 59.0                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29545135  | Ca4                                     | 29545135                      | AATTATTATTATTAT/AATTATTAT<br>TTATTATTATTAT                    | CATACGTGATACGCTG<br>GGTG   | GTGAGGGAGGACCAAA<br>ACAA    | 60.0                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29564954  | Ca4                                     | 29564954                      | ATTTTTTTTT/ATTTTTTTTT                                         | GCATAAGGATCGGGGA<br>AACT   | GATCGTCTCGGGTTG<br>GTTA     | 60.3                             | 396                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29582409  | Ca4                                     | 29582409                      | TAAAA/TAAA                                                    | AGCTGTATTGGGCCTC<br>CTTT   | GCCGAATAAAACCCTC<br>ACAA    | 60.1                             | 212                                           | INTERGENIC                                        | --                                  | --                    | --  |





| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                         |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_29670240  | Ca4                                     | 29670240                      | TAAAAAA/TAAAAAA                                               | TGGGGGATACCATCTTGA        | TGCCCTTGAGCTTTGAGTTT    | 60.1                             | 479                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_29701374  | Ca4                                     | 29701374                      | G/GTTTAAATTC                                                  | AGATCTTCCCTCATGGCT        | CCTTGACAAGAAGCAACACG    | 60.0                             | 474                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_29705345  | Ca4                                     | 29705345                      | ACCCCC/ACCCCC                                                 | CGGTAAGGTGAAGGCTGAAA      | CAAATTCGAGTGCAGATCA     | 60.2                             | 357                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_29712689  | Ca4                                     | 29712689                      | CAA/CAA                                                       | TTTGCTTACTCAAACCCCA       | AGTTCGGTAGTGGCTTCCCT    | 60.5                             | 837                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_29712921  | Ca4                                     | 29712921                      | TA/TTATATTTAA                                                 | TCATGTTGAGCAAAGC<br>CAAA  | TCAGTTCGGTAGTGGCTTCC    | 60.4                             | 406                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_29717512  | Ca4                                     | 29717512                      | GAAATAAATA/GAAATAAATAAATA                                     | GTTGGCATTCTCCACTCGT       | GTGCCCAACAACAAGGACT     | 60.1                             | 458                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_29717836  | Ca4                                     | 29717836                      | CTCACATTTTACTC/CTCACATTTTA<br>CTCATCACATTTTACTC               | AGTCCTTGTTGTTGGGCAC       | TAACAGCTCAACTGCCCTCC    | 60.0                             | 373                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_29730514  | Ca4                                     | 29730514                      | CTTTTT/CTTTTTT                                                | AAAACCTTGTTGGAAGTTTCATTTT | TGAATGTGAAGTGGATGGTCA   | 59.8                             | 247                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_29769001  | Ca4                                     | 29769001                      | CTTTTTTTTT/CTTTTTTTT                                          | CCGATGAAGAAGAAAAAGCAA     | TTGCAGTTGGATTTGTAGGG    | 59.5                             | 479                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_29769710  | Ca4                                     | 29769710                      | ATTTT/ATTT                                                    | CCCTACAAAATCCAACCTGAA     | GCTCCCAAGACAAAACCTGA    | 60.0                             | 686                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_29811970  | Ca4                                     | 29811970                      | AGGCGCGC/AGGCGCGCAGGGCGC<br>GC                                | GCGTTTTATGTTGC<br>TGGT    | ACTTTCATGAAGACACC<br>GGG | 60.0                             | 152                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29821605  | Ca4                                     | 29821605                      | CTTTTTTT/CTTTTTTT                                             | GACTCATCCAAGGTTG<br>CCAT  | TTTGATGGCTCAGAAA<br>GCCT | 59.9                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29823817  | Ca4                                     | 29823817                      | AG/AGGG                                                       | CCAAAATTGGTTGCAA<br>ACTTC | TCATGTTTTGTTGGTCT<br>GCC | 59.5                             | 233                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29826827  | Ca4                                     | 29826827                      | GTGTTGTT/GTGTT                                                | CGAACCTACGAGGCTA<br>AACG  | GGGTGTCGAAACATTC<br>CATC | 59.9                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29848231  | Ca4                                     | 29848231                      | TGAAGA/TGAAGAAGA                                              | GCATTGTTGAAACCAA<br>ACTCG | TTTGGGAGACAGACC<br>TCAC  | 60.5                             | 907                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29863037  | Ca4                                     | 29863037                      | GTTATTATTATTAT/GTTATTATTAT<br>ATTAT                           | TCGGGGTGTTACAGTA<br>TGGA  | ACATCCAAACCCCTCAT<br>TCA | 58.8                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29874025  | Ca4                                     | 29874025                      | TAAAAAA/TAAAAA                                                | GGCCCTATGCAGCGTA<br>TAAA  | ATCATCTCAGAGTCGG<br>CCC  | 60.1                             | 103                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29910860  | Ca4                                     | 29910860                      | TAAAA/TAAAAA                                                  | TATCCGCAATCAAGGG<br>AGAG  | ACAGCATTTTGTGCCAT<br>TGA | 60.2                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29911237  | Ca4                                     | 29911237                      | TATGTTGA/TATGTTGATGTTGA                                       | GTCAATGGCACAAAAT<br>GCTG  | GCAGAAGGGTGTGGA<br>AAAA  | 60.1                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29911402  | Ca4                                     | 29911402                      | CTTTTTTTTT/CTTTTTTTTT                                         | GTCAATGGCACAAAAT<br>GCTG  | GCAGAAGGGTGTGGA<br>AAAA  | 60.1                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_29911958  | Ca4                                     | 29911958                      | TAAAAAAAAA/TAAAAAAAAA                                         | TTTTTCCAACACCTTC<br>TGC  | TAGATTGAGTGCCCA<br>TCGC   | 60.1                             | 684                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29912693  | Ca4                                     | 29912693                      | GATGTC/GATGTCATGTC                                            | TGAGATCCCAACAGGC<br>CTAA | TGGTCTTTGGAAAGCC<br>TCAC  | 60.6                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29930444  | Ca4                                     | 29930444                      | CAAAAAAAAA/CAAAAAAAAAA                                        | CCGACACGGTCTTTT<br>CCTA  | AATGACCCGCAATTAT<br>GAGC  | 60.1                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29930687  | Ca4                                     | 29930687                      | TTTGATCTT/TTT                                                 | GCTCATAATTGCGGT<br>CATT  | AGGTATGGACAAAATT<br>GCGG  | 59.9                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29931076  | Ca4                                     | 29931076                      | A/AGTAACAATAAGT                                               | TGTGCACCAATATCTG<br>CCAT | GAAGAAAACCCGGGAT<br>CAGT  | 60.0                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29931458  | Ca4                                     | 29931458                      | CTTTTT/C                                                      | CCGCAATTTTGTCCATA<br>CCT | CCAAAAAGTAGGGGA<br>GAGAA  | 59.8                             | 545                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29933754  | Ca4                                     | 29933754                      | ATTTTTTT/ATTTTTTTT                                            | AGCCACACGATGTTGA<br>TTGA | TGATTAGGAATCACC<br>CGTT   | 60.1                             | 845                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29939743  | Ca4                                     | 29939743                      | CAA/CA                                                        | TCCTTTTCGAGACTCA<br>GGGA | GCACCACCTGTTTGAT<br>TTCC  | 59.9                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29943561  | Ca4                                     | 29943561                      | AATC/A                                                        | GTGAAAGGTGAGGAGA<br>AGCG | TCAACCTTTTATTTCAT<br>GCCA | 60.0                             | 131                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29945038  | Ca4                                     | 29945038                      | TA/TAA                                                        | AAATGCAATAGCAGGT<br>TGCC | CGATGAGGATAAAAGG<br>AGCG  | 60.1                             | 904                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_29957864  | Ca4                                     | 29957864                      | TAAAAAAAAA/TAAAAAAAAA                                         | AGGACTGAACGTAACC<br>CACG      | ACCTAAGTTCATTGCG<br>CCCT    | 60.0                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29962177  | Ca4                                     | 29962177                      | AC/A                                                          | CACTCCTACGTACCCC<br>CAAG      | TTTACCACCGGCTACT<br>TCG     | 59.5                             | 261                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29962305  | Ca4                                     | 29962305                      | GA/G                                                          | CACTCCTACGTACCCC<br>CAAG      | TTTACCACCGGCTACT<br>TCG     | 59.5                             | 261                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29962434  | Ca4                                     | 29962434                      | GTAT/GTATATAT                                                 | CTAGTCGAAGTAGCCG<br>GTGG      | TTTGGAAGCATTGTGG<br>TTGA    | 59.9                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29986497  | Ca4                                     | 29986497                      | GTGCGAATACATGCG/GTGCG                                         | AAAAAGGATATAAATAC<br>CCGCAA   | AAAAATCTTCTCCACAA<br>GATGAA | 58.1                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_29986966  | Ca4                                     | 29986966                      | A/AGT                                                         | CAACCACTGCGAATAC<br>ATGC      | CACCTGGAGCAGAGGT<br>GATT    | 60.1                             | 923                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30040492  | Ca4                                     | 30040492                      | TC/T                                                          | TAGCCGCGGTTAAGTG<br>AAGT      | TGGAACAAGAGAGGGA<br>TTGG    | 59.9                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30046973  | Ca4                                     | 30046973                      | GAAAAAAAAA/GAAAAAAAAA                                         | TGAATGAAATTTCTGG<br>CAGG      | CGTTTTGTTGTGGCA<br>CATT     | 58.7                             | 280                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30049126  | Ca4                                     | 30049126                      | G/GAA                                                         | TGAGGGCAACAACATA<br>TTCAA     | TTTGACCAATGTGCAAT<br>TCAA   | 58.3                             | 771                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30049460  | Ca4                                     | 30049460                      | C/CTAGT                                                       | GAGTGGGAGAGAAATG<br>TTTAGTGAA | TGACAAATCCCCTTTTC<br>CAA    | 60.1                             | 233                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_30052378  | Ca4                                     | 30052378                      | TG/T                                                          | TAAGCACAAATGACGT<br>TGGG | TCCATTGGGTATTGAG<br>CACA   | 59.6                             | 963                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30072648  | Ca4                                     | 30072648                      | TAAAAAAA/TAAAAAAA                                             | TTTTCATGTTTCCGCAT<br>TCA | CGGGGTGAGTTAAATG<br>TACGA  | 60.1                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30075059  | Ca4                                     | 30075059                      | CTAA/CTAATTGTTTTATAA                                          | TCGAAACCAACCACCT<br>TTTC | GCAATTCGACAATGCA<br>CAAC   | 59.9                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30076786  | Ca4                                     | 30076786                      | GTTTTTTTT/GTTTTTTTTT                                          | GCACTTCGCTAAAAG<br>CATC  | AAGCGCTCCCAAATAT<br>GCTA   | 60.0                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30077034  | Ca4                                     | 30077034                      | TAAATTAATAATTAAT/TAAATTAAT<br>ATTAAATTAATAAT                  | GCATATTTGGGAGCGC<br>TTTA | TGGATGATTGTGACAA<br>AATTGC | 60.2                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30077287  | Ca4                                     | 30077287                      | CTTTTTTT/CTTTTTTTTT                                           | GCATATTTGGGAGCGC<br>TTTA | TGGATGATTGTGACAA<br>AATTGC | 60.2                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30081791  | Ca4                                     | 30081791                      | CCTT/CCTTTCTT                                                 | TTGTCGTTGCAATGGT<br>TCAT | TTACAAAAAGGGGGTG<br>AAAG   | 60.0                             | 467                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30083166  | Ca4                                     | 30083166                      | ATTTTTTTTTTT/ATTTTTTTTTT                                      | AACGGAGGAACAAACC<br>AGAA | CAACCTCGATCTCGAC<br>CAAT   | 59.6                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30084699  | Ca4                                     | 30084699                      | GTTTTTTTTT/GTTTTTTTTT                                         | CGAAATTTGTAGCCG<br>GAAA  | AAGTTGATTGTGGTG<br>GTCA    | 60.1                             | 277                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30086898  | Ca4                                     | 30086898                      | ACTTTCT/ACT                                                   | ACGCCGAAAAACACTT<br>TCAC | TCCATTGCACTGTCCTT<br>CAA   | 60.2                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_30092930  | Ca4                                     | 30092930                      | GTTTTT/GTTTTTTT                                               | GATGCGACCATCTACT<br>GCAA     | TGATGTGTCCCTAATAT<br>TTTCCG | 59.8                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30098960  | Ca4                                     | 30098960                      | ATTTTTTTT/ATTTTTTTT                                           | TGGCGAATCGTTGATC<br>ATAA     | ATATGGCTTGAAGCAA<br>ACGC    | 60.0                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30102122  | Ca4                                     | 30102122                      | CTCTCCAAT/CTCTCCAATTCTTC<br>CAAT                              | TGATTCTTCAATTGCCA<br>CCA     | ACGAGAGACAAGTGAG<br>GGGA    | 60.0                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30102440  | Ca4                                     | 30102440                      | TG/T                                                          | TCCCCTCACTTGCTC<br>TCGT      | GTGTTTGGGATTGGGA<br>AATG    | 59.8                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30102999  | Ca4                                     | 30102999                      | CC/CCCCTC                                                     | ATTTCCAATCCCAAC<br>ACA       | ATCCTTGCTAGCCACG<br>AAAA    | 60.0                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30114713  | Ca4                                     | 30114713                      | TAAAAAAA/TAAAAAAA                                             | GCTCAAGTTATAGCCT<br>ACAAAGGG | CAGTTTTGGTCAATCG<br>CTCA    | 59.7                             | 974                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30116632  | Ca4                                     | 30116632                      | ATTTTTTTTT/ATTTTTTTT                                          | GATCACGCCAGTTGTT<br>GGTA     | TGTCGATTGCGAAGAG<br>TTGT    | 59.6                             | 896                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30118773  | Ca4                                     | 30118773                      | TG/TGG                                                        | CTCCTTCATTCCTCCC<br>TCC      | AAGGTGGGTAAAGAA<br>CCGC     | 60.0                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30120661  | Ca4                                     | 30120661                      | TAAAA/TAAA                                                    | TTTGACATCCATCTTAT<br>GCAGC   | CCCTTGGGTGCGTTAG<br>TTAT    | 60.1                             | 379                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30122538  | Ca4                                     | 30122538                      | ATT/AT                                                        | ATGTCAATGGGCCACT<br>TAGC     | TTGTTTGTGTGCTTTG<br>ACCA    | 60.0                             | 764                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                   | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                 |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_30131966  | Ca4                                     | 30131966                      | CTT/CTTT                                                                                                                                        | TCATGTACGCACTGAT<br>GGAAA  | CTCTTTAAGACGTTTCG<br>CGG   | 60.1                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30138209  | Ca4                                     | 30138209                      | CAAAAAA/CAAAAAA                                                                                                                                 | GCATGCAACATGGCT<br>CTAA    | CAAATTTGGTTGGGTC<br>TTGG   | 59.8                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30142911  | Ca4                                     | 30142911                      | C/CTTG                                                                                                                                          | TGATGCATTGATGTTG<br>TCAAAG | AAAGGAAAGGGGACGT<br>GTCT   | 59.6                             | 701                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30172032  | Ca4                                     | 30172032                      | G/GA                                                                                                                                            | CTCAACAGCCTTATGT<br>GCGA   | GCATGGAGACTCAAAA<br>ATCCA  | 60.0                             | 673                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30172265  | Ca4                                     | 30172265                      | TC/T                                                                                                                                            | CTCAACAGCCTTATGT<br>GCGA   | TGCGATGGAATAATGT<br>GTCG   | 60.0                             | 752                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_3017713   | Ca4                                     | 3017713                       | ATTATTTTAAATTTATTTTAAATTTAT<br>TTTAAATTTATTTTAAATTTATTTTAA<br>ATT/ATTATTTTAAATTTATTTTAAAT<br>TTATTTTAAATTTATTTTAAATTTATT<br>TTAAATTTATTTTAAATTT | GACAAATTAGTGGGGC<br>AACC   | TTGTATTGTTGGTGAG<br>GCCA   | 59.3                             | 902                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30184775  | Ca4                                     | 30184775                      | TG/T                                                                                                                                            | ACAACGGAACAAATC<br>TCGC    | GGGGGTTAGGAGTAAG<br>AAAGGA | 60.1                             | 116                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30196665  | Ca4                                     | 30196665                      | CTTTTT/CTTTT                                                                                                                                    | TCAAACCATGATTTTGG<br>TGC   | TGGATGGGAAAAAGGA<br>CAAG   | 59.4                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30197320  | Ca4                                     | 30197320                      | CAAAAA/CAAAAA                                                                                                                                   | CTTGTCTTTTTTCCCAT<br>CCA   | GGCCTAATTAAACATG<br>GGCA   | 59.9                             | 793                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30211443  | Ca4                                     | 30211443                      | T/TA                                                                                                                                            | ACATCAAACAACAGC<br>GCAC    | CCGCTAAATTGCCCA<br>ATAA    | 59.8                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_30212032  | Ca4                                     | 30212032                      | ATGCATTGCAT/ATGCAT                                            | TTATTGGGCAATTTAG<br>CGG    | AGCTTTGTGGCAAGA<br>CACT   | 59.9                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30225198  | Ca4                                     | 30225198                      | T/TC                                                          | AGGCAAACAAGAACCG<br>AAAA   | ATGTGCTTTTAGCACCA<br>GGG  | 59.7                             | 424                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30237136  | Ca4                                     | 30237136                      | GTTTTTTTTTTT/GTTTTTTTTTTT                                     | CGGGAGTATTTGGTC<br>ACTTT   | CCTCTTGTTGCTTCCTC<br>TGG  | 58.1                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30240512  | Ca4                                     | 30240512                      | ATTTTTTTTTT/ATTTTTTTTTT                                       | TTGGGCATTTTGATGA<br>TTGA   | GACAACCGATTGAGCC<br>TGAT  | 59.9                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30252991  | Ca4                                     | 30252991                      | TAAAAAAAAAAAAA/TAAAAATAAAAA<br>AAAAAAAAAAAA                   | GGGCAGCGAACTTAGT<br>CAAG   | CGGTGGAAGTTTCG<br>GATA    | 60.0                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30266952  | Ca4                                     | 30266952                      | CAAAAAAAAA/CAAAAAAAAAAAAA                                     | ATTTTTCCTTCTTGCGG<br>GTT   | GTTGAGGATGTCCAGG<br>AGGA  | 59.9                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30327391  | Ca4                                     | 30327391                      | ATTTTTTT/ATTTTTTTTT                                           | CTCACGACTAAGGGTG<br>GGAA   | TTTTTCCTTCTTGGGC<br>TCT   | 60.1                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30337279  | Ca4                                     | 30337279                      | ATTTTTTTTTT/ATTTTTTTTTTT                                      | CGAACTTAAATCCTTG<br>CACGA  | TTTTGGTCCTCCAAACA<br>AAAT | 60.3                             | 726                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30351459  | Ca4                                     | 30351459                      | CTTTTTTT/CTTTTTTTTT                                           | TCTTTGAAACACATCAC<br>TTTCG | AAAATTGATCGGTGG<br>TGGA   | 57.9                             | 314                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30373191  | Ca4                                     | 30373191                      | AATATATATATATAT/AATATATATAT<br>ATATATATAT                     | ATTGGAGCAGTGGGGT<br>ACAG   | ATATCGCTGTGCCTTTC<br>CAC  | 60.0                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_30383364  | Ca4                                     | 30383364                      | CAAAAAAAAAAAAA/CAAAAAAAAAA<br>A                               | CGGCAAGACATTTAC<br>GACA  | TCAAGTGGTGGATTGT<br>TGGA | 59.7                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30404870  | Ca4                                     | 30404870                      | AATAACAT/AAT                                                  | TTAACTGTTGGTGCGC<br>AGTC | CGTCACATTTAACACG<br>CCAT | 59.9                             | 798                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30408440  | Ca4                                     | 30408440                      | TAAAA/TAAA                                                    | TGCCTACGTCGTGGGA<br>TTAT | TCATCAAATCCGTAACG<br>CAA | 60.4                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30408471  | Ca4                                     | 30408471                      | TAAAAAAA/TAAAAAAA                                             | TGCCTACGTCGTGGGA<br>TTAT | TCATCAAATCCGTAACG<br>CAA | 60.4                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30408624  | Ca4                                     | 30408624                      | TC/T                                                          | TGCCTACGTCGTGGGA<br>TTAT | TCATCAAATCCGTAACG<br>CAA | 60.4                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30408872  | Ca4                                     | 30408872                      | AA/AAAAGA                                                     | TTGCGTTACGGATTTG<br>ATGA | AGACTTTCGACCGACG<br>CTAA | 60.1                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30426524  | Ca4                                     | 30426524                      | AC/ACC                                                        | TCGTTCAACCTCCCAA<br>TTTC | TTGCACCCATGTTAAC<br>CAAA | 59.9                             | 317                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30429188  | Ca4                                     | 30429188                      | T/TGA                                                         | TGATCGCCATATCCTTA<br>GCC | GTACCGCATGAGCAAT<br>TGTG | 60.0                             | 315                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30433017  | Ca4                                     | 30433017                      | CAAAAA/CAAAAA                                                 | GACTGACATTCGATG<br>AGCA  | TGCAACACGATAAGGG<br>AACA | 59.8                             | 721                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30445654  | Ca4                                     | 30445654                      | CTATATATATATATA/CTATATATATA<br>TA                             | AGGTCAGGTCAGGCTT<br>TGAA | TGCACTCACTCCAACA<br>AACA | 59.8                             | 802                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_30445761  | Ca4                                     | 30445761                      | GTATATATATATATAT/GTATATATAT<br>ATAT                           | AGGTCAGGTCAGGCTT<br>TGAA  | TTTCCATTGCACTCACT<br>CCA   | 59.8                             | 809                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30452386  | Ca4                                     | 30452386                      | ATTTTTTT/ATTTTTTTT                                            | TGAAGCAGATACCCAG<br>ACGA  | TGCTATTGTTGTTGATG<br>ATGGA | 59.4                             | 705                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30453970  | Ca4                                     | 30453970                      | TAAAA/TAAGTACTTTAAAAA                                         | GTGTTGCGGATATCTG<br>GGTT  | ATTCTATCACACAGCG<br>CACG   | 60.0                             | 545                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30456018  | Ca4                                     | 30456018                      | AT/A                                                          | GGCGAGAAAAGTTTGT<br>TGATG | TCGTTGATTTCAACCA<br>CCA    | 59.7                             | 377                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30458112  | Ca4                                     | 30458112                      | C/CCTT                                                        | CAGGCAATGGGACATG<br>ACTT  | AAGATTCGCTTTGATAC<br>GTGG  | 60.9                             | 830                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30459877  | Ca4                                     | 30459877                      | GTTTTTTTTTTT/GTTTTTTTTTTT                                     | AAACCCTTTGCAACCA<br>ATGA  | TGCCTGTTGAAATTGTT<br>GGA   | 60.3                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30463898  | Ca4                                     | 30463898                      | ATTTTTTTTT/ATTTTTTTT                                          | GGGGGAAAAGTGATAA<br>TGGG  | AATGGCATGCAAAAC<br>ATCA    | 60.4                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30464438  | Ca4                                     | 30464438                      | CTTTTTTT/CTTTTTT                                              | TGTGTTAGTGCGACCC<br>ACAT  | TGTGAAGGGAGTGAGT<br>TGCTT  | 60.0                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30464759  | Ca4                                     | 30464759                      | GACAACAACAA/GACAACA                                           | TGATGTTTTGCATGC<br>CATT   | TTGGATCATCACACTC<br>CAACA  | 59.9                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30470866  | Ca4                                     | 30470866                      | GAT/GATAT                                                     | GGCTTCGTTCAAAGTG<br>GTTT  | ACGCACCTCTTACCAC<br>ATCC   | 59.2                             | 786                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_30496363  | Ca4                                     | 30496363                      | CTTTTTTTTT/CTTTTTTTTT                                         | TCTCTGGCAACCGTTC<br>TTCT     | GACTCACTCCCCAAGT<br>GGAA   | 60.0                             | 177                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30497066  | Ca4                                     | 30497066                      | GAAAAA/GAAAAAA                                                | AACATGTTGGCGAGAA<br>CCTT     | TCCCAATGTGGAGGTC<br>TTTC   | 59.6                             | 189                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_3049939   | Ca4                                     | 3049939                       | CATATATATATATATA/CATATATATA<br>TATATATA                       | GCCGAATGGACCAAC<br>ATAC      | GGCAACAAAATAGAAT<br>CGGG   | 60.2                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30535832  | Ca4                                     | 30535832                      | TATAAATAAATAAATAAATAAATA<br>AATAAATAAATAAATAAATAA             | CCATTGAGAATTAGAAA<br>ATCACCA | CCAAATTTCCAAGGG<br>TTCT    | 59.4                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30552355  | Ca4                                     | 30552355                      | TG/T                                                          | TGTCGCATGCAACCTC<br>TTAG     | ACCTGTGTGTTCCCTT<br>CCAC   | 60.0                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30552695  | Ca4                                     | 30552695                      | ATTTTTTT/ATTTTTTTTT                                           | CCAATTGAGAAGGGAA<br>TGGA     | AATGACCCAACAAAATT<br>GCC   | 59.9                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30560828  | Ca4                                     | 30560828                      | T/TC                                                          | CAGATTGTTCTTCCTC<br>CCCA     | CCACATCATCTCCAAC<br>CAAA   | 60.0                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30570798  | Ca4                                     | 30570798                      | TAAAAAA/TAAAAAAA                                              | TGCTTCTCAATGACTAA<br>CACCAA  | TGTTGGTGTGACTTTTC<br>CTTCT | 59.8                             | 881                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30582999  | Ca4                                     | 30582999                      | AC/ACC                                                        | GGAGGGATGCAATATT<br>AAGCA    | ATTCATAGACGCACC<br>CGAG    | 59.0                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30585117  | Ca4                                     | 30585117                      | CT/CTTT                                                       | GCAATGAATGTGCCTT<br>CCAA     | TGTTGGGATGACTGA<br>CCTTT   | 59.5                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_30585901  | Ca4                                     | 30585901                      | CTTTTCTAATTTTCTA/CTTTTCT<br>A                                 | AAAGGTCAGTCATCCC<br>AAACA  | GAAACAGAAAACGGGA<br>ACCA  | 59.4                             | 381                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30605971  | Ca4                                     | 30605971                      | AATATATATATATATATAT/AAAT<br>ATATATATATATATATATATATA<br>TAT    | TCCGACATCACACACC<br>AAAC   | TCGGTGTTAAAAATCG<br>GAGTG | 60.4                             | 850                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30619694  | Ca4                                     | 30619694                      | CAAAAA/CAAAA                                                  | ACTCACTCTGCCCTG<br>TGTT    | CCAACTTGGTCCAAC<br>AAAAA  | 59.8                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30620479  | Ca4                                     | 30620479                      | GTTATTATTATTAT/GTTATTAT<br>ATTAT                              | GCCTGAAGAAGATGAT<br>CAACAA | CTAGGGTTGTCAGGAT<br>GGGA  | 59.3                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30621604  | Ca4                                     | 30621604                      | ATTTTTTTTTT/ATTTTTTTTTT                                       | TGGGCTTCAATTTAGT<br>CCTTG  | CTGATGACAAAAGGGG<br>GAGA  | 59.2                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30628637  | Ca4                                     | 30628637                      | ATTCTGGTTCTG/ATTCTG                                           | ATCGGGTTTGTCTGAT<br>GGTG   | ACAAACCAAGACCCAA<br>CCAG  | 60.8                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30641293  | Ca4                                     | 30641293                      | CTGTTT/CT                                                     | TGCATTTTGGTGCATT<br>TGT    | TGTGTGCAGTGCTGCT<br>ATGA  | 60.0                             | 171                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_3065355   | Ca4                                     | 3065355                       | CATA/CATATA                                                   | ACAAAGGTCACCCTCG<br>TCAC   | CCAAACTGGGGAAAA<br>ACAA   | 60.0                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30662877  | Ca4                                     | 30662877                      | CTTTTTTTTTT/CTTTTTTTTTT                                       | TCGACATGTTGCATCA<br>CTCA   | TCGCCGCCAATTTATT<br>TTA   | 59.8                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30684801  | Ca4                                     | 30684801                      | GGT/GGTGT                                                     | TGTTAGGGATTGTGTG<br>GGGT   | GAAGTTGGGGATGAGG<br>ACAA  | 60.1                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                 | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_30687261  | Ca4                                     | 30687261                      | TA/TATCA                                                                                                                      | TCATCATTATAGCTTG<br>GGCT    | AAATTTCCCAAGCAAAA<br>GGG  | 59.7                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30690853  | Ca4                                     | 30690853                      | TAAAAAAAA/TAAAAAAAAA                                                                                                          | GAAACGAGTTGTTGCA<br>CTTGA   | TTGAGTTGCACGAGAA<br>TTGC  | 59.0                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30715317  | Ca4                                     | 30715317                      | AAT/AATTAT                                                                                                                    | CCACTTCAAGCAATCG<br>TTCA    | TTTGCTTCGAGCACAT<br>GATT  | 59.8                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30723844  | Ca4                                     | 30723844                      | CTAATTAA/CTAA                                                                                                                 | TGCTCATGAAGTAGCA<br>AAATTGA | TCATCTTTGGCATGAG<br>AATCA | 59.9                             | 837                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30730238  | Ca4                                     | 30730238                      | ATTGTGAAA/ATTGTGAACTTTTTG<br>TGAAA                                                                                            | TGTGGATTTTCAAGGT<br>TCTCG   | TCGAAAAAGCGGGATG<br>TTAC  | 60.1                             | 667                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_307324    | Ca4                                     | 307324                        | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTA/ATATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTA | TATGGAACCCCATTC<br>TTCA     | GTTGATGCATGCCCTA<br>AACA  | 60.1                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30773724  | Ca4                                     | 30773724                      | A/AT                                                                                                                          | ATCCGATTGGACGGTT<br>CATA    | GCAAAATCAATTTATGC<br>TGGA | 60.2                             | 855                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30775212  | Ca4                                     | 30775212                      | CTTTTTTTTT/CTTTTTTTTT                                                                                                         | TGAACTCGTAACATAA<br>GCCCAA  | TGGGAATGCTTTCTTAT<br>GGG  | 59.6                             | 931                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30783657  | Ca4                                     | 30783657                      | TTT/TTTATT                                                                                                                    | GCCAATAATTAGGGG<br>CTTG     | GGATGGTAAGTCATT<br>AGAGCG | 60.6                             | 905                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30790861  | Ca4                                     | 30790861                      | TAAAAAAAA/TAAAAAAAAA                                                                                                          | GAATTTTGGCCATCAC<br>CACT    | TGTCTCGCACACCCAT<br>TTTA  | 59.8                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_30955630  | Ca4                                     | 30955630                      | TAAAAAAAAA/TAAAAAAAAA                                         | CAAAGCCATGTTTCTT<br>CCA    | TGAGCAAATGAGGCAA<br>AATG    | 58.7                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30956675  | Ca4                                     | 30956675                      | CAATTTT/CAATTTTAAATTTT                                        | TTGTTGGTGAAATTTC<br>GGT    | AGTGCATCGTTTCCTT<br>GCTT    | 60.2                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30957181  | Ca4                                     | 30957181                      | CAAAAAAAAA/CAAAAAAAAA                                         | AAGCAAGGAAACGATG<br>CACT   | AGTTCCAATGTCACTTT<br>CAATCA | 59.9                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30957575  | Ca4                                     | 30957575                      | AC/A                                                          | AAGCAAGGAAACGATG<br>CACT   | CCAATCAACTGGTGTT<br>GCTG    | 59.9                             | 854                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30958639  | Ca4                                     | 30958639                      | GAAAAAA/GAAAAAA                                               | GCCAAACCAACTCATT<br>CTTACA | CCCATCATAAATCTTC<br>AAAACAA | 59.1                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_30965662  | Ca4                                     | 30965662                      | GCAAAAAATCAAA/GCAAAAAATCAA<br>AAAATCAAA                       | ATTGGCTCGTTGATCC<br>ATCT   | TTGCCTTCTTGTTTTG<br>AATTG   | 59.5                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31001884  | Ca4                                     | 31001884                      | GAAAAAA/GAAAAAA                                               | GCTGTTGAAAGATGCA<br>ACCA   | CCTTGCTCCTTGTTG<br>CTCC     | 59.8                             | 395                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31016017  | Ca4                                     | 31016017                      | AG/A                                                          | TCAACCCTGATTCGAC<br>CTTC   | TGAACCAAACTCACG<br>CAAG     | 60.1                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31023487  | Ca4                                     | 31023487                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA<br>AA                           | GGAATCCAGACTTTC<br>ACCA    | TTGCACAATCAATGG<br>CAAG     | 59.9                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31055489  | Ca4                                     | 31055489                      | TT/TTCAT                                                      | CATGCACAAC TTGTT<br>AATGG  | TGTAATTGGTGGCGTT<br>TGAA    | 59.0                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_31055592  | Ca4                                     | 31055592                      | TAAAAACAAAAACAAAA/TAAAAAC<br>AAAAACAAAAACAAAA                 | CATGCACAAC TTGGT<br>AATGG  | TGTAATTGGTGGCGTT<br>TGAA | 59.0                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31101573  | Ca4                                     | 31101573                      | TGTCATTCCC/T                                                  | AATCGGACAAGAAACC<br>GATCT  | AGTTGTGACCCTCCGA<br>TACG | 60.0                             | 260                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31106310  | Ca4                                     | 31106310                      | CTTTTTTTTTTT/CTTTTTTTTTT                                      | ATAAGAGTGTGGCGGT<br>TTGG   | TGGTTGAAATGGACGA<br>CAAA | 60.0                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31106521  | Ca4                                     | 31106521                      | CCTT/CCTTCTT                                                  | ATAAGAGTGTGGCGGT<br>TTGG   | TGGTTGAAATGGACGA<br>CAAA | 60.0                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31107634  | Ca4                                     | 31107634                      | GTTTT/GTTTTT                                                  | GCCTGATTTCTTGTT<br>GAGC    | GGGACTGAATCCGACT<br>TGAA | 59.8                             | 394                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31113293  | Ca4                                     | 31113293                      | AT/ATT                                                        | AATGTGTTTAACGGGC<br>AAGC   | AGGGGGACTACTTTTG<br>CGAT | 60.0                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31114996  | Ca4                                     | 31114996                      | CT/CTGT                                                       | CTTCTTCAAGTCGGTG<br>GCTC   | TTTGCAAGTCTGGAAT<br>ACCC | 60.0                             | 213                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31116686  | Ca4                                     | 31116686                      | GC/GCC                                                        | CAATCTTGGCAGGATC<br>CACT   | TAAACAGTCAGGCA<br>ACCC   | 60.1                             | 709                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31128772  | Ca4                                     | 31128772                      | GATA/GATACATA                                                 | CAACCTACGTTCTCGT<br>GTTTGT | TCTTTAAATGCGGGGA<br>TGTT | 59.2                             | 619                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31129446  | Ca4                                     | 31129446                      | ATTTTTTTT/ATTTTTTTTTT                                         | TGGGTATCCAAACCAT<br>ATCCA  | TGATTCACGTGGATGG<br>AGAA | 59.9                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_31150025  | Ca4                                     | 31150025                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                     | TGAACGAAAAGCTTAT<br>GGATATGT | AATCGACCCAATCAAG<br>AACG   | 59.1                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31172721  | Ca4                                     | 31172721                      | TG/TGG                                                        | TCTTTGGATGGGTTCC<br>ATGT     | TTACACCAATTCCCCA<br>AGA    | 60.2                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31172943  | Ca4                                     | 31172943                      | TA/T                                                          | TCGCCTAAGGTAAGGG<br>CTTT     | TTACACCAATTCCCCA<br>AGA    | 60.2                             | 421                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31192815  | Ca4                                     | 31192815                      | TGG/TG                                                        | TTGAAGGAGAAGCCAG<br>AGTCA    | TGAGGCATGCAGAAAC<br>GTAG   | 60.1                             | 238                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31220879  | Ca4                                     | 31220879                      | G/GTTAA                                                       | GCCACATAGTTCCAAC<br>CTTCA    | TTGTGAAATTCTGCCAC<br>GAG   | 60.0                             | 228                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31221206  | Ca4                                     | 31221206                      | TAAAAAA/TAAAAAA                                               | CTCGTGGCAGAATTC<br>ACAA      | CAGGTACAAAACCCCG<br>TCAC   | 59.8                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31235171  | Ca4                                     | 31235171                      | GTATATATATAT/GTATATATATAT<br>AT                               | GCCACCCTTAGGAGGA<br>AAAG     | ATTTAAATGTCGTGACC<br>GGC   | 60.1                             | 607                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31250934  | Ca4                                     | 31250934                      | ATT/ATTTT                                                     | AGTTTTCGCCATTGTG<br>ACC      | AACCACTTGAGCATGG<br>GTTC   | 60.0                             | 196                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31251511  | Ca4                                     | 31251511                      | GTTTTTTT/GTTTTTTT                                             | AACCCATGCTCAAGT<br>GTTC      | CAAGCGCATTGTCCC<br>TTAT    | 60.0                             | 894                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31270910  | Ca4                                     | 31270910                      | GTTTTTTTTT/GTTTTTTTTT                                         | TGCATTCCTTTAAATT<br>CCTTGT   | TTTGAGAAACATGCATC<br>AAGAA | 59.1                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_31284485  | Ca4                                     | 31284485                      | ATT/ATTT                                                      | ATGGCTACTCCAATGC<br>ATCC   | ACATGGCTCCCCCTTA<br>CTCT   | 59.9                             | 962                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31316566  | Ca4                                     | 31316566                      | GAAA/GAA                                                      | CATTGTTTTGCTGTTGT<br>GGG   | CCTCACGAGCTGCTTT<br>AACC   | 60.0                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31322872  | Ca4                                     | 31322872                      | GAAAAAAAA/GAAAAAAAA                                           | CTCCTAAGGGTGGCCT<br>TTTC   | GGGTTGTTCTTGACC<br>TTCA    | 60.1                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31332105  | Ca4                                     | 31332105                      | ATTTT/ATTT                                                    | GCACATGTGTGGTTG<br>ACTC    | TTGAACCAACATGATCC<br>AATTC | 60.0                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31334123  | Ca4                                     | 31334123                      | CTTTGT/CTTTGTTTGT                                             | TGCTCTCCCACTGAGA<br>GTCAT  | AAGGTTGTTGCCACTA<br>TCGG   | 60.0                             | 214                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31392404  | Ca4                                     | 31392404                      | AT/A                                                          | CTCAATCGAACCCCTC<br>CAAA   | AAGCCAGGTGGTTGTT<br>TGAC   | 60.0                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31414937  | Ca4                                     | 31414937                      | GTTTTTTT/GTTTTTTT                                             | GGAATACCGCATGCAA<br>ATCT   | TGGTATCGGGAGAGAG<br>GAGA   | 59.9                             | 847                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31445256  | Ca4                                     | 31445256                      | ATT/ATTT                                                      | AGATCTATGCATCGGC<br>AACC   | AGGGTACTACAGCTGC<br>CCCT   | 60.1                             | 338                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31453756  | Ca4                                     | 31453756                      | G/GC                                                          | CGCTAAATTCATCTCAT<br>GTTGG | CCCTTTGGAGCAATAA<br>TTTGA  | 59.6                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31463756  | Ca4                                     | 31463756                      | CTTTTTTT/CTTTTTTTT                                            | GGCTCCTTGCATCAGT<br>TAGC   | GAAAACCGATTAGGGA<br>TTCG   | 60.0                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                              | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                            |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_31514043  | Ca4                                     | 31514043                      | CAAAAAAAAA/CAAAAAAAAA                                                                                                      | AGCCAAAGCAGGTTGG<br>TTTA   | ACCAATCCGAAGACGA<br>TCAC | 59.7                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31523716  | Ca4                                     | 31523716                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAA/A<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAA | GAAACTCTCACAAAGGG<br>TGGC  | TGGCTTTAGGAACCGT<br>GTTT | 59.7                             | 832                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31528243  | Ca4                                     | 31528243                      | GACACCTATTATAACAC/GACACCT<br>ATTATAAACACCTATTATAACAC                                                                       | ATCCAATCCTTGCTCA<br>CGAT   | TCTGCTTCCGTCAAC<br>CTTT  | 59.5                             | 396                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31534458  | Ca4                                     | 31534458                      | CAAAAAA/CAAAAAA                                                                                                            | CAAGCCAACGTGTGT<br>TGTT    | TGTGGGGATCAAAT<br>GTTT   | 59.7                             | 371                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31549191  | Ca4                                     | 31549191                      | TAAAAAA/TAAAAA                                                                                                             | TGTTTTATGAATGGTC<br>AGGGA  | CCAAACTGCAATTGAA<br>AGGA | 59.3                             | 884                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31558178  | Ca4                                     | 31558178                      | GTT/GT                                                                                                                     | CCCTAATTTGTGTGAA<br>GCATGA | TATCACTTCGACCCGT<br>ACCC | 60.0                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31560045  | Ca4                                     | 31560045                      | ATTTTTTTTT/ATTTTTTTT                                                                                                       | GGATATCCCACTGCAA<br>GGAA   | AACCTGTATTCCACAA<br>GCG  | 59.9                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31611840  | Ca4                                     | 31611840                      | GTTTTTTTTT/GTTTTTTTTTTT                                                                                                    | CGTTTTCAGCTGAGCA<br>AATTC  | TTGATCCATTGGGATT<br>GTGA | 60.0                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31611867  | Ca4                                     | 31611867                      | AAT/AATAT                                                                                                                  | CGTTTTCAGCTGAGCA<br>AATTC  | TTGATCCATTGGGATT<br>GTGA | 60.0                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31612473  | Ca4                                     | 31612473                      | TAAAAAA/TAAAAA                                                                                                             | TAAATCCAAACCGC<br>AAGC     | CACTTAAGCAAACGGG<br>GTGT | 60.1                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                         | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                       |                          |                            |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_31620059  | Ca4                                     | 31620059                      | ATTTTTTT/ATTTTTTTT                                                                                    | TATGAATTGGGTGGGG<br>AATC | TGATCTTCTGGGAAGT<br>ATTCAA | 59.4                             | 578                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_31629266  | Ca4                                     | 31629266                      | TAAAAAAAA/TAAAAAAAA                                                                                   | ATGCGTGCTCGCTTCT<br>TTAC | CCCAAAGATATTCCAG<br>GCAA   | 60.6                             | 712                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_31632708  | Ca4                                     | 31632708                      | ATTTTTTT/ATTTTTTTT                                                                                    | AATTGCTCCTTCATCAA<br>CCG | TGGTATGTGGTTGCAG<br>CATT   | 60.1                             | 502                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_31634027  | Ca4                                     | 31634027                      | CAA/CAA                                                                                               | CACTTGGCTTGGAGGA<br>GAAG | TTCCACCAAGTGTGA<br>GTGA    | 60.0                             | 315                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_31636819  | Ca4                                     | 31636819                      | CAA/CAA                                                                                               | TCTCAACATCTCGTAG<br>CGCA | TTCATGATTCATTGGGT<br>CATCT | 60.7                             | 771                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_31639620  | Ca4                                     | 31639620                      | GTTTT/GTTTTT                                                                                          | ATTTGGAGAATGATTT<br>GGCG | GTGTTTGGTTCAAGGG<br>GAGA   | 59.9                             | 412                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_31640017  | Ca4                                     | 31640017                      | AATCACTCATATAT/AATCACTCATA<br>TATATCACTCATATAT                                                        | TGATTTGGCGATTGTT<br>TTGA | CTAGATGTCTCCAGAC<br>GCCC   | 60.1                             | 617                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_31714419  | Ca4                                     | 31714419                      | ATTTTTTTTTT/ATTTTTTTTTT                                                                               | CAAAGAGAGAGTGGGC<br>AAGG | TGAGTCCCAAACTCA<br>AGGAA   | 60.0                             | 883                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_31752393  | Ca4                                     | 31752393                      | TC/T                                                                                                  | GGTAACCAATCCGAAG<br>ACGA | GACCAAGTCGGGAAAA<br>CAAA   | 59.9                             | 351                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_31753116  | Ca4                                     | 31753116                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATA | TTTCATCAAATTCGTCA<br>CGC | AGCCATATGTTGTGTG<br>CCAA   | 59.7                             | 673                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                             |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_31763705  | Ca4                                     | 31763705                      | TAAAAAAAAA/TAAAAAAAAA                                                       | TGCGAGCATGAGAATT<br>TGTT   | TTTGATAAACATGATT<br>TCCCTCA | 59.4                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31806633  | Ca4                                     | 31806633                      | ATGTGACTAATTTT/ATGTGACTAAT<br>TTTGTGACTAATTTT                               | ACAAAAGCCTGGATAG<br>CGAA   | TCACATATACCCTTAAA<br>ATCGCA | 59.8                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31822803  | Ca4                                     | 31822803                      | ATTTTTTT/ATTTTTTTT                                                          | CACAGATTTCTCGAGG<br>CACA   | TCTAAAGCTCATGTCC<br>CGCT    | 60.0                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31837452  | Ca4                                     | 31837452                      | ATTTTTTTT/ATTTTTTTTT                                                        | TGGAGACCATGGAAT<br>GCTT    | TTTTGTGAATAGTCCAT<br>GCTTCA | 60.5                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31852769  | Ca4                                     | 31852769                      | TAAAAAAAAA/TAAAAAAAAA                                                       | TTTGTCATGGCGAAAC<br>AAAC   | GGTTTGTCTTTGCACC<br>CATT    | 59.6                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31859597  | Ca4                                     | 31859597                      | TAAAAAAAAA/TAAAAAAAAA                                                       | GTTGGAGCCCCACTT<br>TATT    | TGCAAGCAGCATCAGA<br>GAAC    | 60.2                             | 793                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31873869  | Ca4                                     | 31873869                      | TTATATATATATATATATATATATAT<br>T/TTATATATATATATATATAT                        | CCCTGTTCAATTCATCC<br>TTTTT | TCCCTTCAGTTCTTGGA<br>TGC    | 59.4                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31885649  | Ca4                                     | 31885649                      | TTA/TTATAGTA                                                                | GTGATTGATTGGGAT<br>TGGG    | TTGGTTGTTGGAATG<br>CAAA     | 60.0                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31886261  | Ca4                                     | 31886261                      | TTTAAATTTAAATTTAAATTTAAAT<br>TAAAT/TTTAAATTTAAATTTAAAT<br>TAAATTTAAATTTAAAT | TGCATTTCCAACAACC<br>AAGA   | TGGAGATCCCAATAG<br>ACCA     | 60.1                             | 964                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31886599  | Ca4                                     | 31886599                      | CATTAT/CATTATTAT                                                            | AGCTAGTTGCATAGCG<br>AGGG   | TGGAGATCCCAATAG<br>ACCA     | 59.6                             | 210                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_31892250  | Ca4                                     | 31892250                      | CTTTTTTTT/CTTTTTTTTT                                          | AACCGTTAACCACCGA<br>AACA      | TGCGGTCAACACACTT<br>AGGA  | 60.3                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31892313  | Ca4                                     | 31892313                      | TTTTCTT/TTT                                                   | AACCGTTAACCACCGA<br>AACA      | TGCGGTCAACACACTT<br>AGGA  | 60.3                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31916653  | Ca4                                     | 31916653                      | AATTACATTACATTACA/AATTACATT<br>ACA                            | GGTGATGAGGGAGAAA<br>CACC      | CAGGTCTGAAGGTTTCA<br>TGGT | 59.4                             | 945                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31918515  | Ca4                                     | 31918515                      | ATTTTTTTTT/ATTTTTTTT                                          | ATTCCACATGAACTTC<br>CGC       | GAAAGTAGGGGTGG<br>GAAAC   | 59.9                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31948251  | Ca4                                     | 31948251                      | AAAA/AAAAATAAA                                                | AAATGCATATATTAAT<br>TCATCCCAA | CTGCATGTGCAATTGT<br>GTCA  | 59.0                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31973044  | Ca4                                     | 31973044                      | GTTTTTTTT/GTTTTTTT                                            | ATGTCCTATGCTGCTG<br>GACC      | AAACAACCGTGCTATT<br>AGCCT | 60.1                             | 279                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31973405  | Ca4                                     | 31973405                      | TGG/TG                                                        | GTGTCCAATGTGTTGC<br>TCCA      | ACCACACCCACTTTTTC<br>AGC  | 60.6                             | 911                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31973453  | Ca4                                     | 31973453                      | AA/AATA                                                       | GTGTCCAATGTGTTGC<br>TCCA      | ACCACACCCACTTTTTC<br>AGC  | 60.6                             | 911                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31974935  | Ca4                                     | 31974935                      | ATTT/ATT                                                      | TCACAGCCAACAGCAC<br>TCTC      | TCGTGCAATGTCCATT<br>CATT  | 60.2                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_31977289  | Ca4                                     | 31977289                      | T/TG                                                          | CATCGAACTCGTCCCG<br>TTAT      | CATGTCGCTACCTGCA<br>CAGT  | 60.0                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_31989643  | Ca4                                     | 31989643                      | CTTTTTTTT/CTTTTTTTTTTT                                        | GAAAGATTCTCCAC<br>TCCC     | TGCACATTGGAAAATT<br>GGTG   | 59.9                             | 246                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_3199026   | Ca4                                     | 3199026                       | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATAT             | TCAAAACCCCAAACCA<br>CAAT   | CCAAAGTTACTTCGCAT<br>GATGA | 60.1                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32001207  | Ca4                                     | 32001207                      | TC/T                                                          | CTTGTTGCATCCAAA<br>CACG    | GCCAAGCAGAAAGTTC<br>ATCC   | 60.1                             | 207                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32006547  | Ca4                                     | 32006547                      | CTTT/CT                                                       | CAAAGAAGGGGAAT<br>GACC     | TCCTTCTCCAACTTTT<br>CCAA   | 60.7                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32016200  | Ca4                                     | 32016200                      | TGAGATACC/TGAGATACCGAGATA<br>CC                               | TCTAAATGTGGGTCGT<br>GCAA   | GAAGGATAAACATTGG<br>GGCA   | 60.1                             | 279                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32021071  | Ca4                                     | 32021071                      | ATT/ATTT                                                      | TCATGTGGCGTAAGTT<br>CCAA   | GAGTTGGGATGAAGGG<br>ACAA   | 60.1                             | 744                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32038234  | Ca4                                     | 32038234                      | G/GA                                                          | ACAATGCCCGACTTTA<br>CTGG   | ACTATGAGGTTTTGGT<br>GGCG   | 60.0                             | 812                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32048513  | Ca4                                     | 32048513                      | TAAAAAAAA/TAAAAAAAAA                                          | CGATTTTGTGCGGTCAA<br>TCTCT | TCACCGTAGGAAAGCT<br>GGAT   | 59.2                             | 355                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32048901  | Ca4                                     | 32048901                      | ATTTTTTTTT/ATTTTTTTT                                          | CGAAATCCAGCTTTCC<br>TACG   | TTTGGGCCTCCTTGAG<br>ATAA   | 59.8                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32049087  | Ca4                                     | 32049087                      | ATTTTTTTTT/ATTTTTTTTTT                                        | CGAAATCCAGCTTTCC<br>TACG   | TTTGGGCCTCCTTGAG<br>ATAA   | 59.8                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_32049749  | Ca4                                     | 32049749                      | AAA/AAAGAA                                                    | CCAAATCATTGGCATT<br>CACA  | TTCTATCACATTGCAT<br>ATCAAAAA | 60.3                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32051935  | Ca4                                     | 32051935                      | ATTTTTTTTTTT/ATTTTTTTTTT                                      | TTGAAGATGGTGAATG<br>TGGAA | TATGACCCGTTGGATT<br>CGAT     | 59.0                             | 797                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32053695  | Ca4                                     | 32053695                      | ATTTTTTTTT/ATTTTTTTTTT                                        | AGGTCAACATCCACTC<br>CAGG  | ATGCTCCCCTGACATT<br>CTTG     | 60.0                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32053743  | Ca4                                     | 32053743                      | GTTTTTTTTTTTT/GTTTTTTTTTTTTT                                  | AGGTCAACATCCACTC<br>CAGG  | ATGCTCCCCTGACATT<br>CTTG     | 60.0                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32057189  | Ca4                                     | 32057189                      | AATATAT/AATAT                                                 | CGCTGCTCTTCCTTGT<br>TCTC  | AAAGCGAAGCGAAGCA<br>ATAA     | 60.3                             | 294                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32057338  | Ca4                                     | 32057338                      | TG/T                                                          | TATTGCTTCGCTTCGC<br>TTTT  | GGGAAACTGCCCTAA<br>TTCT      | 60.1                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32057442  | Ca4                                     | 32057442                      | TAAAAAAA/TAAAAAAA                                             | TATTGCTTCGCTTCGC<br>TTTT  | GGGAAACTGCCCTAA<br>TTCT      | 60.1                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32058252  | Ca4                                     | 32058252                      | CTG/C                                                         | GGCAAAGCCTCTCATT<br>ACCA  | TGACCAATGTTGCCAT<br>GTCT     | 60.2                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32118876  | Ca4                                     | 32118876                      | TAAAAAAAAA/TAAAAAAAAA                                         | CCGATGCAATGAAGAA<br>ATCA  | GGGCCAAGACACCATT<br>TTT      | 59.6                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32121497  | Ca4                                     | 32121497                      | TAAAAAAAAA/TAAAAAAAAA                                         | TGGCATACGACCAACT<br>CAAA  | TTTGCTTTACAAGCTTG<br>GGG     | 60.1                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_32121752  | Ca4                                     | 32121752                      | ACCC/ACC                                                      | CCCCAAGCTTGTAAG<br>CAAA    | AATGAAAGCGTTGATT<br>GGGT    | 60.2                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32121836  | Ca4                                     | 32121836                      | AATA/AATATA                                                   | CCCCAAGCTTGTAAG<br>CAAA    | AATGAAAGCGTTGATT<br>GGGT    | 60.2                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32137832  | Ca4                                     | 32137832                      | CAAAAAAAAA/CAAAAAAAAAA                                        | CGACAGCACATTAGAT<br>AAACCG | ATGGATGATGGGCAGT<br>AAGC    | 59.7                             | 806                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32138975  | Ca4                                     | 32138975                      | CATATATAT/CATATAT                                             | TGGTGTGTGTGTGT<br>GAGG     | TGAAAAACCCAATCCAA<br>ACC    | 60.1                             | 892                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32141276  | Ca4                                     | 32141276                      | GTG/GTGGCACGTTG                                               | ACCAACCTGTTGAAG<br>AAGC    | CCCTCATGATATCCAC<br>GACC    | 59.2                             | 636                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32143759  | Ca4                                     | 32143759                      | GATATATA/GATATA                                               | CGTTATCATTGCTTGAA<br>CGG   | TTGAGCACTTACTGGT<br>GGGA    | 59.2                             | 941                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32147675  | Ca4                                     | 32147675                      | AATATAT/AATAT                                                 | TTGCACAAAAGAAATC<br>GAAAAA | ACAAATTGGCATTACCC<br>CAT    | 59.7                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32149191  | Ca4                                     | 32149191                      | CTTTTTTT/CTTTTTT                                              | CGGTGAAGGGACCACA<br>CTAT   | TGCCATAACTGCACA<br>ACAT     | 59.8                             | 404                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32149314  | Ca4                                     | 32149314                      | TAGAAGAAGAAG/TAGAAGAAG                                        | GCATGCTCACATGATT<br>CCAC   | TGCCATAACTGCACA<br>ACAT     | 60.1                             | 238                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32149597  | Ca4                                     | 32149597                      | TC/T                                                          | ATGTTGTGCAGTTATG<br>GGCA   | TCATGAATCAATCAAC<br>AAACAAA | 60.0                             | 224                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_32156545  | Ca4                                     | 32156545                      | A/AC                                                          | TTCACTTGGTTGCTTT<br>GCAG  | CTTAAACCATAATCCCC<br>GCA  | 60.0                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32159010  | Ca4                                     | 32159010                      | ATTTTTTTT/ATTTTTTTTTT                                         | TCTCTTTTAATGGGCC<br>ATGC  | ATGCATGGAATCCAGC<br>TTTC  | 60.0                             | 688                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32159052  | Ca4                                     | 32159052                      | TAAAA/TAAA                                                    | TCTCTTTTAATGGGCC<br>ATGC  | ATGCATGGAATCCAGC<br>TTTC  | 60.0                             | 688                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32167743  | Ca4                                     | 32167743                      | A/AG                                                          | GCAGCATATGATCGCA<br>AAAA  | AAAGTCCCACTTGATG<br>GTGG  | 59.8                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32174509  | Ca4                                     | 32174509                      | ATCT/AT                                                       | ACAATTGGTTGAAATG<br>GGGA  | CCGCACTTCGCATTTTT<br>AAT  | 60.0                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32179682  | Ca4                                     | 32179682                      | CAATAATCAACAAA/CAATAATCAA<br>ACAAATAATCAACAAA                 | TTGCATACCTCATACCA<br>TCCC | TTGATGCATTACCTCCC<br>ACA  | 59.7                             | 731                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32181880  | Ca4                                     | 32181880                      | ATTTT/ATTTT                                                   | AGATTTAAGGGAGGGG<br>GCTC  | CGAACAATTCGTCCTT<br>GGTT  | 60.8                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32216199  | Ca4                                     | 32216199                      | ATTTTTTTT/ATTTTTTTT                                           | ATAAAGGTCAACGCAC<br>GCTT  | GAAATCAACGGATCTC<br>CATCA | 59.8                             | 384                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32220024  | Ca4                                     | 32220024                      | G/GCC                                                         | CGTGGGGGTATTTTC<br>ATTG   | GCCTCCAGAATATGG<br>ATCA   | 60.0                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32224229  | Ca4                                     | 32224229                      | A/AT                                                          | TCTTCTCCACAGGGG<br>ATTG   | ATATGGGCCAAAAGCA<br>ACAA  | 60.0                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_32224834  | Ca4                                     | 32224834                      | ATTTTTTTTT/ATTTTTTTTT                                         | ATATTTGTTGCTTTTGG<br>CCC   | GCGGAAAAATTTGATG<br>AGTTG | 58.9                             | 328                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32225442  | Ca4                                     | 32225442                      | TTATATAT/TTAT                                                 | TCAATTCCAATCATTCA<br>ACCA  | ACATTACACCAATGCG<br>ACGA  | 58.8                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32225516  | Ca4                                     | 32225516                      | TTA/TTATA                                                     | TCAATTCCAATCATTCA<br>ACCA  | ACATTACACCAATGCG<br>ACGA  | 58.8                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32227293  | Ca4                                     | 32227293                      | AAAAA/AAAAATTAAAA                                             | TCTTCACAACCCCTTG<br>AACC   | TTCTTCCAAACGAGCC<br>TCTC  | 59.9                             | 868                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32227396  | Ca4                                     | 32227396                      | GT/GTT                                                        | TCTTCACAACCCCTTG<br>AACC   | TTCTTCCAAACGAGCC<br>TCTC  | 59.9                             | 868                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32241433  | Ca4                                     | 32241433                      | ATT/A                                                         | ACAATTGTTGCACCAC<br>GAGA   | ATCGCAAAAGTAGTCC<br>CCCT  | 60.2                             | 148                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32242240  | Ca4                                     | 32242240                      | TATTAAATTTAA/TATTAAA                                          | TGCTAATGCTTTTCAAG<br>GGC   | GCGATGCACAGGTAAA<br>CAAA  | 60.3                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32256317  | Ca4                                     | 32256317                      | A/AC                                                          | AAACAAAATCATCCTT<br>CCCAA  | CGTGAGTCTCGTTGAA<br>GCAA  | 59.9                             | 336                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32257454  | Ca4                                     | 32257454                      | GTTTTTTTTTTT/GTTTTTTTTTTT                                     | TGCACCTTGTTAACCA<br>ACAATG | TGTGGGAGACCGATT<br>CTCT   | 59.6                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32263608  | Ca4                                     | 32263608                      | ATTTTT/ATTTTTTT                                               | ACACATGTCCCAGTTG<br>ACGA   | TGACGATGGAGGCTTT<br>TAGG  | 60.0                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_32263960  | Ca4                                     | 32263960                      | TAAAAAAA/TAAAAA                                               | GATCAAATCCCCTATG<br>TATGTGC  | TGACGATGGAGGCTTT<br>TAGG  | 59.6                             | 191                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32264283  | Ca4                                     | 32264283                      | TAAAAA/TAAAAA                                                 | CCTAAAAGCCTCCATC<br>GTCA     | TGCTTGTGAGCTTGT<br>GTGTC  | 60.2                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32264601  | Ca4                                     | 32264601                      | TA/TAA                                                        | GATCAAATTCTCTATGC<br>ATGTGCT | CCAATTGAAGGGTAAG<br>TGCC  | 59.7                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32264980  | Ca4                                     | 32264980                      | AAT/AATAT                                                     | GCACTTACCCTTCAATT<br>GGG     | AGGAGAGGTCCATTTC<br>TCAGG | 59.4                             | 262                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32290820  | Ca4                                     | 32290820                      | AAGA/AAGAGA                                                   | GGATCAGAGAAGAGAC<br>GGGA     | TTACTTGTAGGGCAGG<br>TCCG  | 59.3                             | 703                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32297893  | Ca4                                     | 32297893                      | CTGAAT/CTGAATGAAT                                             | GCGGTGCGATATTCTT<br>TGTT     | TGGAAATGTTGGAGC<br>ATGA   | 60.1                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32298040  | Ca4                                     | 32298040                      | CT/CTTGATAAAGAT                                               | GCGGTGCGATATTCTT<br>TGTT     | TGGAAATGTTGGAGC<br>ATGA   | 60.1                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32335179  | Ca4                                     | 32335179                      | AAAGAAGAAGAAGAAGAA/AAA<br>GAAGAAGAAGAAGAA                     | AAAGTCCGTTTGTGAA<br>TCCG     | TGGGCATTCAAATCAAA<br>CAA  | 60.0                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32351537  | Ca4                                     | 32351537                      | TCTTTTTTTA/T                                                  | CAAAGGTAACCGATCC<br>TCCA     | GCAACGAAAACGGAGA<br>ACAT  | 59.9                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32373608  | Ca4                                     | 32373608                      | ATTTTTTTT/ATTTTTTT                                            | TCCACTTTTCAAACGA<br>GATGG    | AAGATCACGTTTCACAT<br>CGG  | 60.1                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_32373685  | Ca4                                     | 32373685                      | TAAAAAAAAA/TAAAAAAAAA                                         | AGACGGGCAATTTAG<br>TCTCA    | CGATGTGATCTCTTGT<br>TCCC      | 58.8                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32380091  | Ca4                                     | 32380091                      | GAAAAA/GAAAA                                                  | CAACACAATTCAATCC<br>CCC     | CCTTTGCTTCTTGACCT<br>TGC      | 60.0                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32388627  | Ca4                                     | 32388627                      | CTTTTTTTTT/CTTTTTTTT                                          | CGGCCCTTTGTTATGT<br>CTCT    | AGACCGTGAACGGCTT<br>ATAGA     | 59.2                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32388983  | Ca4                                     | 32388983                      | AAAT/A                                                        | CGGCCCTTTGTTATGT<br>CTCT    | TTTGGGCGAATTCATT<br>TTA       | 59.2                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32395281  | Ca4                                     | 32395281                      | TA/TAA                                                        | GGTTAACAAATCTCCTA<br>AAGGCA | TTTTGTAAAGAATTGC<br>GACCTC    | 58.7                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32395719  | Ca4                                     | 32395719                      | TAAAAAAAAA/TAAAAAAAAA                                         | GGTTAACAAATCTCCTA<br>AAGGCA | CCAAACAAAGAAATGA<br>CGAACA    | 58.7                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32409897  | Ca4                                     | 32409897                      | T/TTTTATATTTA                                                 | CACGCGAGCAAGATGT<br>TCTA    | TGGTTTGCATCTTGTG<br>GTCT      | 60.2                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32410631  | Ca4                                     | 32410631                      | AT/ATT                                                        | TTATTCCACCCACCT<br>CAAA     | CTCAGCTCATTGGTTT<br>GGTG      | 60.2                             | 262                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32413475  | Ca4                                     | 32413475                      | AAT/AATAT                                                     | TTGTGCAACCCTTGAA<br>ATGA    | CAATTTTCCATTCTAA<br>GCTTCTC   | 60.1                             | 722                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32432200  | Ca4                                     | 32432200                      | CATAATTTA/CA                                                  | TGATAAATTGGGTCAT<br>GTATTTT | TTGGATCATAGATTCT<br>GAATGATAA | 57.9                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_32450619  | Ca4                                     | 32450619                      | ATTTTTTTT/ATTTTTTTT                                           | TCCCCCTTCGTCTTTT<br>CTT       | AAAATAAGGGACACATT<br>TTTGTCAT | 60.0                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32457295  | Ca4                                     | 32457295                      | AC/A                                                          | TGTGCTCAACCCAAAT<br>TGAA      | ACAAGTTGTGGGAGTG<br>GGAC      | 60.1                             | 278                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32464896  | Ca4                                     | 32464896                      | CTTTTTTTTT/CTTTTTTTT                                          | CCTGTTTTGTGGGAAC<br>CTGT      | TGGAGGAAGCAAGGAA<br>AGAA      | 59.9                             | 684                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32466403  | Ca4                                     | 32466403                      | ATT/ATTT                                                      | GCCAGTAGGAAATCC<br>TCCA       | ACCCAAACAAGAACAA<br>ACGC      | 59.1                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32470160  | Ca4                                     | 32470160                      | GCTATGTTTGC/G                                                 | TGAAACACATTGGAGA<br>CCCA      | GACAACCCTCCGCAAT<br>AAAA      | 59.9                             | 336                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32485754  | Ca4                                     | 32485754                      | CAAAAAAAAA/CAAAAAAAAA                                         | GAAGAGGAATGAGTCT<br>GAGTGGA   | GGAAACTTCTTTCATGT<br>GGACC    | 59.9                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32487077  | Ca4                                     | 32487077                      | GAAA/GAAATAAA                                                 | CGTCAATTTGAGACGA<br>CGAA      | ATTCATCAATTCGGG<br>GTGA       | 59.8                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32489750  | Ca4                                     | 32489750                      | C/CA                                                          | GGGTTTTATTATTATTG<br>ATGGAGGG | GCAAACCCAACATTT<br>TCGC       | 60.1                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32491529  | Ca4                                     | 32491529                      | GTT/GTTT                                                      | GGTGATGGTTTCGCCT<br>AAAA      | TCAAACACACAGAAAA<br>TAGCA     | 59.9                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32494024  | Ca4                                     | 32494024                      | TAAAAAAAA/TAAAAAAAAA                                          | CGTCATTACCCGTTGA<br>AACC      | TCATCCATCCATATCCC<br>CAT      | 60.2                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_32498425  | Ca4                                     | 32498425                      | CAAAAAAAAA/CAAAAAAAAA                                         | TAGCACGGACCCCAAT<br>TAAG   | GGGAAATTTCAAGGCA<br>CAAA  | 60.0                             | 368                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32509855  | Ca4                                     | 32509855                      | TAAAAA/TAAAAA                                                 | GCATTCCCTCTGGACT<br>TTGA   | GAAACTTTGGCCCTA<br>TGGT   | 60.2                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32511208  | Ca4                                     | 32511208                      | GAAAAAAAA/GAAAAAAAA                                           | ACTGTTTTGCCAGAA<br>ATGC    | TGATGCATGTCAGAAA<br>GGGA  | 60.1                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32511542  | Ca4                                     | 32511542                      | A/AT                                                          | TCCCTTTCTGACATGC<br>ATCA   | TCTAGACTAGGCTGCT<br>CCCG  | 60.2                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32511906  | Ca4                                     | 32511906                      | T/TC                                                          | TTTCTCCGTTATGTGT<br>CGG    | TGAGTGCTGGGAAC<br>TACC    | 60.9                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32513097  | Ca4                                     | 32513097                      | TGGGGGG/TGGGGG                                                | GATTTCGATTGGCCTC<br>TTGT   | ACAGTGGTTGCCATTT<br>CCTC  | 60.1                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32514320  | Ca4                                     | 32514320                      | GACATTGACTTTTT/GACATTGACTT<br>TTTTCAACATTGACTTTTT             | ATTACTGGACCAGAGG<br>CACG   | AATGTCCATTCTGGGA<br>CGAG  | 60.1                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32522290  | Ca4                                     | 32522290                      | GAAAAAAAA/GAAAAAAAA                                           | ACTCATTATTCCACAG<br>CCC    | TTGCTAACGGTAACAC<br>AACGA | 59.9                             | 851                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32523002  | Ca4                                     | 32523002                      | GTT/GTTTT                                                     | CGCATGCTAATTCAATT<br>TCAGA | CTCCTTACATTGAGG<br>GGCT   | 60.2                             | 257                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32523554  | Ca4                                     | 32523554                      | TAAAAAAAAAAAAA/TAAAAAAAAA                                     | TGATTTGCGTCGTGTT<br>CAAT   | AGAGAGGAGGAGAGC<br>CCAAG  | 60.1                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_32525507  | Ca4                                     | 32525507                      | CAAAA/CAAAAA                                                  | GTCATGCATATGTTGG<br>ACGC  | AAGTTTTCTTCCCGCTC<br>ACA   | 60.0                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32531473  | Ca4                                     | 32531473                      | TAA/T                                                         | TAAATGGATGCATCG<br>AGCC   | ACAAATCAACCAAGTGT<br>CGCA  | 60.9                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32547296  | Ca4                                     | 32547296                      | AA/AACATTATCAATTA                                             | TGCGAGATTTTGAGTT<br>CAACC | TGCTTATCTTGAACGG<br>GACC   | 60.2                             | 325                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32554394  | Ca4                                     | 32554394                      | A/ATTC                                                        | AAATTAAGTGCAGGAGG<br>GGTC | ACCCATTATGGTGAAG<br>AGCG   | 60.3                             | 832                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32559742  | Ca4                                     | 32559742                      | AAAGAAAGAAGAAAGA/AAAGA<br>AAGAAGA                             | TTCATTCCAGTCTGTG<br>GCA   | ACGGCCGTTATAGGTT<br>TCCT   | 60.2                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32559814  | Ca4                                     | 32559814                      | A/AC                                                          | TTCATTCCAGTCTGTG<br>GCA   | TGAGAACTTTTCCGCT<br>GCT    | 60.2                             | 872                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32562355  | Ca4                                     | 32562355                      | CTTTTT/CTTTTTT                                                | AAATGGAGGAGAAGGA<br>GGGA  | CGGTGAATCCTTTACG<br>GAGA   | 60.0                             | 286                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32567747  | Ca4                                     | 32567747                      | TAAAA/TAAAA                                                   | GAAGGTGAGACAGCAG<br>AGGG  | TGACGTGTGTAGTTTC<br>CCCA   | 60.0                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32586827  | Ca4                                     | 32586827                      | GAAAAAAAA/GAAAAAAAAA                                          | TATCTTTGCCGCTCC<br>AATC   | AAGGACCAAAACCAATT<br>GTCTC | 60.2                             | 750                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32615628  | Ca4                                     | 32615628                      | CAAA/CA                                                       | GCACTTGGAAGGAAC<br>AAAC   | TTTTGCTCGAACTTGG<br>CTTT   | 60.7                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                       | Forward primers (5'-3')        | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------|--------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                     |                                |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_32631880  | Ca4                                     | 32631880                      | CTTTCTTTTTCTTTTCT/CTTTCTTT<br>TTCTTTTCTTTTCT                                        | TTACGTGGAGAGGGAA<br>ATGG       | CACACATCACTTCAACC<br>GTG | 59.9                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32634672  | Ca4                                     | 32634672                      | CTTTATCT/CTTTATCTTTTATCT                                                            | CAGACCCGTGTGAACA<br>CAAA       | AGCAGATGCCTCTATC<br>GCAT | 60.6                             | 937                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32663516  | Ca4                                     | 32663516                      | TTTATTATTATTATTATTATTATT/TTT<br>ATTATTATTATTATT                                     | TGCGTTTCACTCTTCCT<br>TCC       | TGTCAGCCCAAAAAC<br>AAAA  | 60.4                             | 257                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32694376  | Ca4                                     | 32694376                      | ATTTTTT/ATTTTTTT                                                                    | AATCATTTTTGGAAGAC<br>GCC       | TGAAAACGTGCAGCA<br>TGAA  | 59.0                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32696742  | Ca4                                     | 32696742                      | AGG/AGGG                                                                            | TGTATTTGCAGGGACG<br>TGAA       | CTCATGAGAGGCGATT<br>GTGA | 60.1                             | 467                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32696837  | Ca4                                     | 32696837                      | TAAAAAAAAA/TAAAAAAAAA                                                               | TGTATTTGCAGGGACG<br>TGAA       | CTCATGAGAGGCGATT<br>GTGA | 60.1                             | 467                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32697443  | Ca4                                     | 32697443                      | TAAAAAAAAA/TAAAAAAAAA                                                               | TCAAAGGCTTACCACC<br>TTCG       | CATCGGCCTTGAAAAC<br>AAAT | 60.2                             | 942                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32714134  | Ca4                                     | 32714134                      | GCTCTCTCTCTCTCTCTCTCTCTCT<br>CTC/GCTCTCTCTCTCTCTCTCTCTC<br>TCTCTCTC                 | AAGAACCACGTTTAC<br>ATCC        | AACAATGATGACGAGA<br>GGGG | 59.8                             | 150                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32747280  | Ca4                                     | 32747280                      | GAAAA/GAAA                                                                          | TCTTCCACCCAGTTTT<br>GACC       | GGAGACAGGTGTGGAC<br>GTTT | 59.9                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32795346  | Ca4                                     | 32795346                      | AATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATATA<br>TATATATATATATATATATATAT | CCTGATATGAGTTGAG<br>TTAGAAACCA | AATTCATGGACTGCAC<br>CCTC | 60.0                             | 796                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)  | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_32873081  | Ca4                                     | 32873081                      | ATTTT/ATTTT                                                    | GTCATTGACCGGGAT<br>ATTG   | ACGGTTGCACCGAATA<br>AAAA  | 60.0                             | 162                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32886390  | Ca4                                     | 32886390                      | AC/ACC                                                         | AATCATCCCATGTTGC<br>CATT  | CGAGATTTCACACCA<br>GGGT   | 60.0                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32907762  | Ca4                                     | 32907762                      | ATTTTTTTTTT/ATTTTTTTTTT                                        | TCTGATGGACGAGTTC<br>AAACA | TTGCGTCCTTTTTACCC<br>AAC  | 59.3                             | 344                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_32913108  | Ca4                                     | 32913108                      | TAAATTAATAATAAT/TAAATTAATA<br>TTAATAATAATAAT                   | GGGTTTTTCAGAAAGA<br>AACGG | AACGGTGAACCTTAACA<br>CGGG | 60.0                             | 438                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33053978  | Ca4                                     | 33053978                      | ATGTT/AT                                                       | TGCTTTCATCTTTGGAA<br>CCC  | TTTGCAATACGGATTG<br>ATGA  | 60.1                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33054018  | Ca4                                     | 33054018                      | TAA/TAAA                                                       | GGAATGGCAAACCTTC<br>ATGC  | TTTGCAATACGGATTG<br>ATGA  | 60.5                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33054232  | Ca4                                     | 33054232                      | TAAAAAAAA/TAAAAAAAA                                            | TCATCAAATCCGTAATG<br>CAAA | GCATATGGGGTACCAG<br>ACTT  | 59.0                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33064079  | Ca4                                     | 33064079                      | ATTGTTGTTGTTGTTGTTG/ATT<br>GTTGTTGTTGTTGTTGTTGTTG              | TCGGGCCACTATCTGG<br>ATTA  | GTGTGCCGTCACAAAC<br>AATC  | 60.4                             | 810                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33083922  | Ca4                                     | 33083922                      | CATATATATATATATATATATATAT<br>T/CATATATATATATATATATATAT<br>ATAT | AGGAAGAAGAAGCTGG<br>GAGC  | GCTGTTAGCCCAAGTTT<br>TTGG | 60.1                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33145619  | Ca4                                     | 33145619                      | TAAAAAAAA/TAAAAA                                               | AAACCGTCGTTCCAGT<br>TGTC  | AGGCAACAAACATAGA<br>ATCGC | 60.0                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_33176390  | Ca4                                     | 33176390                      | A/AC                                                          | ATCCACGGACAATCCA<br>TTTG | TGGATGTCTTGTCTG<br>GGTTC      | 60.6                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33186066  | Ca4                                     | 33186066                      | A/AG                                                          | GCGCACAACAACAAGA<br>AAAA | CGGGTTGTGAAACACC<br>TTCT      | 59.9                             | 620                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33204821  | Ca4                                     | 33204821                      | AATATATATATATATATATAT/AA<br>TATATATATATATAT                   | GCCACACTCCGAAACA<br>AAAT | ATGGAAGTAGGTGGCA<br>GTGG      | 60.0                             | 823                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33212027  | Ca4                                     | 33212027                      | TT/TTAT                                                       | TCACAATCCACTAATG<br>CGGA | TTGATAACATGAAAATG<br>AAACGAAA | 60.1                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33212339  | Ca4                                     | 33212339                      | AATATATATATATATATATATAT<br>/AATATATATATATAT                   | CAAACTGCTGGCAC<br>ATCT   | GAAATGCCACACTCCG<br>AAAT      | 59.9                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33213558  | Ca4                                     | 33213558                      | CTTTTT/CTTTTT                                                 | AATGATACGGACCGCA<br>TAGC | GCCACTAGGCATGTGG<br>AAAT      | 60.0                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33256637  | Ca4                                     | 33256637                      | ATTTTTTTTT/ATTTTTTTTT                                         | CATTGATCATGGTTCTT<br>GCC | GGCTTGTGAAAACAAA<br>TGGA      | 58.9                             | 329                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33260832  | Ca4                                     | 33260832                      | TGAAGAAGAAGAA/TGAAGAAGAAG<br>AAGAA                            | ACATCTGGAATTTGCTT<br>GCC | CGACTTTGGCACCATA<br>TCCT      | 60.1                             | 968                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33283356  | Ca4                                     | 33283356                      | G/GAATTAATTTA                                                 | TTGGGATGGTTGACCT<br>TTGT | ATCGGGCCAATTTACA<br>AGAA      | 60.2                             | 681                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33293560  | Ca4                                     | 33293560                      | CTA/C                                                         | GGAGGATCCATCGAAG<br>ATGA | TTGGAACAGACATTGA<br>CCCA      | 60.0                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_33315743  | Ca4                                     | 33315743                      | CTT/CTTT                                                      | ACATGAGTCTTTGTG<br>CCCC    | TGGCACGTGATTTGTT<br>TGAT  | 60.0                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33321015  | Ca4                                     | 33321015                      | AATATA/AATATATA                                               | TATTGTTGCACCCCCA<br>ATTT   | ATGTCTGCCCATTTTC<br>TTG   | 60.1                             | 229                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33327000  | Ca4                                     | 33327000                      | CA/C                                                          | AATATCCCCGTCAAT<br>GTGC    | TTTATTGCAACATCGCC<br>TTTT | 59.8                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33336961  | Ca4                                     | 33336961                      | ATTTTTTTT/ATTTTTTT                                            | CACGGAGTTTAACGAT<br>GTGAGA | CATCCCCTAACCCACT<br>CAAA  | 60.2                             | 911                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33342440  | Ca4                                     | 33342440                      | TTTTTCTTCTT/TTTTTCTTCTCT<br>TTTTCTTCTT                        | TGAAATTCACCTCAC<br>CTCC    | TTGGTTGAGTTTATG<br>CGTG   | 59.9                             | 155                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33346959  | Ca4                                     | 33346959                      | TT/TTAT                                                       | TTTTCGGTTTGTTCAAA<br>GGC   | GGAAACATTGGGAAA<br>CCCT   | 60.1                             | 766                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33348179  | Ca4                                     | 33348179                      | ATT/AT                                                        | AGGTTGAGCGATTGGA<br>GAAA   | TCCTAAAAGACTGCCC<br>GCTA  | 59.8                             | 378                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33362903  | Ca4                                     | 33362903                      | TCATACACA/TCATACACAACATACA<br>CA                              | CGTTTGTTGCACTGA<br>TGTC    | CCAGACGCAACAGTCA<br>AATG  | 60.2                             | 119                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33386822  | Ca4                                     | 33386822                      | ATAAAATTAATAATAATAATAATA<br>AAATTAATAATAATA                   | CCCTCCTTTGTGACGG<br>TTTA   | TTCGCACCTACACGAT<br>CAAG  | 60.0                             | 763                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33392310  | Ca4                                     | 33392310                      | ATTTTTTTTTTTT/ATTTTTTTTTTT                                    | CGACCCAAGTCATTGG<br>ATT    | CTCGAAAAATTGAAACC<br>CCC  | 59.8                             | 177                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_3356082   | Ca4                                     | 3356082                       | A/AGCCAAGCGTAACG                                              | TCACCGGAAAGTAACT<br>CGCT  | ATCGATATTCTCCGCA<br>CCTG | 59.9                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33566311  | Ca4                                     | 33566311                      | ATTTTTTTTTTT/ATTTTTTTTTTTTT                                   | TCCATCCTCCTCATCT<br>GACC  | TTGTCTCAACAATCTCC<br>CCC | 60.0                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33615467  | Ca4                                     | 33615467                      | ATT/ATTT                                                      | GGTCCTTGTTGAGTCC<br>AACG  | CTCAAAACCTGAGCA<br>TGGC  | 60.5                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33617340  | Ca4                                     | 33617340                      | CTTTTTTTTT/CTTTTTTTTT                                         | TTTTCTAAATTTCGAG<br>GACGA | TTTCCCGATTGGTCC<br>TTT   | 60.1                             | 798                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33617796  | Ca4                                     | 33617796                      | AAAAGAA/AAA                                                   | CCCCGATTGGTCCTT<br>TATT   | TGCTAGTTGTTGCGAC<br>CAAA | 60.0                             | 765                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33619155  | Ca4                                     | 33619155                      | CGTGT/CGTGTGT                                                 | GAACATGCTGAAAACG<br>GGAT  | TGAGGGCAATGACAAA<br>CAAA | 59.9                             | 122                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33619321  | Ca4                                     | 33619321                      | TAAAAAAA/TAAAAA                                               | GAACATGCTGAAAACG<br>GGAT  | CCAATTCCAAGGTCAT<br>CTGG | 59.9                             | 448                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33627666  | Ca4                                     | 33627666                      | TATTTAAATTTAAATTTAAATTTA<br>AAAT/TATTTAAATTTAAATTTAA<br>AT    | AGTGACATGACGGAAG<br>TAGCA | TTGTTCCAGTGTGCA<br>TGTT  | 58.4                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33633372  | Ca4                                     | 33633372                      | GTTTTTTT/GTTTTTT                                              | ACGAGGAAACATATCG<br>TCCG  | ATGTCCACATTGGG<br>TGTC   | 60.0                             | 726                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33714267  | Ca4                                     | 33714267                      | T/TCTTAATC                                                    | GAACACGTTGTTAGAC<br>CGGC  | TGACAAAATGGGGAGA<br>AAGG | 60.6                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_33714529  | Ca4                                     | 33714529                      | ATT/ATTGTT                                                    | CGTTGTTAGACCGGCT<br>CTTG  | TGGGCTGACATAATCA<br>CCAA | 60.8                             | 940                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_33715942  | Ca4                                     | 33715942                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA<br>AAAAAA                       | TTGGGTACGTTGGTGT<br>AGCA  | ATTGACTGGGCACCAT<br>GATT | 60.0                             | 634                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_33717821  | Ca4                                     | 33717821                      | TAAAAAAAAAAAAAAAAA/TAAAAAA<br>AAAAA                           | CCAAAAACCCCTCTTTT<br>TCC  | CCACAAAATTTGTCCA<br>ACC  | 59.8                             | 730                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_33733792  | Ca4                                     | 33733792                      | AATATTTGTTTATATT/AATATTTGTT<br>TATATTTGTTTATATT               | CGTTATTCCCATATGA<br>GAGGC | TGTGATGTTGGACGTG<br>TGTG | 58.5                             | 280                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_33739294  | Ca4                                     | 33739294                      | ATTTTTTTTT/ATTTTTTTTT                                         | CGTCTTGATTTGGT<br>GGTG    | GTAGTGGGTGAACGTG<br>GCTT | 60.0                             | 456                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_33746638  | Ca4                                     | 33746638                      | CAAAAAAAAA/CAAAAAAAAA                                         | CGTGGACAAAGATCGT<br>GATG  | AAGCCACGTTACCCCA<br>CTAC | 60.1                             | 289                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_33773434  | Ca4                                     | 33773434                      | AC/ACC                                                        | GGATGTCTCCATGGGA<br>ATTG  | GCATACAATTGCTTCTC<br>GCA | 60.1                             | 528                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_33777332  | Ca4                                     | 33777332                      | GAAAAAAAAA/GAAAAAAAAA                                         | TGGGTTACCAACAAT<br>AGTGG  | TCGTGCTGACACCTTC<br>AATC | 57.4                             | 749                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_33795008  | Ca4                                     | 33795008                      | TTATATATATATATAT/TTATATAT<br>ATATAT                           | GTCGTGCAATGCAAC<br>AACC   | TCGACTAAGGACATTG<br>GGCT | 60.0                             | 514                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_33804679  | Ca4                                     | 33804679                      | CAT/CATAT                                                     | TCAGAAATGTTTGAAT<br>CGCA  | TCGTATGCGTCAATCC<br>GATA | 60.2                             | 262                                           | INTERGENIC                                           | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_33813940  | Ca4                                     | 33813940                      | ATTT/ATTTTT                                                   | TGAAGCATGGACCAAT<br>CAAA    | GTCCAATCACATGCAC<br>AAGG  | 60.0                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33833551  | Ca4                                     | 33833551                      | ATTTTTTT/ATTTTTTTTT                                           | TCGGAGAGGAGATTGA<br>TGCT    | TCCAACCTCGCAAGGCT<br>ATCT | 59.9                             | 803                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33833847  | Ca4                                     | 33833847                      | TA/TAAC TGCA                                                  | GCGTCATCGTCCCTAC<br>AAAT    | TCCAACCTCGCAAGGCT<br>ATCT | 60.0                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33835105  | Ca4                                     | 33835105                      | CAAAAAA/CAAAAAAAA                                             | TTTTCACCAATCACTT<br>GAAAGAA | TCGAGCCTTATTGTGG<br>ATGA  | 60.0                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33835153  | Ca4                                     | 33835153                      | AAGCT/A                                                       | TTTTCACCAATCACTT<br>GAAAGAA | TCGAGCCTTATTGTGG<br>ATGA  | 60.0                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33835234  | Ca4                                     | 33835234                      | TAAAAAAA/TAAAAAAA                                             | CCAATCAAATTGAGCA<br>TACCC   | TGTGTTTGCTTTGCATG<br>CTT  | 59.3                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33835524  | Ca4                                     | 33835524                      | TAA/TAAA                                                      | TGCATCCAGACATGAG<br>TCAAA   | TGTGTTTGCTTTGCATG<br>CTT  | 60.3                             | 309                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33836766  | Ca4                                     | 33836766                      | GAAAAAAAA/GAAAAAAAAA                                          | GTTTTGTGATGGGGGA<br>TGAC    | CCATTGAAAAACGAAC<br>GACC  | 60.0                             | 205                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33837766  | Ca4                                     | 33837766                      | CAAAAA/CAAAA                                                  | TCATTGTCTATGCCCG<br>ATCA    | GGTTTGATCTGTGTTT<br>GCGA  | 60.0                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33856380  | Ca4                                     | 33856380                      | CTTTTTTTTT/CTTTTTTTTTTT                                       | CGGGAATTAAGAGGAG<br>AGGG    | AAATTTAATGCCGTGA<br>CCG   | 60.0                             | 719                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_33858628  | Ca4                                     | 33858628                      | ATTT/ATTTT                                                    | GCAAACGCAGATCAAG<br>TCAA    | ATTATTGGGAAATCT<br>GGGC   | 60.0                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33865093  | Ca4                                     | 33865093                      | GAAAAAAAA/GAAAAAAAA                                           | TTTGATGTTGTTGGAG<br>ATGAAAA | CGTTTCAGAGGTGAAC<br>CGTAA | 59.5                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33865441  | Ca4                                     | 33865441                      | GTTTTTTTT/GTTTTTTTTT                                          | TGTTTACGGTTCACCT<br>CTGAAA  | ATAACCCAGCTGAAAG<br>GTGC  | 59.6                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33873292  | Ca4                                     | 33873292                      | CTTTTTTTTTTTTT/CTTTTTTT                                       | GCGAGGTTGAGAAAC<br>AAGC     | TTGAGGGACCAAACT<br>GAAGA  | 60.0                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33878589  | Ca4                                     | 33878589                      | CGTTTTCTGTT/CGTTT                                             | CTTCAACAGCCTCCA<br>AAGC     | CGTGAATGGATCAGAT<br>GTGC  | 60.0                             | 748                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33884406  | Ca4                                     | 33884406                      | GTTTTTTTT/GTTTTTTTTT                                          | AGGCTAGTGCATCATC<br>CAGG    | GTACCCAATTTTCCC<br>GTT    | 60.2                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33953368  | Ca4                                     | 33953368                      | CAT/CATATCATAT                                                | TATTTTGGGATTGTGG<br>GCTC    | AGATTAGGGCCTCAGG<br>AACC  | 59.8                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33954309  | Ca4                                     | 33954309                      | TAAAAAAAA/TAAAAAAAA                                           | CACGACCAATCCATT<br>CTTG     | TGCCAAGATTCGTGAA<br>ACAA  | 59.0                             | 747                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33960188  | Ca4                                     | 33960188                      | TAA/TAAA                                                      | AAATAAGGACCAGGT<br>CGGG     | TTTGCCAGACCACCT<br>TTAC   | 60.2                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_33960521  | Ca4                                     | 33960521                      | GTATATATATATAT/GTATATATAT<br>ATATATATAT                       | TCATGTTCTCCAGCT<br>GCTA     | TTTGCCAGACCACCT<br>TTAC   | 59.5                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_33972054  | Ca4                                     | 33972054                      | AAACAACA/AAACAACAACA                                                          | TGAGTTCCAAAATCGG<br>GAAA    | AATTGGCTAAGCAAGC<br>TCCA   | 60.4                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34056670  | Ca4                                     | 34056670                      | ATAAT/ATAATTAAT                                                               | AGGATGCAACAAACCC<br>AAAG    | GTCCAAATGAAAACGC<br>CAAT   | 60.0                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34136044  | Ca4                                     | 34136044                      | AATATATATATATATATA/AATATATA<br>TATATATATATATATA                               | TTTTTGTGGAAAGGCC<br>TACG    | GCAAAGCCTCTTCAGT<br>CTGG   | 60.1                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34169705  | Ca4                                     | 34169705                      | CAATGA/CAATGATAATGA                                                           | TCAAAGTGGCTCACA<br>GTGC     | TCGACTCAAGAAGCA<br>AGTG    | 60.0                             | 781                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34229083  | Ca4                                     | 34229083                      | GTTTTAACTT/GTTTTAACTTTTTAAC<br>TT                                             | AATTAACCCCCACGC<br>CTAC     | CTCATCCCACGCTAGG<br>AAAA   | 60.1                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34247514  | Ca4                                     | 34247514                      | TTATATATATATATATATATA/TTA<br>TATATATATATATATATATATATA                         | TCATTAGCTCAATCAAT<br>TACGCA | TTGATAAGATTGATCCG<br>TTGGA | 59.8                             | 434                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34262481  | Ca4                                     | 34262481                      | TAAAAAAAA/TAAAAAAAAA                                                          | GACCACCTACGCCACA<br>CTTT    | TGTTCCAATTCCTCGTG<br>TCA   | 60.0                             | 807                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34262689  | Ca4                                     | 34262689                      | AATAAATATATATATATATATATAT<br>ATATATATATATAA/AATATATATATA<br>TATATATATATATATAA | TCTTGCCACCAACAAA<br>ACAA    | TGTTCCAATTCCTCGTG<br>TCA   | 60.1                             | 223                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34308809  | Ca4                                     | 34308809                      | TAAAAA/TAAAAA                                                                 | GTTGAGCATACCGACC<br>AACC    | ATGGTCGTTTTTCGAA<br>CTTG   | 60.4                             | 870                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34330740  | Ca4                                     | 34330740                      | TAAAAAAAAA/TAAAAAAAAA                                                         | TGCACACATCTACCCC<br>TGAA    | GGCATGGCAACTTCAC<br>TTTT   | 60.1                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_34333563  | Ca4                                     | 34333563                      | TAAAAAAAA/TAAAAAAAA                                           | ACGGTGACAAATTGGA<br>GAGG  | GGTCGCTCAACCTTTA<br>CGAG  | 60.0                             | 744                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34371605  | Ca4                                     | 34371605                      | CAA/CAAA                                                      | ATGCCCTTTGATTACGTT<br>GCC | AACCATGCTTGGA AAA<br>CCTG | 60.0                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34384933  | Ca4                                     | 34384933                      | CAAAA/CAAA                                                    | TACATTC CATCCACA<br>GGGT  | TTCGGTTGGTGACCCT<br>TTAC  | 60.1                             | 103                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34388082  | Ca4                                     | 34388082                      | CATATATATATATAT/CATATATATAT<br>ATATATATAT                     | GTTGGTTCCTAGCAC<br>CGTA   | CTGTCAATTGAGTTGC<br>GACG  | 60.0                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34388181  | Ca4                                     | 34388181                      | GAAA/GAAAA                                                    | GTTGGTTCCTAGCAC<br>CGTA   | CTGTCAATTGAGTTGC<br>GACG  | 60.0                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34410371  | Ca4                                     | 34410371                      | ATGTGTGTGTGTGTGTGTGTGTGT/<br>ATGTGTGTGTGTGTGTGTGTGTGT<br>GTGT | TGAAACAGGATCCAAA<br>AGCC  | GCGCATACACACACAC<br>ACAC  | 60.1                             | 848                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34417460  | Ca4                                     | 34417460                      | CATTTCTTGTA TTTCTTGTA/CATTT<br>CTTGTA                         | CCCAATAGTGGTTGCA<br>TTCC  | CCAAGGATGTGTTTCC<br>CTGT  | 60.2                             | 371                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34432600  | Ca4                                     | 34432600                      | ATTTTTTT/ATTTTTT                                              | GGGTGAGGATTGGTCA<br>GTCA  | ACCTTTGGGTCTTGCC<br>TTTT  | 60.9                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34462526  | Ca4                                     | 34462526                      | TAAAAAAAA/TAAAAAAAA                                           | GTGGGAAAAGATGTGG<br>GAGA  | TCGAAAGGATTTTCCA<br>TGC   | 59.9                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34468802  | Ca4                                     | 34468802                      | GTTTTTTT/GTTTTTTT                                             | GGGAAGCTTGTTTGCT<br>TCTG  | TAAGAGTGAGTGGGTT<br>GGGC  | 60.0                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_34470233  | Ca4                                     | 34470233                      | TAAAAAAAA/TAAAAAAAA                                           | GCTCAATTTTGTTTAG<br>GTCCTC | GCGTTGTGGTTCACT<br>CAAT       | 59.6                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34471336  | Ca4                                     | 34471336                      | ATTATTTATTTATTTATTTAT/ATTAT<br>TTATTTATTTATTTATTTAT           | AACGTGACATTTTCGG<br>AAGC   | TCAAGTTTTCCGATATA<br>GCCGT    | 60.1                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34503551  | Ca4                                     | 34503551                      | G/GAACTCA                                                     | GGAGGGTTTGGTTTG<br>GAAT    | GTAAGGGTCACCAAC<br>CGAA       | 60.0                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34515993  | Ca4                                     | 34515993                      | TC/T                                                          | CAGTATACCCACG<br>CCAT      | TCACATGAATAAATTTA<br>CAAGCGAA | 59.7                             | 155                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34566172  | Ca4                                     | 34566172                      | GTTTT/GTTTTT                                                  | CGCCTAAGGACTATGC<br>AAGC   | AAAATCCAACAATCTCC<br>CCC      | 60.0                             | 761                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34566424  | Ca4                                     | 34566424                      | ATT/AT                                                        | CCCTGAGACTCACGAA<br>GAGG   | AAAATCCAACAATCTCC<br>CCC      | 60.0                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34605005  | Ca4                                     | 34605005                      | G/GT                                                          | AACCAATCTTGTGCAT<br>CCAA   | TTGGACCAGAATAAGC<br>CGAG      | 59.0                             | 317                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34884584  | Ca4                                     | 34884584                      | T/TCCTCAG                                                     | CCCATGTTGGGAAC<br>AATG     | AGCGACAGAGATACGC<br>GATT      | 60.0                             | 140                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34889805  | Ca4                                     | 34889805                      | AGGGGGGG/AGGGGGG                                              | TGCAGTGCAATGTCCA<br>TTTT   | GTAAGGCATGCCACCT<br>CCTA      | 60.1                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_3492406   | Ca4                                     | 3492406                       | TATCAAATCAAATCAAATC/TATCAA<br>ATCAAATC                        | CGATGATGTCCAGTTC<br>ACGA   | TTTTCTGTTGCATTGG<br>CAG       | 60.7                             | 365                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_34944690  | Ca4                                     | 34944690                      | ACTTC/ACTTCCGGCTTC                                                      | GCTTCTTGGTGCGAGT<br>CATT  | CGTGTGAAGTCGGGA<br>AAAT   | 60.4                             | 114                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_34965051  | Ca4                                     | 34965051                      | ATTTTTT/ATTTTTTT                                                        | TTGGGATTAGAGCAAG<br>GTCG  | CATGAGACCTTCATGTT<br>GTCG | 60.2                             | 212                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_35114842  | Ca4                                     | 35114842                      | CAAAA/CAAAAA                                                            | TTGATTGTACCCTTGT<br>GCCA  | AACTGTGGAGGAATCC<br>ATGC  | 60.0                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_35405054  | Ca4                                     | 35405054                      | ATTTTTTTT/ATTTTTTT                                                      | AGCCTGTCAACACAAA<br>TCCA  | TCACTCTCCAATTTTT<br>GGC   | 59.1                             | 296                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_35431597  | Ca4                                     | 35431597                      | CCAA/C                                                                  | CCCTCACAATTGACAT<br>TTGG  | TTTTTGAATGCTTGTT<br>TGGA  | 60.2                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_35432013  | Ca4                                     | 35432013                      | TTAT/TTATAT                                                             | TGTTCAACATCCACGA<br>ACAA  | TGCCATACTCATGTGCG<br>GAAA | 58.5                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_35432836  | Ca4                                     | 35432836                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATAT                       | TTTCCGACATGAGTAT<br>GGCA  | TTTGAAAGTAACACT<br>GCACG  | 60.1                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_35432970  | Ca4                                     | 35432970                      | CATATATATATATATATATATATA<br>TATATA/CATATATATATATATATA<br>TATATATATATA   | AAAAATGTCATAAAAT<br>CGGTT | TTTGAAAGTAACACT<br>GCACG  | 57.7                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_35433291  | Ca4                                     | 35433291                      | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATATA<br>TATATATATATAT | CACGTGCAGTGTTACT<br>TTCCA | TGACGAATTTCAAAAC<br>CTGC  | 59.8                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_35445772  | Ca4                                     | 35445772                      | AATATATATATATATATAT/AAAT<br>ATATATATATATAT                              | TGCATTCAATTAAGCTT<br>GCG  | ATGTGGGCAAGTGACA<br>AACA  | 60.0                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                            | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                          |                               |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_35457008  | Ca4                                     | 35457008                      | TTGC/T                                                                                                   | AATTGCAGAAAAATGC<br>GGTC      | TTGTACCAGATATTGG<br>CCCC   | 60.1                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_35818039  | Ca4                                     | 35818039                      | AAATAATAATAATAATA/AAATAATAA<br>TAATA                                                                     | GTTCATAACGAAGATG<br>ACAATAACA | TGCAGTCAAACTTTAA<br>AGGAAG | 57.4                             | 728                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_35822348  | Ca4                                     | 35822348                      | TGG/TG                                                                                                   | GATCAAAATCGAGGACC<br>GAAA     | CGAACAAAACGATGGG<br>AAGT   | 60.0                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_35912616  | Ca4                                     | 35912616                      | CAAAAAAAAA/CAAAAAAAAA                                                                                    | ACGAAGCTCGGTCTGT<br>TGTT      | GATGGATTTAACTTTTCG<br>GTCG | 59.9                             | 287                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_35936788  | Ca4                                     | 35936788                      | TA/TAA                                                                                                   | TTGGGAAAGGCGATT<br>GTAG       | CGGCCTGGTCAAAGTA<br>TGAT   | 60.1                             | 696                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_35975112  | Ca4                                     | 35975112                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTAT/TTTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTAT | AGCCAAAAGTGGGTAA<br>CGTG      | TTTTGTGTAACGCCCA<br>GTCA   | 60.0                             | 193                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36079126  | Ca4                                     | 36079126                      | TTGTG/TTGTGTG                                                                                            | ATTTTGATGCTCACGG<br>TTCC      | CGGAGATGATGGTTCA<br>GGTT   | 59.9                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36088961  | Ca4                                     | 36088961                      | GNNNNNNNNN/GNNNNNNN                                                                                      | TACCAACGAATCCCCT<br>TCAG      | TTTGGGATAAGTGGA<br>CCCA    | 59.9                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36138277  | Ca4                                     | 36138277                      | ATT/AT                                                                                                   | ACCATGAAAGACATGG<br>GAGC      | CGGAGTACCCGACCA<br>ACTA    | 59.9                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36204013  | Ca4                                     | 36204013                      | AATATATATATATATATA/AATATA<br>TATATATATATATA                                                              | GAATGAGATTGCACAT<br>AATTAGGAA | CAACACGTAACACG<br>CAAAA    | 58.6                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_36335313  | Ca4                                     | 36335313                      | ATTTTT/ATTTTTT                                                | TTGCGACAAGATCAAG<br>CAAC      | TCAACACCAACACAA<br>GGGA   | 60.0                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36336918  | Ca4                                     | 36336918                      | TAAA/TATAAAA                                                  | ACAACAAGGGTGACCT<br>CCAC      | TGCTTGTCTATTCTGC<br>GTCAA | 59.9                             | 736                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36337139  | Ca4                                     | 36337139                      | GC/G                                                          | TGCAATGTCAATATGAA<br>CCAAA    | CCACAACCACTCATCA<br>CGAC  | 58.9                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36337264  | Ca4                                     | 36337264                      | AT/ATT                                                        | TGACGCAGAATAGACA<br>AGCAA     | CCACAACCACTCATCA<br>CGAC  | 59.6                             | 341                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36337395  | Ca4                                     | 36337395                      | A/ATTATTATT                                                   | TGACGCAGAATAGACA<br>AGCAA     | CCACAACCACTCATCA<br>CGAC  | 59.6                             | 341                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36390176  | Ca4                                     | 36390176                      | TATAATAATAA/TATAATAATAATAA                                    | TATGCACGCTCTCTCT<br>CCCT      | AGGAGGAACCAAAACC<br>GTCT  | 60.1                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36392790  | Ca4                                     | 36392790                      | TT/TTGACT                                                     | CCCTCAACAAGCATTG<br>AACA      | TTCTTTTGCTCGTGTG<br>TTG   | 59.7                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36408080  | Ca4                                     | 36408080                      | ATTTTT/ATTTTT                                                 | CAACGATCCTTCATTG<br>ATGC      | ACTATTTTCGCGAAGG<br>CTGA  | 59.1                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36419271  | Ca4                                     | 36419271                      | A/ATTTTTTTTTT                                                 | CGTCCAAGGTCACCA<br>ACTT       | GGAAATCCTATGTCTA<br>CCCCA | 60.0                             | 275                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36420752  | Ca4                                     | 36420752                      | CTTTATTTTTATTTTTATTTTT/CTTT<br>ATTTTTATTTTTATTTTTATTTTT       | TGACTTTTGTCTTAACA<br>TGAGGATG | TTTCTTTTCCTTCTGA<br>TTGG  | 58.7                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_36438574  | Ca4                                     | 36438574                      | TA/TAA                                                        | GGATAATTTTTCGCCTA<br>TTCAAA   | CTCCTTTTCACGATTCT<br>CGC      | 58.6                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36453533  | Ca4                                     | 36453533                      | TATATTTATAATATTTATAATATTTA/<br>TATATTTATAATATTTA              | TGTTGGGTGGTTAGCA<br>TACG      | GGGGTTAGAGTAAGAG<br>GCCA      | 59.5                             | 597                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36471974  | Ca4                                     | 36471974                      | TG/T                                                          | CCTCGGCTGTAAGTAA<br>CGGA      | ATGGTTCCAAACCAAT<br>GCT       | 60.3                             | 827                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36472245  | Ca4                                     | 36472245                      | TTGGTAC/TTGGTACAATGGTAC                                       | TTGCTGTTGTGAATTT<br>CCATC     | ACCACGTTTCTGTCC<br>TACG       | 60.0                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36474350  | Ca4                                     | 36474350                      | ACATAATTCA/ACATAATTCATAATT<br>CA                              | CAAACCACATCACCCCT<br>CCTT     | GCTACACCGACCACCT<br>GAAT      | 59.8                             | 585                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36495365  | Ca4                                     | 36495365                      | CGTTTTTGTTTTTGTT/CGTTTTTGTT<br>T                              | TTTTCTCCTATTGATTG<br>GATATTGG | CCCAAACTCTTCTCTTC<br>TTCCA    | 59.6                             | 888                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36502639  | Ca4                                     | 36502639                      | TCCCC/TC                                                      | GTGGCAAAATGGATCG<br>AACT      | GCCGTCTAGTGTTCCT<br>TTAATGACT | 59.9                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36510171  | Ca4                                     | 36510171                      | T/TC                                                          | CGGGCTAATTGACTCT<br>CAGC      | CCGACGAAACGAAAA<br>CAAT       | 60.0                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36510514  | Ca4                                     | 36510514                      | GTTTTTTTT/GTTTTTTTTT                                          | ATTGTTTTTCGTTTCGT<br>CGG      | GCAATGCCATAGAAGC<br>CAAT      | 60.0                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36527807  | Ca4                                     | 36527807                      | TTATAT/TTAT                                                   | AATCCCATGCATTAG<br>GCAG       | TTTGATGCCGTTTACC<br>TCA       | 59.9                             | 346                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_36560970  | Ca4                                     | 36560970                      | TAAAAAAAAA/TAAAAAAAAA                                         | CCGCATTGTTCCTT<br>CTTA        | TTGCAAAATCAATCCA<br>AACA   | 60.1                             | 746                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36561766  | Ca4                                     | 36561766                      | CTTTTTTT/CTTTTTTTTT                                           | GAACATGTTAATTTGGT<br>TCATTCCG | TTCAACTCAATGGAATT<br>TTGGA | 59.7                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36622848  | Ca4                                     | 36622848                      | ACCCC/ACCC                                                    | CTGTGAGTTGCAGGGA<br>ATGA      | GCCAAAGTGGCTTAAC<br>GTCTG  | 59.8                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36623599  | Ca4                                     | 36623599                      | T/TA                                                          | GAAAATATTGGGGGC<br>ATGA       | TCCTGAAATGTCTTTG<br>TTGCT  | 59.6                             | 292                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36631595  | Ca4                                     | 36631595                      | TC/TCC                                                        | CCCCCACTATGAAACA<br>CACC      | CTGAATGTTTAATCCCC<br>GGT   | 60.1                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36633157  | Ca4                                     | 36633157                      | AAATAAAT/AAATAATAAAT                                          | GTCCCTTCCAATAACG<br>TGGA      | GCTTTGATGGTGTAGC<br>CACTT  | 59.8                             | 411                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36693901  | Ca4                                     | 36693901                      | ACTCT/ACT                                                     | CCGCTTTCGTCAATTT<br>CAT       | TCCAGCTGTTTCTCGA<br>GGT    | 60.1                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_3683925   | Ca4                                     | 3683925                       | ATTTTTTTTT/ATTTTTTTTT                                         | CGACTGACCACATGGA<br>TTGT      | CGAGTCATCTATTGTT<br>TGCCA  | 59.4                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36854161  | Ca4                                     | 36854161                      | GCA/GCATCA                                                    | TGTTCATGATGCTTCCT<br>CTCC     | CCAAACGATTATCCAAC<br>CCT   | 60.2                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36902625  | Ca4                                     | 36902625                      | GTTTTTTTTTT/GTTTTTTTTTT                                       | TTTTCTCCTTCTCCGGT<br>TCA      | CACATAGAATTTGTGC<br>GCGT   | 59.8                             | 562                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_36957693  | Ca4                                     | 36957693                      | GTT/GTTT                                                      | GCCGAAAAAGTCCTCA<br>CAAA  | GCGGCTAGAAGTATCA<br>ACGG   | 60.2                             | 381                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36959669  | Ca4                                     | 36959669                      | CAAAA/CAA                                                     | CGGCAGACTTTTTCGT<br>CAAT  | AAAAATCACACGTGG<br>GGTC    | 60.2                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36960688  | Ca4                                     | 36960688                      | ATATCTTTGTTATTAT/ATATCTTTGT<br>TATTATCTTTGTTATTAT             | TTGATTTTGATGCAGG<br>TGGA  | CAAATACCTGTTGCCG<br>AGGT   | 60.0                             | 818                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36966828  | Ca4                                     | 36966828                      | ATTTTTTTTT/ATTTTTTTTTT                                        | AGACGACGAATAGGG<br>TGTG   | TTCGTGGTTTCATTGTT<br>AAACG | 60.0                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36968132  | Ca4                                     | 36968132                      | ATTTTTTTTT/ATTTTTTTTTT                                        | GGCGAAAGTACCCAAA<br>CAAA  | GACTTCTGCAAAGGAC<br>CTCG   | 60.0                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36968194  | Ca4                                     | 36968194                      | TAAAAAAAA/TAAAAAAAAA                                          | GGCGAAAGTACCCAAA<br>CAAA  | GACTTCTGCAAAGGAC<br>CTCG   | 60.0                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36969491  | Ca4                                     | 36969491                      | TAAAAAAAAA/TAAAAAAAAA                                         | CATGGGCCAAAAATAA<br>AAAGA | GAGCTGTGGAGAAGAA<br>AAGCA  | 59.0                             | 814                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36972358  | Ca4                                     | 36972358                      | CTTT/CTT                                                      | ACAACCAACAAATGC<br>GACA   | AGCCTTGAGCGACCAC<br>TTTA   | 60.0                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_36972540  | Ca4                                     | 36972540                      | AATATATATATATA/AATATATATATA<br>TATATATATA                     | TAAAGTGGTCGCTCAA<br>GGCT  | TCTACATTCAAATTGGG<br>GGC   | 60.0                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37011834  | Ca4                                     | 37011834                      | GTAACAACTAACTAA/GTAACAACTAA<br>TAACAACTAA                     | GGCCAAGCATTGTAAG<br>GGAA  | ACCATTGAACCCAAAC<br>CGTA   | 60.1                             | 816                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_37034691  | Ca4                                     | 37034691                      | ATTTTT/ATTTT                                                  | CTCCATTCCTTCCACT<br>CCA        | AGGGAAAACAAGGGTT<br>TTGG  | 60.0                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37038560  | Ca4                                     | 37038560                      | TGAGA/TGAGAGA                                                 | TGGTTTATAACACCGC<br>TTATATTCA  | AGGATTCAACCACAAA<br>GGACA | 59.0                             | 242                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37039222  | Ca4                                     | 37039222                      | TGGG/TG                                                       | CAATCTTTCTTTCAATT<br>CTCTACAAA | TGATTCTTGACACGGT<br>GGAA  | 57.5                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37040426  | Ca4                                     | 37040426                      | TAAAAAA/TAAAAAA                                               | GCGCTACAGAGACCT<br>TCAC        | GGTCATAACAAAGGC<br>CAGA   | 60.3                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37043985  | Ca4                                     | 37043985                      | TAAAA/TAAAA                                                   | CTAGTCCGGTGGACCC<br>GTAT       | TCACGAAATTAGCCCT<br>CCAA  | 61.1                             | 861                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37045715  | Ca4                                     | 37045715                      | AAT/A                                                         | CCAGCTGGCCATTTGT<br>AAAG       | TACCCCATATGGACAA<br>GGGA  | 60.6                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37047002  | Ca4                                     | 37047002                      | TAAAAA/TAAAAA                                                 | TTGACAATGAATTAAG<br>AAACTGGA   | TCAAACCCATTTCCAC<br>TTC   | 59.1                             | 227                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37047718  | Ca4                                     | 37047718                      | GTTT/GTT                                                      | ATACTCTGCACCACAC<br>ACGG       | ATGATTGTGCCTCGTG<br>AACA  | 59.6                             | 241                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37055356  | Ca4                                     | 37055356                      | TAAAA/TAAAA                                                   | TTCAAAACACTCCCT<br>CCAA        | AAACACAATACACTGTC<br>CGGC | 59.1                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37055534  | Ca4                                     | 37055534                      | ATTTTT/ATTTT                                                  | TGCTTTAAAGAGTGA<br>GAGGGAA     | AAACACAATACACTGTC<br>CGGC | 59.5                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_37057125  | Ca4                                     | 37057125                      | CTTTTT/CTTTTTT                                                | TGCACAGTCAATCCTC<br>TTCTG | TCATGTGTGTATGGAG<br>CACAAA | 59.0                             | 474                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37057389  | Ca4                                     | 37057389                      | ATTTTTTTTT/ATTTTTTTTT                                         | TGCACAGTCAATCCTC<br>TTCTG | TCATGTGTGTATGGAG<br>CACAAA | 59.0                             | 474                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37059654  | Ca4                                     | 37059654                      | CAAAAA/CAAAAAA                                                | ATTGATCCACATCGTC<br>CCAT  | TGGGGACTGGAAATG<br>GTTA    | 60.0                             | 345                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37070263  | Ca4                                     | 37070263                      | TC/TCAACTTTAC                                                 | TCAACTCCAATTCAAGT<br>GCG  | TGTTGCGTAGCCTCTG<br>AAAA   | 59.8                             | 206                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37092034  | Ca4                                     | 37092034                      | TGGGG/TGGG                                                    | CCAAGTTTTGTGCAT<br>TCCT   | CACCACAAATTTCAACA<br>ACGA  | 60.0                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37099831  | Ca4                                     | 37099831                      | TAAAAAA/TAAAAA                                                | TGAATAATTCGCGTAC<br>GGCT  | TGTGAGGAGCTCTTTG<br>TGGA   | 60.6                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37104817  | Ca4                                     | 37104817                      | ATATTAT/ATATTATTAT                                            | ACTACGCCATCATTTG<br>GAGG  | GGGGTGAGAGACCATT<br>TGAA   | 60.0                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37105871  | Ca4                                     | 37105871                      | TGA/T                                                         | AAGATTCTGTCTTTCCA<br>CCGA | ACGAAGGTCAAGCTCA<br>AGGA   | 58.8                             | 367                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37107564  | Ca4                                     | 37107564                      | TAAAAAAA/TAAAAAA                                              | CGACGAATTTGCAGAG<br>TCAA  | TCCCGCATTCAAATCCT<br>ATC   | 60.0                             | 751                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37108408  | Ca4                                     | 37108408                      | A/AATAT                                                       | GATAGGATTTGAATGC<br>GGGA  | TCATGCTGGCATGTTAT<br>GCT   | 59.9                             | 745                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_37110290  | Ca4                                     | 37110290                      | GC/G                                                          | TCCAACCCCGTACCTA<br>TTCA    | AATGCCAAAGGGTAT<br>GAAG   | 60.2                             | 804                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37119880  | Ca4                                     | 37119880                      | CTT/CTTCTTT                                                   | TGGGAAAAATTTGCAC<br>AACA    | ACGAAAATTCATGGCT<br>GTCC  | 59.9                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37119914  | Ca4                                     | 37119914                      | TTATA/TTATATA                                                 | TGGGAAAAATTTGCAC<br>AACA    | ACGAAAATTCATGGCT<br>GTCC  | 59.9                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37121983  | Ca4                                     | 37121983                      | ATTTTTTT/ATTTTTTTT                                            | TCAACATGACCTCCTTA<br>TGCTTT | TCCAAACACTCCAAACA<br>CCA  | 60.0                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37128859  | Ca4                                     | 37128859                      | G/GC                                                          | TTTGACGATGGATGCA<br>TAAGA   | TTTAGGTTGGCTTTGG<br>ATGC  | 59.1                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37128959  | Ca4                                     | 37128959                      | TGAG/TGAGAGAG                                                 | TTTGACGATGGATGCA<br>TAAGA   | TTTAGGTTGGCTTTGG<br>ATGC  | 59.1                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37131217  | Ca4                                     | 37131217                      | TC/T                                                          | TTGTGACCAAAGGTTG<br>GAGG    | AATTTGCGAGCATTAC<br>CTGC  | 60.9                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37131327  | Ca4                                     | 37131327                      | TAA/TAATAGTTTAAAAA                                            | CAACTCAAACCACCTT<br>CATTCA  | AATTTGCGAGCATTAC<br>CTGC  | 60.0                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37131533  | Ca4                                     | 37131533                      | TAA/TAAA                                                      | GACTCGCAGGTAATGC<br>TCG     | TTCCACGATTTCCCTT<br>CAC   | 59.6                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37132221  | Ca4                                     | 37132221                      | CTAT/CTATAT                                                   | GTGAAGGGAAAAATCGT<br>GGAA   | GGGCTCTCATAATCTT<br>GGAGG | 59.9                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_37149399  | Ca4                                     | 37149399                      | CTATAACTATAATAATATAACTATAA<br>TAA/CTATAACTATAATAA             | TTGGGAGGAGACAATA<br>TCCAA   | TCCATAACCGACCATG<br>AAGA     | 59.4                             | 337                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37156938  | Ca4                                     | 37156938                      | AG/AGG                                                        | CCATTGTATTTCCCAA<br>TGC     | AAGAATGAATGACGTT<br>GAATTTGA | 60.0                             | 210                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37194041  | Ca4                                     | 37194041                      | GAAAA/GAAA                                                    | GACACCAAAAGTAACC<br>ATGTCAA | TCCATGCACCTACATCT<br>TGC     | 58.9                             | 787                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37196987  | Ca4                                     | 37196987                      | AC/A                                                          | TTTTCATCGCCAACAAC<br>ATC    | AATTTACACCCCAACGA<br>ACC     | 59.5                             | 856                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37202310  | Ca4                                     | 37202310                      | CAAAAAAAAAAAAAAAAA/CAAAAAA<br>AAAAAA                          | AGAGTTTTGATTTGCA<br>CCCG    | AACCGTGACAAGGACA<br>CACA     | 60.1                             | 424                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37202681  | Ca4                                     | 37202681                      | TACA/TA                                                       | TGTGTGTCCTTGTCAC<br>GGTT    | GGGATCGATTTTCAAA<br>CAAAA    | 60.0                             | 335                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37203651  | Ca4                                     | 37203651                      | ATTT/ATT                                                      | TGATTCTGCATTGCTTC<br>TGC    | ATGGCAAGTGCAAGTC<br>AACA     | 60.1                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37204010  | Ca4                                     | 37204010                      | A/AAG                                                         | TGCCATGTACAGAGGA<br>CACAA   | TAGTGAAAAGGCATGT<br>GCAA     | 60.2                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37221016  | Ca4                                     | 37221016                      | A/AG                                                          | TGGTTGTCGACTTGTC<br>TTGC    | ATGCGGTAGCTTTTGA<br>TTGC     | 59.9                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37221300  | Ca4                                     | 37221300                      | GAAAAA/GAAAAAA                                                | CGAATCAAAAGCTACC<br>GCAT    | TGCAACAATTTTCACAT<br>AGCG    | 60.2                             | 150                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')         | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                 |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_37245007  | Ca4                                     | 37245007                      | GTAGCATA/GTA                                                  | AAGCGAGAGAGATTG<br>GGACT        | TTTTCATCCCCATTT<br>GAA      | 59.5                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37249911  | Ca4                                     | 37249911                      | GAAAAA/GAAAAAA                                                | TCGTCGATGAGATCAA<br>ATATGC      | GGCACAAAAGAGCTGG<br>TCAT    | 60.1                             | 251                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37270731  | Ca4                                     | 37270731                      | G/GTA                                                         | GCGGGGATTGAGGAAT<br>AAAT        | CCATTTCCTTAACACT<br>GCCA    | 60.1                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37283555  | Ca4                                     | 37283555                      | GT/GTT                                                        | TGAATGAAATATTGGAT<br>ACGTTTATGA | GCAGGGCATTGTCTC<br>TAGC     | 59.9                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37293607  | Ca4                                     | 37293607                      | GTATAT/GTATATAT                                               | TCGAACGACAATTATG<br>CTGC        | TACGAAGTTGACGCCA<br>CAAA    | 59.8                             | 259                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37305722  | Ca4                                     | 37305722                      | TGGG/TGGGG                                                    | TGCTGCAAAATATCAA<br>CGTACA      | CTTGTTACGTGGGAC<br>TTCA     | 59.3                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37306375  | Ca4                                     | 37306375                      | CTTT/CCTTTT                                                   | TCAATGAAGTCCCACG<br>TGAA        | TGCAGTCGAAACCAAA<br>AGTG    | 60.1                             | 381                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37308252  | Ca4                                     | 37308252                      | ATT/A                                                         | TCGCAACAACCATTTA<br>CCA         | TGCATGCAGAAAAGAC<br>ACAA    | 60.0                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37308462  | Ca4                                     | 37308462                      | GAGTA/GA                                                      | TTTTCTGCATGCAATAT<br>TTGG       | TGCAACCACATTCAAC<br>GACT    | 58.7                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37331887  | Ca4                                     | 37331887                      | CAA/CAAAA                                                     | TGACCGACGACTACAA<br>TTTCA       | AATGGATCACAAAAATC<br>ATGTGT | 59.2                             | 782                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                              |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_37332359  | Ca4                                     | 37332359                      | TC/T                                                                         | CACACATGATTTTGTG<br>ATCCAT  | ATTGGGCGATCAGCAA<br>ATAG   | 59.6                             | 243                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37332662  | Ca4                                     | 37332662                      | TAA/TA                                                                       | TCTGTAATCGGTTTGG<br>GCTC    | TCGACCAATGAACACG<br>CTAA   | 60.1                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37344294  | Ca4                                     | 37344294                      | AATTTATT/AATTTATTATT                                                         | TGTTGAATGTGTGTG<br>CTTCTATG | GAACCGGCTCAACGTG<br>TTAT   | 60.1                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37344783  | Ca4                                     | 37344783                      | TATTTAA/TA                                                                   | AGCCGGTTCTGACCAT<br>AAGA    | GGTGCAAGTCCTAAA<br>GCAAA   | 59.7                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37346206  | Ca4                                     | 37346206                      | TTTTATTTATTTATTT/TTTTATTTATT<br>TATTTATTT                                    | GCCCCAACGTGAACAT<br>TATT    | TCAATAATGCTGCCATC<br>CAA   | 59.7                             | 208                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37390225  | Ca4                                     | 37390225                      | TC/T                                                                         | CGCATCCATTAAAGAC<br>GGTT    | ATTTCTTTGGCGGAAT<br>GATG   | 60.0                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_3739769   | Ca4                                     | 3739769                       | TACCTCCGGAGGAAACCTCCGGAG<br>GAAACCTCCGGAGGAA/TACCTCCG<br>GAGGAAACCTCCGGAGGAA | GTTCCAAATGCGGTTG<br>ACTT    | CGAACGTTAACCTCGTC<br>GTCA  | 60.0                             | 906                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37403650  | Ca4                                     | 37403650                      | CTTTT/CTTTTT                                                                 | CTTATCCAAAAGCGAG<br>GCAC    | TGAGTTGGACTACAAG<br>CCATCA | 59.8                             | 597                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37403954  | Ca4                                     | 37403954                      | AC/A                                                                         | TGATGGCTTGAGTCC<br>AACTC    | TTCTCTCAGCCAATTAC<br>ACCC  | 57.8                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37406028  | Ca4                                     | 37406028                      | CGG/C                                                                        | ATTCATCCCCGACAAAG<br>ATCG   | CTGTAATCCACAATGC<br>CGTG   | 59.9                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_37443931  | Ca4                                     | 37443931                      | CT/CTAT                                                       | CCGCATTTTCTTCATTA<br>GGG      | ACGTTAAGGCATGAGT<br>TGGG   | 59.5                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37480497  | Ca4                                     | 37480497                      | CAAA/CA                                                       | GATCTTCCTTCAATGA<br>GATACCAGA | TTGTTGGCGAAACAAA<br>CAAA   | 60.0                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37483206  | Ca4                                     | 37483206                      | TAAAAAAAAAAAAA/TAAAAAAAAA<br>AA                               | AAATTGGGTGATGTGG<br>TGGT      | CCTAGAAGATGAGGGT<br>GCCA   | 60.0                             | 424                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37508257  | Ca4                                     | 37508257                      | ATTTTTTTTT/ATTTTTTTTT                                         | GGAGCTTTATGTTAG<br>ATGCATTG   | TCGTATCTCCACGATAA<br>GACCA | 59.2                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37540554  | Ca4                                     | 37540554                      | ATAATTAATTAATTAATTA/ATAATTA<br>ATTAATTAATTAATTA               | CGTGCAACCATCAAAT<br>ACAGA     | TGACTGAGTCCACTGC<br>CTTTT  | 59.6                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37608001  | Ca4                                     | 37608001                      | ACTCTCTCTCTCTCTC/ACTCTCTCT<br>CTCTCTCTC                       | TTGGATTCTGACACA<br>CACA       | TAAAAATTTGAGGGGA<br>GGGG   | 58.4                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37618447  | Ca4                                     | 37618447                      | ATAT/A                                                        | CATATGCCCATGTTGG<br>TTTG      | TTTCACACATCATCTTT<br>CACGA | 59.7                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37671559  | Ca4                                     | 37671559                      | CAA/CA                                                        | TTTCCACCCAGAAAGC<br>AATC      | GCAAAACAGAGGCAAC<br>ATCA   | 60.1                             | 250                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37695722  | Ca4                                     | 37695722                      | TTGTGTGTGTGTGT/TTGTGTGTGT<br>GT                               | TCGATCCTCACTCTCA<br>ACCA      | TTTTCAATGCATCTTCA<br>GCG   | 59.3                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37696000  | Ca4                                     | 37696000                      | TTGGCAATGGCA/TTGGCA                                           | CGCTGAAGATGCATTG<br>AAAA      | CGGATGAATCAAAACA<br>ATCCA  | 60.0                             | 273                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_37696707  | Ca4                                     | 37696707                      | TA/TATAGACATAA                                                | AATGTTTTGGTAATCC<br>CGGT | AACATTGGTGGTGCAA<br>GACA | 59.5                             | 607                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37703958  | Ca4                                     | 37703958                      | C/CAAG                                                        | TAGTGGGGAAGGTCTG<br>TTGG | TGTTGCTGCGTCTTGA<br>AATC | 60.0                             | 733                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37704077  | Ca4                                     | 37704077                      | AG/AAGAAGTCG                                                  | TAGTGGGGAAGGTCTG<br>TTGG | TGTTGCTGCGTCTTGA<br>AATC | 60.0                             | 733                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37704228  | Ca4                                     | 37704228                      | T/TG                                                          | AGGAGGGATCAAACCG<br>AACT | TGTTGCTGCGTCTTGA<br>AATC | 59.9                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37704299  | Ca4                                     | 37704299                      | T/TCAAA                                                       | AGGAGGGATCAAACCG<br>AACT | TGTTGCTGCGTCTTGA<br>AATC | 59.9                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37707068  | Ca4                                     | 37707068                      | C/CTGGCAAGGAGCTACT                                            | TGAGGCCTTAGCTTCG<br>TGAT | CACAAGGACCTGACGG<br>TTTT | 60.0                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37707135  | Ca4                                     | 37707135                      | C/CGCCCCCTCCCC                                                | TGAGGCCTTAGCTTCG<br>TGAT | CACAAGGACCTGACGG<br>TTTT | 60.0                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37707688  | Ca4                                     | 37707688                      | T/TTC                                                         | AAAACCGTCAGGTCCT<br>TGTG | TGAGCGTTTTCTCGGT<br>CTTT | 60.0                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37710631  | Ca4                                     | 37710631                      | CTTTT/CTTTT                                                   | ACGTGTTGAGCTAACC<br>CTGC | TCTACCTGCCATTTC<br>GATT  | 60.3                             | 275                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37746382  | Ca4                                     | 37746382                      | GTTTTT/GTTTT                                                  | TTGCAATAGGCATAGG<br>ACCC | TTGTTTCTCCCCAGTTT<br>TGG | 59.9                             | 448                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_37751701  | Ca4                                     | 37751701                      | TTCTCTCTCTCTCTCTCT/TTCTCTCTCTCTCTCT                           | GCGTGGAGTGAAAGAG<br>GAAG    | AGGAAAATCACAATGC<br>AGCC  | 60.0                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37751797  | Ca4                                     | 37751797                      | ATT/ATTT                                                      | GCGTGGAGTGAAAGAG<br>GAAG    | AGGAAAATCACAATGC<br>AGCC  | 60.0                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37760565  | Ca4                                     | 37760565                      | ACAAC/A                                                       | AAACCAAAAGAACACC<br>GCAC    | CCGAACCGGTTTTTCAG<br>TTTA | 60.0                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37788269  | Ca4                                     | 37788269                      | TT/TTAT                                                       | AAAATTGGTCCCAAGA<br>CTTCAA  | TGTTTGTGTTTCATCGG<br>CAT  | 59.9                             | 246                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_3779072   | Ca4                                     | 3779072                       | ATT/ATTTT                                                     | TTCTAACAACGTGTT<br>GATGC    | ACGTGCCTTTCGATTG<br>TTTC  | 60.0                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37817066  | Ca4                                     | 37817066                      | AATCTCTCTCTAT/AATCTCTCTCTA<br>TCTCTCTCTAT                     | CCCTTCAAAAGGTGGT<br>TCAA    | ACAACACTCACCTCAA<br>GCC   | 59.9                             | 816                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37850626  | Ca4                                     | 37850626                      | TG/T                                                          | CTGTATTTGCTCGCAT<br>CCAA    | TGTCCTCTCTTGAAT<br>TTTG   | 59.8                             | 722                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37871651  | Ca4                                     | 37871651                      | ATTTTT/ATTTTT                                                 | ACCCTACCCATTGTCA<br>ACCA    | TGGATGGTTATGATTT<br>GCTGA | 60.1                             | 668                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37872697  | Ca4                                     | 37872697                      | CAAA/CAAAA                                                    | TGATTTGGTTTGAGTAT<br>TATGCG | TTCTATTCTCAAAGGC<br>GGA   | 59.1                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37881000  | Ca4                                     | 37881000                      | ATTT/ATT                                                      | ACTTCGGGAAGAACTC<br>GTGA    | CATCGTGTTCCTGTGT<br>GGG   | 59.8                             | 172                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')        | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|--------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                       |                                |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_37891409  | Ca4                                     | 37891409                      | TA/TAAAAACA                                                           | GGATGTCACACAGGCT<br>TTCA       | AGTCCCATGTAATTGT<br>CACG  | 59.7                             | 764                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37895622  | Ca4                                     | 37895622                      | TATAGGAGATAGGAGAT/TATAGGA<br>GAT                                      | GCCAAACTTTGTCATT<br>GTATATGG   | TGTTAGACGGAGAACA<br>TGCG  | 59.7                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37909050  | Ca4                                     | 37909050                      | GTTTTTTT/GTTTTTTTTT                                                   | TGCATTTTAGGTCCAT<br>GATGA      | ATTTGACCACCGAAAG<br>ATGC  | 59.0                             | 190                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37977728  | Ca4                                     | 37977728                      | CGTGGTGGT/CGTGGT                                                      | GTTCCCAACTTGTGTG<br>CCTT       | TGCATTTATCACAGAC<br>ATTGA | 60.0                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37989911  | Ca4                                     | 37989911                      | TTATATATA/TTATA                                                       | CGTTGACTCGTTAATG<br>GAGC       | TCAATTACCAAAAGGG<br>CCAG  | 58.4                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37992000  | Ca4                                     | 37992000                      | TTATATATATA/TTATATA                                                   | ATCTCGAACATTTCCCA<br>CCC       | AGTGGAGGATTTTCCT<br>GGCT  | 61.1                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_37993885  | Ca4                                     | 37993885                      | CTATATATATATATATATATATAT<br>ATATATA/CTATATATATATATATATA<br>TATATATATA | GAAGGTCTTGCAAGTG<br>AGTGC      | CAAACGTGTGATGGAT<br>CTTCC | 60.1                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38015157  | Ca4                                     | 38015157                      | A/AG                                                                  | CAACGATGCTACTTAC<br>AAACGG     | TCATTTATTGAGGTG<br>GCAA   | 59.7                             | 723                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38017134  | Ca4                                     | 38017134                      | AAAACCTATAAA/AAAA                                                     | TGACAATCAAAGTACAA<br>TGAGTCAAA | AAAAGTTGTTGTGGCA<br>TCGG  | 60.0                             | 673                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38024785  | Ca4                                     | 38024785                      | GTATATATATATATATATATATAT<br>A/GTATATATATATATATATATATA                 | AAGTGAACCCCAAA<br>GGCT         | GCATGTGCCTCATTTT<br>GTTG  | 60.0                             | 230                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                   |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_38040589  | Ca4                                     | 38040589                      | CTAATA/CTAATATAATA                                                | CAACAAATATGTGCC<br>GTGC     | TGGTGGTTCCTTCC<br>TATC     | 60.0                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38074525  | Ca4                                     | 38074525                      | AC/A                                                              | TCCTTAAGCGTTGGTT<br>TGCT    | GAGTGGGGCATGTTGG<br>TACT   | 59.9                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38085487  | Ca4                                     | 38085487                      | AT/A                                                              | TCCCTTTCTTACGAAT<br>CCC     | CACTTGAAGAGGGCA<br>ACAT    | 60.3                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38108114  | Ca4                                     | 38108114                      | ATC/A                                                             | TCCACAACACACAA<br>AAAGG     | AATGCTATTGGGGCAG<br>TTCA   | 59.5                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38108391  | Ca4                                     | 38108391                      | CATATATATATATATATATATATA/<br>CATATATATATATATATATATATA<br>TATATATA | GGAAGAATGAAAATTG<br>CAGAAAA | CAATGCTATTGGGGCA<br>GTTC   | 59.6                             | 311                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38123299  | Ca4                                     | 38123299                      | TGTCTTC/T                                                         | ACGATGAGAATCGCAT<br>TTCC    | CCATTGCAAAACCAAG<br>CATA   | 60.0                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38124061  | Ca4                                     | 38124061                      | AT/ATT                                                            | TTACATTTTCATGGCC<br>TCA     | TGCTACCAAGGGAGCA<br>AAAT   | 60.0                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38137988  | Ca4                                     | 38137988                      | TG/T                                                              | TCGAGACCAATATGC<br>AAGA     | GCTCTCCGGACTTTT<br>CAAT    | 59.2                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38139279  | Ca4                                     | 38139279                      | CTA/CTATA                                                         | GTCGGAGGTGGTGAT<br>GAGTT    | TCAAGGTAATCCATCTA<br>GTCGC | 60.0                             | 686                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38169564  | Ca4                                     | 38169564                      | ATCTCT/ATCT                                                       | CCCAAAGGATATGCGT<br>GAAT    | ACGATCTGTCTCTGCA<br>AAGC   | 59.8                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_38204868  | Ca4                                     | 38204868                      | AATATA/AATA                                                   | CTGGTATCGTAGAAGG<br>AAGGAA    | GGCGGCGCTATTTATA<br>TTGA      | 57.5                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38284143  | Ca4                                     | 38284143                      | GAA/GA                                                        | AGACAATGTACGGTGC<br>CTCC      | TGATTTGGTTAAAGTG<br>GATGTTG   | 60.0                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38297090  | Ca4                                     | 38297090                      | CAA/CAAA                                                      | TGATCTGTTTGATGAC<br>CAAGATAAA | AAAAACAAAATCATGAC<br>TAACCAAA | 59.9                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38297845  | Ca4                                     | 38297845                      | GACCCTTAAAGTAC/GAC                                            | AAAGGTTTCCAGTCCA<br>CATTTT    | CATGATTCTTCGGTGT<br>CGTG      | 58.9                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38311670  | Ca4                                     | 38311670                      | TAA/TA                                                        | TGTAGGAACAAGGGCC<br>AAAG      | AGATCATGGCTATTCA<br>CCCAA     | 60.1                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38317091  | Ca4                                     | 38317091                      | AAA/AAACAA                                                    | TTTTAAATTTCCGAAA<br>CACAATG   | TCCAAACACACTTGATC<br>CCA      | 59.4                             | 211                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38317513  | Ca4                                     | 38317513                      | GTATATAAATATA/GTATA                                           | TGGGATCAAGTGTGTT<br>TGGA      | GGTTGCTCACTCCTTT<br>GGAC      | 59.9                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_3832898   | Ca4                                     | 3832898                       | ATTT/ATTTTTT                                                  | CGGAGGGTACGAACCT<br>GTAA      | ACTGTTGTGGAATCT<br>GGGC       | 60.0                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38354604  | Ca4                                     | 38354604                      | AT/ATT                                                        | CAATTTTCTCCGAAC<br>AGAA       | CAGGGACATTTAATTG<br>AACTTGA   | 59.2                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38368647  | Ca4                                     | 38368647                      | A/ATTCTACTTCAATT                                              | TATGTTTGGATTTTCC<br>GCTC      | TTGTCTTCCCGTTTAG<br>TGG       | 59.9                             | 751                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_38376891  | Ca4                                     | 38376891                      | ATT/AT                                                        | CCTAGAAAAAGGGCT<br>GATG    | TTTACGGTGCATCACA<br>ATCA   | 58.8                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38377327  | Ca4                                     | 38377327                      | TTT/TTTGAATT                                                  | TGATTGTGATGCACCG<br>TAAAA  | AGCGAAAGTTCCTTGA<br>GGGT   | 60.0                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38378071  | Ca4                                     | 38378071                      | TATATA/T                                                      | TTCTATTCAACAACG<br>GTGG    | CTTCTGTGCTGTGCTT<br>TGG    | 59.5                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38379738  | Ca4                                     | 38379738                      | ATTTAAATTAT/ATTTAAATTATTTTA<br>AATTAT                         | AATTTATCCACATCTT<br>CAAAAA | CTCCGTGTTAAGCCGA<br>AAAA   | 57.7                             | 712                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38457252  | Ca4                                     | 38457252                      | CTGTGT/CTGT                                                   | CGATCACCAAGTCCCC<br>TAAA   | CCACTCCCTCCAATCTT<br>CAA   | 59.9                             | 344                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38479454  | Ca4                                     | 38479454                      | CAAAA/CAAA                                                    | GGTGGGATCCATTGA<br>GTTG    | CCGAAGGCTTTCTTCA<br>ACAG   | 60.2                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38480745  | Ca4                                     | 38480745                      | TGG/TG                                                        | GTGGAGCTTCTTTGGG<br>TGAC   | ATCACCACCGAAAACT<br>TGG    | 59.7                             | 844                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38482887  | Ca4                                     | 38482887                      | CAAAAA/CAAAA                                                  | CAATGAGAGCGTTAA<br>GGCAG   | TGTCCTTCAATTCATT<br>TCCAA  | 60.0                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38482961  | Ca4                                     | 38482961                      | A/AC                                                          | TTGGAAATGAAATTGAA<br>GGACA | TTGTTGATTCTAACCT<br>TGCTCA | 59.4                             | 193                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38483289  | Ca4                                     | 38483289                      | AATATATATA/AATATATATATA                                       | TTGGAAATGAAATTGAA<br>GGACA | TTGGTTTCCTTTGCACA<br>CTG   | 59.4                             | 636                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_38483484  | Ca4                                     | 38483484                      | AATA/AATATATA                                                 | TGAGCAAGGTTAGAAA<br>TCAACAA | ACCATTGTTTCCTTG<br>CAC    | 58.9                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38567221  | Ca4                                     | 38567221                      | GAATAAAA/GAA                                                  | GACAAAAATGAGAAAG<br>ACCTGGA | AAATGCTGCCGAAGAA<br>GCTA  | 59.6                             | 824                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38568371  | Ca4                                     | 38568371                      | TAAAAAAAAAAAAA/TAAAAAAAAA                                     | TCTCGACTTTTAAGCAA<br>GCCA   | TGTCCATGAAGAAAGA<br>GCCC  | 60.1                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38568495  | Ca4                                     | 38568495                      | ATATT/ATATTATT                                                | CGAAATTGACAAAATCA<br>CAATCA | TGTCCATGAAGAAAGA<br>GCCC  | 59.9                             | 340                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38573939  | Ca4                                     | 38573939                      | TAAA/TAA                                                      | TGGGAATTGGAATTG<br>GAAA     | TCATTTGCTTTGTGAG<br>GAACA | 60.1                             | 767                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38585075  | Ca4                                     | 38585075                      | ATTCTTCTTCTTCTTCTTCTC/ATTC<br>TTCTTCTTCTTCTC                  | AGGCCCAAATTTGTT<br>GTTG     | TCGATTTGCAATACCA<br>CGA   | 59.8                             | 457                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38585148  | Ca4                                     | 38585148                      | ATTTTTTTTT/ATTTTTTT                                           | AGGCCCAAATTTGTT<br>GTTG     | GGGAGTGGTGTGTAC<br>ATCG   | 59.8                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38604351  | Ca4                                     | 38604351                      | TA/TAA                                                        | GCGAACGTATTGGACT<br>GGTT    | GAAACCAATTTCTCC<br>GTGA   | 60.0                             | 619                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38615844  | Ca4                                     | 38615844                      | TAAGAAGA/TAAGA                                                | GGTGAGCCACGGAAAA<br>ATAA    | TTTGGAGACACCAAGC<br>CTCT  | 59.9                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38618852  | Ca4                                     | 38618852                      | CATAA/CA                                                      | GCCGACAGAGAAAATC<br>CAAA    | ATTGGGGAAGGCCTTG<br>ATAA  | 60.2                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_38619240  | Ca4                                     | 38619240                      | TAAA/TAAAA                                                    | TTATCAAGGCCTTCCC<br>CAAT    | CCAGCAGTTTCATT<br>GGTT    | 60.6                             | 545                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38626043  | Ca4                                     | 38626043                      | AATTATTATT/AATTATT                                            | TTGATTCTCTTTGTGTG<br>TGTGCT | GACCGCAGATGTAATT<br>TAGCC | 59.8                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38644984  | Ca4                                     | 38644984                      | GTTT/GTT                                                      | TAGAGGCCCAACAACG<br>TAGC    | ACCTCGACAACCACTT<br>GCTC  | 60.3                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38648334  | Ca4                                     | 38648334                      | GTACAA/GTACAATACAA                                            | AACGAAAACGAGGAGA<br>GCAA    | GAGACACGGTTTTTGG<br>CAAT  | 60.0                             | 258                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38649330  | Ca4                                     | 38649330                      | AG/AGG                                                        | TGTGCTGCATTCCAAC<br>TCTC    | CGATGATTATCCCTG<br>CCAA   | 60.0                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38656963  | Ca4                                     | 38656963                      | TAAAA/TAAAA                                                   | TTGACTTGCATTGATGT<br>GCC    | TGGTGAAAAATCGACGA<br>ATCA | 60.7                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38668986  | Ca4                                     | 38668986                      | CCA/CCACA                                                     | AAAACCAACATTGGC<br>AAGC     | GCTGTCCCTGAAGCAA<br>GTTC  | 60.0                             | 307                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38682900  | Ca4                                     | 38682900                      | TACAAACATAA/TA                                                | TTTAAATTTGAATTGTC<br>CCCG   | GTCAATTCGCTTGCACT<br>TGA  | 58.8                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38686412  | Ca4                                     | 38686412                      | AA/AAGGTGGAAGA                                                | AGGTCAAGCACCCACT<br>TCAG    | TTACAATCTTCGGGT<br>CCTC   | 60.3                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38691498  | Ca4                                     | 38691498                      | CA/CATGTGACTA                                                 | TTGGCCCTATTGAAA<br>GATG     | ATGGTGACACCCCCCT<br>ACTA  | 60.0                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_38705713  | Ca4                                     | 38705713                      | ATTTTTTT/ATTTTTTTTT                                           | TTGGGTACAACCTCCGT<br>CACA  | TCAAAATCTTCCTTCAA<br>TGCAA | 60.0                             | 715                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_38710772  | Ca4                                     | 38710772                      | TCACAAAA/TCACAAAAATAAAA<br>CACAAAA                            | TGGTGACACAAATGGC<br>AAAC   | TCCCTTTCAATTGCCAA<br>ATC   | 60.4                             | 309                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_38714491  | Ca4                                     | 38714491                      | TTTGAAC/TTTGAACCTGAAC                                         | AAGGAGAAACCAAAAA<br>TGTCAA | TTTTTCGTTTGAATGG<br>AAGATT | 57.8                             | 444                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_38726989  | Ca4                                     | 38726989                      | TA/T                                                          | TACCTGACTACCCAC<br>TGCC    | TGTTTACAATTTGACG<br>AGCA   | 60.0                             | 501                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_38733548  | Ca4                                     | 38733548                      | TT/TTTAACCTCGTGT                                              | TTTGTCTGCCTAACT<br>CGCT    | CGCTAGATGCAAAATG<br>GGAA   | 60.0                             | 360                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_38734510  | Ca4                                     | 38734510                      | T/TTTCATGCACCTAAGA                                            | GAGACCAAATCTCATC<br>CCCA   | AAGTTGGAAAAATCGG<br>AGGT   | 59.9                             | 180                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_38739330  | Ca4                                     | 38739330                      | CATA/CA                                                       | ACTTCAACATCCAAC<br>CCG     | GGAAAAATGAGAGAAG<br>GGGC   | 60.0                             | 112                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_38742074  | Ca4                                     | 38742074                      | TTATATATATATATATAT/TTATATAT<br>ATATATAT                       | GCCATAAACACAACCC<br>TTTCTT | AAAATTCAGCGAGATT<br>CTTTG  | 59.4                             | 954                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_38743790  | Ca4                                     | 38743790                      | ACC/AC                                                        | TTCCCATAAATGGAAT<br>GCAA   | GCCAACCCTATGTGCA<br>TTTT   | 58.8                             | 205                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_38744817  | Ca4                                     | 38744817                      | CAAAAA/CAAAA                                                  | GAAGCACCATCGACCA<br>CTTT   | TGGTGGCACTAGGTGT<br>ATTGA  | 60.1                             | 194                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                   |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_38750092  | Ca4                                     | 38750092                      | GAAA/GAAAGAGAGAAAA                                                | GGAGATGAGGACAGG<br>GACAA    | CAAGTGGGGTGGGAGT<br>AAGA   | 60.0                             | 155                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38772029  | Ca4                                     | 38772029                      | GTTT/GTT                                                          | AATAGGTGGCGATGAG<br>TTCG    | GCTCTGCAATAGTTCT<br>CCCG   | 60.1                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38772279  | Ca4                                     | 38772279                      | ATT/ATTT                                                          | CGGGAGAACTATTGCA<br>GAGC    | AAATGCCACGTAGGTG<br>AAAA   | 60.0                             | 159                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38772463  | Ca4                                     | 38772463                      | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATAT                 | CGGGAGAACTATTGCA<br>GAGC    | CTGATAGAAGGTTGGA<br>TTTGGA | 60.0                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38806144  | Ca4                                     | 38806144                      | AA/AATGTTA                                                        | TGTTGGTCTCCGTAAC<br>TTCTCA  | CCATGACCCGAGTCTA<br>TTGAA  | 59.8                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38806212  | Ca4                                     | 38806212                      | TA/TAA                                                            | TGTTGGTCTCCGTAAC<br>TTCTCA  | GGATGCCATGAATGAA<br>GCAT   | 59.8                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38822967  | Ca4                                     | 38822967                      | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATA<br>TATATAT | TCTATGGCAACCTAAG<br>CCGT    | CATGTGCAATGTACTT<br>GGTTCC | 59.7                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38830492  | Ca4                                     | 38830492                      | A/ATTGTTG                                                         | CAACGCCACAACCTCTT<br>CTCA   | AGCTCGGTCATTTTC<br>AACT    | 60.0                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38859836  | Ca4                                     | 38859836                      | GATAT/GAT                                                         | TGTTGCTTCATCTGGT<br>TTATACG | TGATAATGGTGGAAGT<br>GGCA   | 59.2                             | 299                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38874560  | Ca4                                     | 38874560                      | ATTATTTAAAT/ATTATTTAAATTT<br>ATTTAAAT                             | TGATTCAATACCCGC<br>GAAA     | CCAAGCATGAACCTAC<br>TCCC   | 60.1                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_38885489  | Ca4                                     | 38885489                      | ATT/AT                                                        | CATAGCATAGGGTGGT<br>GCCT   | GCACGCAATTCCTCCA<br>TATT  | 60.0                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38886119  | Ca4                                     | 38886119                      | ATT/ATTTT                                                     | ATTGGTTACGCGACCA<br>ACTC   | AAATTTTGAGCGGTTG<br>ATGC  | 60.0                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38886399  | Ca4                                     | 38886399                      | AATATATATATATATATATA/AATATA<br>TATATATATATATATATATA           | TATTGCATCAACCGCT<br>CAAA   | TACACATGCATAGGTG<br>GCCT  | 60.2                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38887313  | Ca4                                     | 38887313                      | CG/C                                                          | TCATTGCTATGACCCC<br>AGTTT  | GGGGAGGATCACGGA<br>CTATT  | 59.4                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38887574  | Ca4                                     | 38887574                      | AAAATAAA/AAAA                                                 | AATAGTCCGTGATCCT<br>CCCC   | TTTGTGTTGTTTCCCCAA<br>TCA | 60.2                             | 240                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38895087  | Ca4                                     | 38895087                      | AT/ATT                                                        | CACGGATGTAATTTAG<br>CCGAA  | TGATGGACCTGGGTTT<br>TGAT  | 60.0                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38895946  | Ca4                                     | 38895946                      | AGTGT/AGT                                                     | TGCAATCGATCTAGTTT<br>AAGCC | GCATAAAGATGGTGGT<br>GCCT  | 58.5                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38915071  | Ca4                                     | 38915071                      | AAGAGAGAGA/AAGAGAGA                                           | ATCTCTTCATTACCAC<br>CCG    | CCCTCATTGAAAGTGC<br>CATT  | 59.9                             | 155                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38937830  | Ca4                                     | 38937830                      | ATTT/ATT                                                      | GTTTTCTCAAAAATTT<br>CCCAA  | TCAAAACAAGATTACG<br>GGGC  | 57.4                             | 377                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38943074  | Ca4                                     | 38943074                      | ATTTTTTTTT/ATTTTTTTT                                          | ATGCGGGTATGGAGGT<br>GATA   | AGAAAAGGGAGAAGAT<br>CGGC  | 60.2                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_38944216  | Ca4                                     | 38944216                      | AACGTG/A                                                      | TGATTCCGTCATGTG<br>TTTT   | CAAAATCCATCATTCT<br>CCCA   | 60.0                             | 246                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38949129  | Ca4                                     | 38949129                      | GTGGTTATGGT/GTGGTTATGGTTA<br>TGGT                             | GAAGCGACGGTCTCAG<br>TTTC  | CGCTTCGCATACTGAT<br>TTGA   | 60.0                             | 979                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38949892  | Ca4                                     | 38949892                      | GT/G                                                          | TCAAATCAGTATGCGA<br>AGCG  | ACCCACACAACACACA<br>TGCT   | 60.0                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38950263  | Ca4                                     | 38950263                      | CA/CAA                                                        | AGCATGTGTGTTGTGT<br>GGGT  | TTAATCATCCATGAAATC<br>GCAA | 59.9                             | 743                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38955357  | Ca4                                     | 38955357                      | GATAAAATA/GATA                                                | GAGTTTTGGGGTGACA<br>TGCT  | CATCCTGCACAATGCT<br>GTTC   | 60.0                             | 251                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38970599  | Ca4                                     | 38970599                      | CCTT/C                                                        | AGCGTACGAGAAGGAG<br>TCCA  | ACCAAAATGGCAATGA<br>GGAC   | 60.0                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38987085  | Ca4                                     | 38987085                      | GTTTTTT/GTTTTTTTT                                             | GAGCGGCTAAATGGAT<br>CAAA  | AAAGTTTGGAGGGGAG<br>GAAA   | 60.2                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38994620  | Ca4                                     | 38994620                      | ATGTATT/ATGTATTGTATT                                          | GCATACCCTTTTCCGG<br>TCTT  | GCATGCTCTAATCCATT<br>CCAA  | 60.3                             | 769                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_38997590  | Ca4                                     | 38997590                      | TCAA/T                                                        | ACCCACCACTGATTCC<br>ATGT  | TGCTTCAACTAGCACT<br>CGGG   | 60.1                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39001801  | Ca4                                     | 39001801                      | AG/A                                                          | TTGGGTCTGTAAATTG<br>CAAGC | TTCAAATGCAAAACGAA<br>TGAA  | 60.1                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_39002456  | Ca4                                     | 39002456                      | ATT/AT                                                        | TTCATTGTTTTGCATT<br>TGAA   | TTTGACGGAAGTTTTCC<br>ACTTT  | 59.2                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39013296  | Ca4                                     | 39013296                      | GTATATATATATAT/GTATATATATAT                                   | ACCAACGGAGAGTTTG<br>CCTA   | TTCACCTTCGACAGCAAA<br>ACG   | 59.7                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39020294  | Ca4                                     | 39020294                      | GTCACGA/GTCACGACTCACGA                                        | ACTCCGTGCAAGGAAT<br>TTGA   | TTTGCCACATTTGAGG<br>AAATAG  | 60.6                             | 278                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39020809  | Ca4                                     | 39020809                      | TAAAA/TAAAAA                                                  | TCCAATTACCAATAAC<br>AAATGC | CCCCAATGTATTGGAA<br>CCAC    | 60.0                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39027557  | Ca4                                     | 39027557                      | CCAAACA/CCA                                                   | CGGTGTTTTGAGTGAG<br>AGAGTT | CAGCCACCAACAAC<br>ATTG      | 58.5                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39062674  | Ca4                                     | 39062674                      | TA/TAATGCA                                                    | GGTCCGTGTGGTTAAT<br>TTGG   | AATTGCATGTTGGTTCA<br>TGG    | 60.1                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39074802  | Ca4                                     | 39074802                      | AGGGGG/AGGGG                                                  | AGAAGCCCTGAAAGCA<br>ACAA   | AATTTATGCCATTGCTT<br>CGG    | 60.0                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39078155  | Ca4                                     | 39078155                      | ATTTTTT/ATTTTTTT                                              | TGTGTGCAATAGAAGG<br>TCGC   | CATCACTAGGATGCGA<br>TCACC   | 59.9                             | 347                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39078527  | Ca4                                     | 39078527                      | AAATAA/AAA                                                    | GTGTGCAATAGAAGGT<br>CGCA   | CGAAGTAACAATTGTG<br>TAAGGGG | 59.9                             | 860                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39079360  | Ca4                                     | 39079360                      | TATTTAC/TATTTCACTCACATTT<br>AC                                | TGACGCCTGTTTGTC<br>ATGT    | GTTGAGGAAAAAGAG<br>TGCG     | 60.2                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_39156446  | Ca4                                     | 39156446                      | TAAAAAAAAA/TAAAAAAAAA                                         | GAGCATCGCAGGTTGA<br>ATT   | CCGCATGAGATATTT<br>GCATT   | 60.2                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39165742  | Ca4                                     | 39165742                      | TAAAAATAAAAAATAAAAA/TAAAAA<br>TAAAAATAAAAAATAAAAA             | CGTATACCGCTGCTCA<br>TCAA  | TGATGTGATTGTGCC<br>ATGA    | 59.9                             | 259                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39249438  | Ca4                                     | 39249438                      | CTTTTTTT/CTTTTTTT                                             | ATTGTTTGGCTCCACA<br>CCTC  | TTCAACAGGAGTATT<br>TTATGCG | 60.0                             | 245                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39257138  | Ca4                                     | 39257138                      | ATTTTTTTTT/ATTTTTTTTT                                         | TTTGCATTACGAATTTG<br>ATGA | TGAATTTCCGACTTG<br>GTC     | 59.2                             | 181                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39356109  | Ca4                                     | 39356109                      | CCTCTC/CCTCTCTC                                               | TCTCTACCTGTGGTT<br>GCCT   | ACTTTTTCGGAGAAGC<br>ACAT   | 59.7                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_3951674   | Ca4                                     | 3951674                       | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATATAT           | GCACAACCAAGTCACCA<br>CTCA | AGGAAGCAAGGGATCA<br>AACA   | 60.8                             | 918                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39641904  | Ca4                                     | 39641904                      | CATATATATATATATATATATATA<br>T/CATATATATATATATATATATAT         | CCTTTAGCGTATGCAC<br>TGAGC | TAACCATCTCCACCGA<br>CACA   | 60.1                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39642176  | Ca4                                     | 39642176                      | CAAAAA/CAAAA                                                  | CCTTTAGCGTATGCAC<br>TGAGC | TAACCATCTCCACCGA<br>CACA   | 60.1                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39643073  | Ca4                                     | 39643073                      | CA/CACAA                                                      | TCGTACCTTGATCAC<br>CGCA   | AACGCGCGGGTTATAT<br>TCTA   | 60.1                             | 276                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_39644534  | Ca4                                     | 39644534                      | GAA/GA                                                        | TGAGCTTTTAGGTGGC<br>ACAA  | TGACACTCATTGCTCCT<br>CCA   | 59.5                             | 700                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                   | Forward primers (5'-3')     | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------|-----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                 |                             |                                |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_39689187  | Ca4                                     | 39689187                      | AC/ACC                                                                                                          | ATTACCGACATTGCAG<br>AGGG    | CTCCATTCTGCCCTT<br>GATA        | 60.0                             | 329                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_3991086   | Ca4                                     | 3991086                       | ATTCTC/ATTCTCATTCTC                                                                                             | AGCCTTCTCCAGCAAA<br>AACA    | AGCATGCAAATGCAAA<br>CAAA       | 60.0                             | 217                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_39987654  | Ca4                                     | 39987654                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                                                                       | TAAATTCCGCTGTGCA<br>CTTG    | AACTTACCGATCAATTC<br>AAATCAA   | 59.9                             | 191                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_40056699  | Ca4                                     | 40056699                      | AATATATATATATATATATATATAT<br>ATATATATATATATATATATAT/AA<br>TATATATATATATATATATATATAT<br>ATATATATATATATATATATATAT | CAGGACAGGGATGGT<br>GTTTT    | TTGCAATTCATGAATG<br>TTACTCA    | 59.8                             | 639                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_4008216   | Ca4                                     | 4008216                       | TTATATA/TTATA                                                                                                   | GCTTCCTAAGAAACCT<br>CATTCAA | TGGTTTTAATTTAGAGT<br>TGATCCAAG | 58.9                             | 796                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_4008273   | Ca4                                     | 4008273                       | TTTTAAATATATTTAAATA/TTTTA<br>AAATATATTTAAATATATTTAAATA<br>A                                                     | GCTTCCTAAGAAACCT<br>CATTCAA | TGGTTTTAATTTAGAGT<br>TGATCCAAG | 58.9                             | 796                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_40111947  | Ca4                                     | 40111947                      | GAATAATAATAATAATAATAATA<br>ATA/GAATAATAATAATAATAATA<br>ATA                                                      | TGCAAGTTGCTATCCC<br>ATTG    | TTGCAATACGGATCAC<br>AAAAA      | 59.7                             | 753                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_4011481   | Ca4                                     | 4011481                       | ACC/AC                                                                                                          | TTTTGGGCTCAAATTT<br>ACG     | TGAATGGTTAATGGAT<br>GACAGTG    | 59.9                             | 348                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_4013042   | Ca4                                     | 4013042                       | T/TGA                                                                                                           | GCATATTGTGTTTGT<br>GTGCAA   | CACAAACACTAATTTGT<br>TGCCA     | 58.5                             | 539                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_4013283   | Ca4                                     | 4013283                       | GTA/GTAAAGTGTGATGCTATA                                                                                          | TTGCCAACAAATTAGT<br>GTTTGTG | CTTGCCAAGCAAATCA<br>ACA        | 60.0                             | 508                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                   |                         |                         |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_4016329   | Ca4                                     | 4016329                       | T/TA                                                              | CGATGTGACCGACCAGTTTA    | TTGCCCACACTTACTGTGAA    | 59.6                             | 452                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_4025049   | Ca4                                     | 4025049                       | CT/C                                                              | CGA AACATATCCAAATCGGG   | ACCGAGCCATAGTGACCAAC    | 60.1                             | 175                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_40251301  | Ca4                                     | 40251301                      | TTATATATATATATATATATATATATATATA/TTATATATATATATATATATATATATATATATA | ATAATTGAGATGGGATGGCG    | CAATGCTAGGCCACAACCTT    | 59.7                             | 693                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_40265020  | Ca4                                     | 40265020                      | GTTTTTTTT/GTTTTTTT                                                | AATCTGTGTTGACGCA CGAG   | TTTTCTCCTCATTTTT CGTT   | 59.9                             | 681                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_4031680   | Ca4                                     | 4031680                       | AT/ATAACAGT                                                       | AAAATTTCTCTCCCCTCTCC    | AACCACGACTAAAACGACGC    | 59.9                             | 859                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_4032682   | Ca4                                     | 4032682                       | TAA/TTTAATAAGAGAA                                                 | ATCAGTAAAGCAACCC CAGC   | CAACGGTGGAGTTTGG ATCT   | 59.2                             | 346                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_4034664   | Ca4                                     | 4034664                       | ATTT/ATTTT                                                        | CAAACGTGGACGACTTCTCA    | AGCGCGCCCTTAATAGAAAA    | 59.9                             | 352                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_4035364   | Ca4                                     | 4035364                       | AT/A                                                              | TTTTCTATTAAGGGCC GCCT   | GTAACCTTTGCACGCTCCAT    | 60.1                             | 772                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_4037177   | Ca4                                     | 4037177                       | GTTTTTTTTTTTT/GTTTTTTTTT                                          | AAAGTGAAAGCCACTCCAA     | AATGTCGCCACCACTTTTC     | 59.7                             | 369                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_4037315   | Ca4                                     | 4037315                       | ATTTATTTT/ATTTATTTTATTTT                                          | AAAGTGAAAGCCACTCCAA     | AATGTCGCCACCACTTTTC     | 59.7                             | 369                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_4039327   | Ca4                                     | 4039327                       | TACTC/T                                                       | TTTGGTTTGGTAATTG<br>TGGG  | TGATGGAGAAATCCTC<br>ACCC      | 59.6                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4041384   | Ca4                                     | 4041384                       | A/AC                                                          | GGGTTTTGGTTGAAAT<br>TTTTG | TAATGACGACCAGCGA<br>ATGA      | 58.4                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4045322   | Ca4                                     | 4045322                       | CAA/CAAAAA                                                    | CACGATGTTCTACAG<br>TACCA  | AGGAGGAAACAAACCC<br>AACA      | 58.6                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40460183  | Ca4                                     | 40460183                      | AATATATATATATATATA/AATATA<br>TATATATATATATATA                 | CAAGCGTTTTGATAGG<br>GTCA  | CCGTAAATAACAGTACA<br>ATGGTGAA | 58.8                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40487175  | Ca4                                     | 40487175                      | AAT/AATAT                                                     | TTTCCGCGATTTGATC<br>ATT   | GGCTAAATAGCATTCTG<br>CAATC    | 60.4                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40503609  | Ca4                                     | 40503609                      | TA/TACTCTCAA                                                  | GTGGTGTGTGCAAGAA<br>TTGG  | CCAACAAGTAGGGTGG<br>AGGA      | 60.0                             | 800                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40506274  | Ca4                                     | 40506274                      | CAGTATAATAGTA/CAGTATAATAGT<br>ATAATAGTA                       | GTGGCTGTTTATGGAT<br>TGGG  | TGATCCCCCTTCATTCCT<br>TCA     | 60.2                             | 239                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40514871  | Ca4                                     | 40514871                      | AATA/AA                                                       | GGAGAACCAGCTTCCT<br>CCTT  | CGCTCTTGCTTCCTTTC<br>ACT      | 59.8                             | 278                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40515212  | Ca4                                     | 40515212                      | CG/C                                                          | GGAGAACCAGCTTCCT<br>CCTT  | TTCTCGGTTCTCCTTTC<br>TGC      | 59.8                             | 916                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40526310  | Ca4                                     | 40526310                      | CATATATAT/CATATATATAT                                         | CACGGAATTGATCCCC<br>TTATT | TGCATGCCACTAATCG<br>TTGT      | 60.0                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                               |                              |                              |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_40560588  | Ca4                                     | 40560588                      | TAAAAAA/TAAAAAA                                                               | TCATTCTCCCGATCTTC<br>CAC     | TTTCTGTGGACTCACG<br>CATC     | 60.0                             | 636                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_40571712  | Ca4                                     | 40571712                      | T/TG                                                                          | CACTCATCATAGCCCC<br>CTGT     | AGATGCACGACAATGC<br>TTCA     | 60.0                             | 711                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_40573539  | Ca4                                     | 40573539                      | AG/A                                                                          | TATTGCACCGTTGCCT<br>TACA     | TCAACTTCCTTGTTAT<br>ATTTTTGC | 60.1                             | 721                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_40574527  | Ca4                                     | 40574527                      | TA/T                                                                          | TGCAGATGAGTTTTTG<br>TCCA     | TTTAAATGATTTTTCGC<br>AATGA   | 57.8                             | 426                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_40575366  | Ca4                                     | 40575366                      | ATTTTTTTTT/ATTTTTTT                                                           | CAATGTTGAACCTTCCT<br>TTGTCTT | TCACCAGTGACACGTT<br>CGAT     | 58.8                             | 768                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_40601986  | Ca4                                     | 40601986                      | TTATATATATATATATATATATATA<br>TATATATATATAT/TTATATATATATA<br>TATATATATATATATAT | GGTGCCTTATGGGTTA<br>GGAA     | TGTTTGTTGAGTTGGA<br>AGACTTG  | 58.9                             | 935                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_40602662  | Ca4                                     | 40602662                      | GAAAAA/GAAAAA                                                                 | CCATTACGATGCACAT<br>TGCT     | TGAATTGTTCTTACGAG<br>CCG     | 59.6                             | 257                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_40604039  | Ca4                                     | 40604039                      | TGGGGGG/TGGGGG                                                                | TTTGTCGTAGTCACTCT<br>CCGT    | GTGCCCTAAAAAGAG<br>GGTC      | 57.5                             | 719                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_40608520  | Ca4                                     | 40608520                      | GTTTTTTTT/GTTTTTTT                                                            | TTTTTGCAAACGACAAC<br>TTTCT   | TGTGAATACGTGACTTT<br>TCTTTCA | 59.0                             | 432                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_40615032  | Ca4                                     | 40615032                      | TAA/TA                                                                        | GAGCCCAACGATGTTT<br>AAAT     | TGAACCCCAACGAGCAT<br>TATT    | 59.9                             | 793                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_40621809  | Ca4                                     | 40621809                      | AAGA/AA                                                       | TCTTTTGCACGGAGAA<br>TCAA    | TTCCCGTGACGTGTGT<br>ATGT  | 59.4                             | 320                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40624782  | Ca4                                     | 40624782                      | TAAAAA/TAAAA                                                  | TCAAAAGAATGGAGCA<br>AGTTGT  | GGGGGCATTAAAGAAGG<br>AAAT | 58.9                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4063264   | Ca4                                     | 4063264                       | GTTTTTT/GTTTTT                                                | GAACCCGCGTCATTG<br>TAA      | TTGTGTGCGTGTGTGT<br>ATGTG | 59.5                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40633755  | Ca4                                     | 40633755                      | GTTTTTTTTTTT/GTTTTTTTTTT                                      | GTGTGTCCAAAAGTGC<br>GAGA    | CCCATAATTTCTTGG<br>GGC    | 59.9                             | 726                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40638727  | Ca4                                     | 40638727                      | AATATATATAT/AATATATATATAT                                     | TCCTTCTAGCACATGG<br>TCCC    | TTGGAAAAGCCGCAAT<br>CTAT  | 60.1                             | 863                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40639226  | Ca4                                     | 40639226                      | AGG/AG                                                        | AATAGATTGCGGCTTT<br>TCCA    | CAAGAAACCGTTGTGG<br>TCCT  | 59.7                             | 158                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40639974  | Ca4                                     | 40639974                      | AATATATATAT/AATATATATATATAT                                   | CAACGCTATTTACCCA<br>CCCA    | TCCTATGGAACCACCA<br>AAGC  | 60.7                             | 200                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40649020  | Ca4                                     | 40649020                      | ATTTTTT/ATTTTTTTT                                             | TGTGATTATCCGGTAC<br>CACAAAC | TGTATTGAGGACCTCG<br>CAGA  | 59.6                             | 207                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4068418   | Ca4                                     | 4068418                       | ATTTTTTTTTTT/ATTTTTTTTTT                                      | ATAGATGGTCGCATTG<br>TGCG    | TCATCAAATCCGTAACG<br>CAA  | 59.9                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4068531   | Ca4                                     | 4068531                       | T/TTTC                                                        | CGTGCCAAAACAGACA<br>AAAG    | TCATCAAATCCGTAACG<br>CAA  | 59.4                             | 333                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_40700886  | Ca4                                     | 40700886                      | AGAC/A                                                        | TCTTGATGTAACGTTT<br>GTTTCAGA | TGAATATTTGAGTTACG<br>AATTTGATGA | 60.1                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40702737  | Ca4                                     | 40702737                      | ACTCT/ACT                                                     | CCCCCATCATAAAATT<br>GTGC     | AAGATTAGTGGGCGAC<br>CCTT        | 60.0                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40704362  | Ca4                                     | 40704362                      | TA/T                                                          | GCGTAGAATGGGAAAC<br>GAAA     | GAATGCAGTTAGCACG<br>AGCA        | 60.1                             | 230                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40729399  | Ca4                                     | 40729399                      | TAAAAA/TAAAAAA                                                | TTGTGAAATTGAAAAG<br>GTTCCA   | TTGTTTTCAATGAGAAG<br>GTGGTT     | 59.5                             | 256                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40731137  | Ca4                                     | 40731137                      | TC/T                                                          | TCATGGATAAGGTGGA<br>AGACG    | TGAATTCGAAAATCCAT<br>TTCATC     | 59.9                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40743608  | Ca4                                     | 40743608                      | TTCAAT/TT                                                     | GAATTTTGTGTGTTGC<br>GGTG     | GCGGTGTTTTTCAACA<br>CATTT       | 60.0                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40762174  | Ca4                                     | 40762174                      | ATTTTT/ATTTTTT                                                | AATGGCGTATGTGTGA<br>GGGT     | TCACCAAATTGAAAGCA<br>TCC        | 60.3                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40763607  | Ca4                                     | 40763607                      | CAAAAA/CAAAA                                                  | GCTCTGCTTGATTGAA<br>AATGC    | CCAATGCATGAAATTTG<br>TTCTT      | 60.0                             | 696                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40763691  | Ca4                                     | 40763691                      | ATTTT/ATTT                                                    | GCTCTGCTTGATTGAA<br>AATGC    | GGGTCCTCTAACTTG<br>TGAGC        | 60.0                             | 826                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40778747  | Ca4                                     | 40778747                      | T/TA                                                          | GGGAGTTTGAGAAGA<br>AGGG      | AATAAGCAACAGCCC<br>CAAT         | 60.0                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_4078034   | Ca4                                     | 4078034                       | CA/CAGTA                                                      | AGCACGTGTGGAAGAC<br>ATTG     | CCCCTTCCACAAAAG<br>TGAA  | 59.8                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40783665  | Ca4                                     | 40783665                      | TTTAT/TTTATTAT                                                | CCTCTAGTGGGTTTCT<br>TTCATCA  | AATGATGCCTCCATGC<br>TTTC | 59.6                             | 853                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40785871  | Ca4                                     | 40785871                      | ATTTTTTTTT/ATTTTTT                                            | GAGCTATTGTCCTCGG<br>CACC     | CCTTCAAGAGTCGCA<br>TCAT  | 59.8                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40790018  | Ca4                                     | 40790018                      | A/AT                                                          | GCCCATTTTGTCTTTG<br>TTGA     | TCATTGTCCAGTGAAG<br>GCAA | 60.0                             | 667                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40821058  | Ca4                                     | 40821058                      | ACA/ACATGCCTCA                                                | CCGTAAAACGATGGT<br>CGAT      | TTAATTTCCAGCCATG<br>CAA  | 59.8                             | 338                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40833473  | Ca4                                     | 40833473                      | ATTTTTTTTT/ATTTTTTTTTT                                        | TTTTTATTGTCAACCC<br>GCA      | TTCAAACCCCATTTCT<br>TGT  | 59.1                             | 766                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40838372  | Ca4                                     | 40838372                      | GTTTT/GTTT                                                    | AGTTATTTTGTGAGAC<br>AATTACCA | GCCTTTTCCACGCATTT<br>TTA | 57.5                             | 755                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40842793  | Ca4                                     | 40842793                      | TC/T                                                          | CTGGATTGAGTTGAGG<br>CCAT     | TGGACCAACCAAGCA<br>CATA  | 60.1                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40842971  | Ca4                                     | 40842971                      | AGTGTGT/AGTGTGTGT                                             | AAAATTTGTGCATCAAG<br>GGC     | TCAAGATTGGGCAAG<br>AATC  | 59.9                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40845072  | Ca4                                     | 40845072                      | TG/TGG                                                        | CGAAACAAATGTGTA<br>GAGGCA    | GGCAAATTAAGGAGG<br>CACA  | 60.2                             | 870                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_40846133  | Ca4                                     | 40846133                      | ATTT/ATTTT                                                    | CCATCAATTGGGTGGT<br>TGTT    | GGGAGAACATCATGCT<br>CCAT   | 60.5                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4084759   | Ca4                                     | 4084759                       | CAG/CAGAAG                                                    | TAACCATGGCCATCAA<br>GACA    | CGTCTTAACTTTTGCTA<br>TCGGC | 59.9                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40880303  | Ca4                                     | 40880303                      | GA/GAA                                                        | GGAAGTTTCCAAGCA<br>CGAG     | AAGTCCATTGCTTGGT<br>GGT    | 59.9                             | 411                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40881410  | Ca4                                     | 40881410                      | CAAAA/CAAA                                                    | AAGACCCACATTTGGT<br>GAAAA   | ATGAGTTCTTCATCGGT<br>CGG   | 59.3                             | 506                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40895378  | Ca4                                     | 40895378                      | TAAAA/TAAAAA                                                  | TGTGTCCCTAATATTT<br>GCCG    | TGACACATAGTTTGT<br>TGCA    | 59.8                             | 441                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40896370  | Ca4                                     | 40896370                      | CAATAATA/CAATA                                                | AGGTACTTTCAAATGG<br>GTGTGA  | GAACCTGATGAAGTGT<br>GGCA   | 58.5                             | 258                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40933977  | Ca4                                     | 40933977                      | GTTTT/GTTTT                                                   | GGATCATCCACCATTT<br>ATCTGAA | TTCTCACGTTGTTGAC<br>GAGC   | 60.0                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40935936  | Ca4                                     | 40935936                      | T/TC                                                          | TTTTCACGAATGATCCA<br>CCA    | GTCGTTCAATCCAACC<br>TCGT   | 59.9                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40955483  | Ca4                                     | 40955483                      | ATTTTT/ATTTTT                                                 | TTGCATTTCGTCGAAC<br>TACA    | TCCGTTTTTATTTGGT<br>CGC    | 60.4                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40964102  | Ca4                                     | 40964102                      | TT/TTCT                                                       | ATTGGATAGGCCTGG<br>CTTT     | GCACTTTTGTATACGG<br>GAGC   | 59.9                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                           |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_40966159  | Ca4                                     | 40966159                      | GCATTTG/GCATTTGATGCCATTGT<br>CATTG                                        | AACATGCGCTTTGTGCG<br>GGTG   | CTCAAAAACGAGCCAA<br>AAGC | 60.0                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40968955  | Ca4                                     | 40968955                      | TC/TCC                                                                    | CACTGGAATGATTGCC<br>AAAA    | TTCTACCCAAGATCGG<br>ATGG | 59.5                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_40997865  | Ca4                                     | 40997865                      | TAAAAAA/TAAAAAA                                                           | GATGAATGGAGACGAC<br>CGTT    | AACCAATGATGCAGTT<br>GTGC | 59.9                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_41010535  | Ca4                                     | 41010535                      | CTT/CTTT                                                                  | TAGTTGGTCAATGCGG<br>ATCA    | GGACTAACAGGGGAGA<br>AGGG | 60.1                             | 278                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_41015513  | Ca4                                     | 41015513                      | ATTTTTTTT/ATTTTTTT                                                        | CGTCATTGAAAAAGC<br>GACA     | GCCCCATAAAAAGATG<br>CTCA | 59.8                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_41015733  | Ca4                                     | 41015733                      | TAAAAAA/TAAAAAA                                                           | CAAATTTTGATGATCTC<br>ACACGA | GCCCCATAAAAAGATG<br>CTCA | 60.0                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_41027713  | Ca4                                     | 41027713                      | AATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATA<br>TATATATATATATAT | TGAATCCCAAATTTGA<br>ACCA    | TTTGATCGCAAGGGTT<br>TAGG | 60.2                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4115988   | Ca4                                     | 4115988                       | ATTTTTT/ATTTTT                                                            | TGCAATATGAAGGTCC<br>ACCC    | CCCCCTTTTGGTCGT<br>ATCT  | 60.7                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_41172721  | Ca4                                     | 41172721                      | AC/A                                                                      | TCAAGTTAAAGGTGGA<br>GCGG    | TTCTCCCTTTCTTTGA<br>CAAC | 60.2                             | 761                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4118065   | Ca4                                     | 4118065                       | CTTTTTTTTTTT/CTTTTTTTTTT                                                  | AAAAGGAATTTGTGCG<br>AACG    | TTTTGCAATCTATCGAG<br>GGG | 60.0                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                         | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                       |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_41581170  | Ca4                                     | 41581170                      | GA/GATCA                                                                                                              | ACAAAACTCCCAATG<br>GTCG     | TAGCCAACCACACATG<br>GAAA   | 59.8                             | 737                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4158984   | Ca4                                     | 4158984                       | CTT/CTTCAAGTT                                                                                                         | ATATAAGAGGGTGGGG<br>GCAT    | TGAGGAAGGTACGAGG<br>AGGA   | 59.5                             | 625                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_41612820  | Ca4                                     | 41612820                      | ATTG/ATTGTACATAAATACGGTGT<br>G                                                                                        | TGAATTGCGTTAGATG<br>AGCA    | GCAATATACGCCAAAT<br>GCAA   | 58.0                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4162107   | Ca4                                     | 4162107                       | AATTAAATT/AATTAAATTTATTAAT<br>T                                                                                       | AGGGAGAGAGGCATGA<br>GACA    | ATGTGCGACATGAAAA<br>CCAA   | 59.9                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4162204   | Ca4                                     | 4162204                       | GTTTTTTTT/GTTTTTTTTT                                                                                                  | AGGGAGAGAGGCATGA<br>GACA    | ATGTGCGACATGAAAA<br>CCAA   | 59.9                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4162985   | Ca4                                     | 4162985                       | ATTTT/ATTT                                                                                                            | TATTGCAGCAACACAT<br>GCAA    | CAAATTTGTGAAAGAC<br>GTGGA  | 59.9                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4163265   | Ca4                                     | 4163265                       | TAAAT/TT                                                                                                              | TGACCACTTTAGAAAG<br>CATGTGA | TGCAAATCCATAGACTC<br>CAAGA | 59.8                             | 284                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_41634605  | Ca4                                     | 41634605                      | CATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>/CATTATTATTATTATTATTATTAT<br>TTATTATTATTATTATTATTATTA<br>TTAT | TTGATGGAAGTTTACAT<br>CGGC   | TGTTTGTGAGGGGA<br>AAGG     | 60.0                             | 890                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_41637679  | Ca4                                     | 41637679                      | ATTTATTTTTATTTT/ATTTATTTT<br>TTTTATTTTT                                                                               | TTCAAGGAGGAAGGGT<br>GATG    | GGACGAAAGCCACAAA<br>ACAT   | 60.0                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4166322   | Ca4                                     | 4166322                       | T/TAAG                                                                                                                | GCGTTGAGAATCTTGA<br>AATGC   | TCCTCTCACAGGGCTC<br>ACTT   | 59.8                             | 164                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_41666178  | Ca4                                     | 41666178                      | ATTTTTTTTT/ATTTTTTTTT                                         | AGCCCATCTTGACGC<br>AGAT   | GGAGCCAATAAAAGA<br>AAATCG     | 59.7                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4173930   | Ca4                                     | 4173930                       | GAAAAA/GAAAAAA                                                | GGACACCCCAATAACA<br>AGGA  | TCTTGACATAAACTAT<br>TTTTCAGCG | 59.6                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_41799900  | Ca4                                     | 41799900                      | CATATATATATATATATATAT/CAT<br>ATATATATATATATAT                 | CACAAAACACAAGGTG<br>TGGC  | GAAGATTGTATATCCG<br>CTCTACGAC | 60.0                             | 297                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4180652   | Ca4                                     | 4180652                       | AT/A                                                          | CACCATGTCATAACCA<br>ATGGA | TGCTTGCCAACACATAT<br>AACA     | 59.1                             | 186                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_41810917  | Ca4                                     | 41810917                      | C/CA                                                          | ACACAATTTGTCGTCC<br>ACCA  | TGTAAGTAAAAATTCAT<br>CAGCACCA | 59.9                             | 262                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4181784   | Ca4                                     | 4181784                       | GAGAAGAAG/GAGAAG                                              | GGGAGGGTTTGCAATT<br>TTCT  | TCGGATTGTGCTCACA<br>ACAT      | 60.3                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_41823980  | Ca4                                     | 41823980                      | CATCAGA/CA                                                    | CATCAAGACCATTTC<br>AGCA   | CAATTGTTTCGTGTTGC<br>GTCT     | 59.6                             | 114                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4183045   | Ca4                                     | 4183045                       | TAAAAA/TAAAAA                                                 | TTACTTGTTGTGCGGC<br>TGAA  | TTGAGCATGTGGTTGT<br>TGGT      | 60.4                             | 216                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_41832968  | Ca4                                     | 41832968                      | AATATATATATA/AATATATATATA                                     | TTTCCATTGCACTCACT<br>CCA  | CCTATCATGGCCTGAC<br>CTGT      | 60.2                             | 758                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4188614   | Ca4                                     | 4188614                       | TAAAAA/TAAAAA                                                 | TTGCAGAAATTTAGCG<br>GAAA  | TTGAATTGGAATTGTTT<br>TGCAT    | 58.6                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                       | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                     |                           |                             |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_42025518  | Ca4                                     | 42025518                      | AATATATATATATATATATATATA/<br>AATATATATATATATATATATATA                               | CACGGATCTTGAGT<br>GACC    | TCACAAGTCACACAATT<br>TTCACA | 59.1                             | 504                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_42101261  | Ca4                                     | 42101261                      | CGAGAGAGAGAGAGAGAGAGAGAG<br>AGAGAGAGAGA/CGAGAGAGAGAG<br>AGAGAGAGAGAGAGAGAGAGAG<br>A | CCTCATTCCGTTGTTTC<br>GTT  | GCCGAACCGTTTCGTA<br>CTTA    | 60.0                             | 565                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_42332097  | Ca4                                     | 42332097                      | GA/A                                                                                | TCAGGGCCAACTGAA<br>GTCT   | CTGGATGTGCATCCTG<br>TTTG    | 59.8                             | 628                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_42412637  | Ca4                                     | 42412637                      | GA/GAA                                                                              | CTTCTCAAGGGACGCA<br>TCAT  | AATTTGGCAAGTTTGAC<br>ACG    | 60.2                             | 170                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_4242385   | Ca4                                     | 4242385                       | TTATATATATATATATATATATATA<br>TAT/TTATATATATATATATATATA<br>TATATATATATAT             | GAACCATTGAGAGGCC<br>GTT   | TCGGTTTCCGAGTAGT<br>GGAC    | 60.1                             | 359                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_4248584   | Ca4                                     | 4248584                       | CTTTTTTTTT/CTTTTTTTTTTT                                                             | GCTGTAAACAAGGTGCC<br>CAAT | TTTGAGCTCAATGAAA<br>TCC     | 60.0                             | 386                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_42534372  | Ca4                                     | 42534372                      | GTTTTTTTT/GTTTTTTTT                                                                 | TGGGGCAGTGCAATGT<br>ATTA  | CATCGGCAAGAGTTGG<br>GTAT    | 60.0                             | 574                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_42548370  | Ca4                                     | 42548370                      | ATTTTTTTTT/ATTTTTTTTTT                                                              | CGTGCCTTTGTCGTCT<br>CTTT  | AGAGGCCCAATATCCT<br>TGCT    | 60.4                             | 528                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_42574723  | Ca4                                     | 42574723                      | AGGG/AGGGG                                                                          | TCGTCATCACACAAGG<br>TGGT  | CAGGTTGTAAGCAAAA<br>GCCC    | 60.0                             | 227                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_4259095   | Ca4                                     | 4259095                       | CT/C                                                                                | GTTGGCTGAAAAGGGA<br>TTGA  | CGATTTCCACTAACACC<br>TTGG   | 60.1                             | 383                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                  | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_42633986  | Ca4                                     | 42633986                      | TATAATAATAATAATAATAATAAA<br>TAATAATA/TATAATAATAATAAAT<br>AATAATAATAATAATAATAATA                | TTGCTTTAGATGAATCA<br>AATCCC | CGACAGGCTTAGGTTA<br>GACCA  | 59.5                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4269269   | Ca4                                     | 4269269                       | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATATAT                                          | ACACGGTGATCGTCAG<br>TGAA    | ACACGTGACACTTACC<br>TAGCAA | 60.2                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_42693293  | Ca4                                     | 42693293                      | TC/TCC                                                                                         | AAATGCTCGAACGAAA<br>ATGC    | TCGAAGTTGGATGCTT<br>TTGA   | 60.2                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4272031   | Ca4                                     | 4272031                       | CAAATAATTAATAATAATAAA/CAA<br>ATAATTAATAATAATAATAAATT<br>AAAA                                   | TGAAGGGTTCAAATG<br>TTCTGTT  | CTCGCATCTTCAAGCG<br>TTTT   | 59.9                             | 843                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4273619   | Ca4                                     | 4273619                       | ATTTTTTTTT/ATTTTTTTTT                                                                          | GCGCCCGTTGAAAATA<br>ATAA    | ACACGTGTGGACGTGA<br>TTTG   | 59.9                             | 408                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_42961696  | Ca4                                     | 42961696                      | CAAAAA/CAAAAA                                                                                  | CCCGGTGTCTTCATCA<br>AAGT    | GCTTGGGACAAGCAA<br>TAGA    | 60.0                             | 370                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4296519   | Ca4                                     | 4296519                       | ATTTTTTTTT/ATTTTTTTTT                                                                          | CAAAGCCCCACACTA<br>AAAA     | TATGGCGGTTGGACTG<br>TGTA   | 60.0                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43195252  | Ca4                                     | 43195252                      | TA/T                                                                                           | TGTTGGATATTGTCTC<br>CTCCC   | AAGTTCTGTGCCTCTAT<br>GTGGA | 58.9                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43219549  | Ca4                                     | 43219549                      | GTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTA/GTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTA | TCATGAAGATTGGAA<br>GAAAAAGA | CCATCAACCCTAGCCT<br>TCAA   | 59.3                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43222555  | Ca4                                     | 43222555                      | TTATATATATATATATATATAT/TT<br>ATATATATATATATATAT                                                | AAAGATTTAAAGGGCA<br>AAAAGTG | CTGGCAGCTGGGAAAG<br>ATT    | 58.0                             | 908                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_43243761  | Ca4                                     | 43243761                      | GCTTCTTCTTCTTCTTCTC/GCTTC<br>TTCTTCTTCTTC                     | TCTGTTTTTGCCATCAA<br>GCA     | TTTGAGACCAATGGT<br>GACA      | 60.4                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43291624  | Ca4                                     | 43291624                      | TAA/TAAAA                                                     | GAGCGATTACCGGTGT<br>TGTT     | GCCTTCAAATGTAACC<br>CCCT     | 60.0                             | 946                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43298328  | Ca4                                     | 43298328                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATAT             | TGCGTTTGCAAAATCA<br>CAGT     | TTCTAATCGGCACAAT<br>GTTCA    | 60.3                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43301091  | Ca4                                     | 43301091                      | ATAA/ATAATGTAA                                                | ACCATAAAGGGAACA<br>GGGG      | TCATGGTCTGCAATCT<br>CGTC     | 60.0                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43312802  | Ca4                                     | 43312802                      | CAAA/CAA                                                      | GCCCCATTAAGCACAC<br>AAAA     | ATATGGCTTGGTCCCA<br>CGTA     | 60.9                             | 853                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43328071  | Ca4                                     | 43328071                      | ACA/ACATCA                                                    | TCCATTATATCCAAAG<br>GCGA     | TTTCGTTCCGTTTCAGA<br>TCC     | 59.4                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43333325  | Ca4                                     | 43333325                      | ATTTTTTTT/ATTTTTT                                             | TGTGGGGTAAAATGAC<br>TACAAAAA | AAAATGATTGCCGATT<br>TGT      | 59.7                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43339918  | Ca4                                     | 43339918                      | ATT/ATTT                                                      | TCATTCTCTTCATCGAA<br>GATTCA  | TGGAGAATAATTAACAG<br>AGCAGCA | 60.2                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43342892  | Ca4                                     | 43342892                      | TAAAA/TAAAAA                                                  | AGCAGCAGCACAAAGCA<br>ACTA    | TCTTCATCATTGGCCA<br>GAAA     | 60.0                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43350385  | Ca4                                     | 43350385                      | AACA/AA                                                       | GGACTAAATGTTTTAA<br>GCACGG   | TTTCATCATTTTGAGAA<br>AAGAAA  | 59.1                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_43401153  | Ca4                                     | 43401153                      | GAAAAAAAAAAAAA/GAAAAAAAAAA<br>A                               | GCTAAATTACATCCGC<br>GGTC  | GTGCAAGTCCACACAT<br>GGTC   | 59.6                             | 702                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43422683  | Ca4                                     | 43422683                      | GAAGCTAAG/GAAG                                                | CACACTAGCCCTCATT<br>TCCC  | CACCACCAACCTCTTT<br>GGTT   | 59.6                             | 847                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43426940  | Ca4                                     | 43426940                      | CCACACACACACACACA/CCACACA<br>CACA                             | TCCAAAATAGATGCAT<br>CGGAC | TGGACATGTTAGGTGA<br>GACCTG | 59.9                             | 271                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43458722  | Ca4                                     | 43458722                      | TAAAA/TAAAAA                                                  | CTTGGCTCTTTGCATT<br>CGTT  | GCGTCGGATACACCTT<br>TGTT   | 60.4                             | 365                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43459528  | Ca4                                     | 43459528                      | TA/T                                                          | TTGCCCTCTTTTATT<br>CCA    | TTCGCTCGAGTTTGTAT<br>CG    | 59.7                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43460190  | Ca4                                     | 43460190                      | ACC/AC                                                        | CTCGAGCGAAAATATC<br>CCAA  | TGAAACACAACAACAG<br>GGGA   | 60.2                             | 619                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43475384  | Ca4                                     | 43475384                      | AAA/AAAGAA                                                    | TCTCCTTCAAAATCGC<br>CAAT  | TCCAGTTGGCCATTCT<br>TTC    | 59.6                             | 842                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43486688  | Ca4                                     | 43486688                      | GGGCCGG/GGG                                                   | TGAACTCTCATGTGCT<br>TCGG  | CCATCAACAAAAACACC<br>ACG   | 60.0                             | 315                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43536933  | Ca4                                     | 43536933                      | T/TAAGA                                                       | TTGGAAGGGAGGTTCA<br>CGTA  | ATTTTGTCTTCCGCA<br>ACG     | 60.5                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43544345  | Ca4                                     | 43544345                      | CAAAAAA/CAAAAAAA                                              | GACCTAGTCCGCGACT<br>CAAC  | AAACCAGACTGCGTGT<br>AGGG   | 59.9                             | 781                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_43549490  | Ca4                                     | 43549490                      | TA/TAA                                                        | ATGGAAGTGGAAGCCA<br>ACAG    | AAAGAAGCGCGAATAA<br>TCCA   | 60.1                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43549820  | Ca4                                     | 43549820                      | TC/T                                                          | TGGATTATTCGCGCTT<br>CTTT    | TTCCGCTGCTCGTAAA<br>TTCT   | 59.8                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43553592  | Ca4                                     | 43553592                      | TG/T                                                          | AACGGGAGAAGGAGG<br>AAAAA    | CGGTTTCACACTCTGA<br>TCCA   | 60.0                             | 843                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43564232  | Ca4                                     | 43564232                      | CTTTTTTT/CTTTTTT                                              | TCAAACAAAATTGGGTT<br>ACAACA | TTTGTAATCACAAAA<br>TCCAAAA | 59.3                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43566104  | Ca4                                     | 43566104                      | ATTGTGAGTTTTTGTG/ATTGTG                                       | AGATCCTCTCCCTTGC<br>AAAA    | TTCAATTCATTGCCATT<br>CCA   | 58.9                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43570031  | Ca4                                     | 43570031                      | C/CG                                                          | GAACAGGAAAAGAACA<br>CCGC    | TGGTGTGAGATTTGTT<br>GGGA   | 59.7                             | 383                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43659877  | Ca4                                     | 43659877                      | ATTTTTTTTT/ATTTTTTTT                                          | TTTTTGCCACAGCTAG<br>GGAG    | TGGCACATCTATCCAAT<br>CACA  | 60.4                             | 423                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4378608   | Ca4                                     | 4378608                       | CATATATATATATATATATATAT/C<br>ATATATATATATATATATATATATA<br>TAT | TAAATTCACGCGCACG<br>TATC    | GGAGTCCGTGCAATAC<br>ACCT   | 59.7                             | 747                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43895697  | Ca4                                     | 43895697                      | GATATATATATATATATATATATA<br>TAT/GATATATATATATATATATATA<br>AT  | CCCAGTAGTCTCCA<br>TCAA      | CTCCACAGCCTAACT<br>CGAC    | 60.1                             | 920                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_43990162  | Ca4                                     | 43990162                      | GTTTTTTT/GTTTTTTT                                             | TGTTGGCAAGTTTGCT<br>TGAG    | GTTTCGATTCCGCAAAAT<br>GTT  | 60.0                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                              |                          |                          |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_43999007  | Ca4                                     | 43999007                      | TTATATATATATATATATATATATATATATATACATATATATATATATATATAT/TTATATATATATATATATATATATATATATATACA TATATATATATATATAT | ACGTGTATATTTGCGCACCC     | TTTGTTCAGCCCATCCAAT      | 60.8                             | 625                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_44332657  | Ca4                                     | 44332657                      | TAAATAAAATAAAATAAAA/TAAATAA AATAAAATAAAATAAAA                                                                | ACCGAAGTCAACCGCTTACA     | AGTCACTTGCGAATGTCGTG     | 60.7                             | 508                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_44344897  | Ca4                                     | 44344897                      | ATTTTTTTTTT/ATTTTTTTTTT                                                                                      | TTGATTATTGATTACCCACGGA   | TACCATTTGATCCGATT CGT    | 59.2                             | 510                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_44428431  | Ca4                                     | 44428431                      | CATATATATATATATATATAT/CATAT ATATATATATATATATAT                                                               | TGTTGCGGAAATGTTA GTTCA   | TTTCATCCATGCAATAT CAAAAA | 59.2                             | 699                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_44486854  | Ca4                                     | 44486854                      | ATAAA/ATAAATAAA                                                                                              | CTCAGGATGAACAAC TGCCA    | TTTCGTTTATCTCTTCAA TCGCA | 59.8                             | 419                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_44488487  | Ca4                                     | 44488487                      | T/TC                                                                                                         | AAACCAATTGTTGAT GGGGA    | TTGACGGTTGTCAAAT CCA     | 60.0                             | 715                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_44489358  | Ca4                                     | 44489358                      | CTTTT/CTTT                                                                                                   | TTTTGTTTCTCCACCCC AAA    | TGACTGCACACAATAAA CATTGA | 60.3                             | 400                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_44489639  | Ca4                                     | 44489639                      | CTTAATT/CTT                                                                                                  | TTCTGGACTGCTCCAA AACAA   | TCAATCGATCAGTTGCT TTTT   | 59.4                             | 611                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_44490020  | Ca4                                     | 44490020                      | AT/A                                                                                                         | CAACTGATCGATTGAT AGAAGCA | TGCTTCGCAAGATTAG TTAGGA  | 59.4                             | 570                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca4_P4_44493122  | Ca4                                     | 44493122                      | CT/CTT                                                                                                       | CAATCTTGGGAGATAG TTGTTGG | CTCACATGATGCTCGT TGCT    | 59.9                             | 558                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_44493805  | Ca4                                     | 44493805                      | GACA/GA                                                       | TTGAATGCACACAA<br>CCCT    | CCATACCGAGATTATAA<br>CGCC  | 60.0                             | 237                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44507935  | Ca4                                     | 44507935                      | CT/CTT                                                        | AGATATTTGGCGGTGG<br>TCAG  | TTAAGGGAGTGCATGA<br>GCAA   | 60.0                             | 780                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44510870  | Ca4                                     | 44510870                      | GT/GTTT                                                       | GCAAACTTGCCTCTT<br>AGGC   | TTGTTTCATGACCTG<br>CATC    | 60.0                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44524444  | Ca4                                     | 44524444                      | TTTACGAATTACGA/TTTACGA                                        | TTCTTCCTCCTCCTTC<br>GTT   | TGTCCAATCACCAACG<br>TCAT   | 60.2                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44525079  | Ca4                                     | 44525079                      | AGTATTTTCTTA/AGTATTTTCTTA<br>TGTATTTTCTTA                     | ATGACGTTGGTGATTG<br>GACA  | TGGAGTAATCCCTAAT<br>CATTCA | 59.8                             | 357                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44525230  | Ca4                                     | 44525230                      | TAAAAAAAAAAAAA/TAAAAAAAAA                                     | ATGACGTTGGTGATTG<br>GACA  | GCGCTAGCAAAATAG<br>CCAC    | 59.8                             | 884                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44526873  | Ca4                                     | 44526873                      | ACTCCAAA/ACTCCAATGCTCCTCG<br>AAA                              | TTCCAATCTTTTGCCA<br>AGG   | TTGGCTCAAGTGGGAT<br>AAGC   | 60.0                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44527209  | Ca4                                     | 44527209                      | TG/TGG                                                        | CCATCGCTTAGCCAAT<br>TGTT  | AGGCAGAAAGTCGCAG<br>TGAT   | 60.1                             | 852                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44540601  | Ca4                                     | 44540601                      | TAAAA/TAAAAA                                                  | AACAATGGGGTCTATC<br>GTGTG | GGACCCATGGTCAAGA<br>AAGA   | 59.7                             | 678                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44540632  | Ca4                                     | 44540632                      | TAAA/TAAAA                                                    | AACAATGGGGTCTATC<br>GTGTG | GATTGGAACCATCGAG<br>GAGA   | 59.7                             | 896                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)      | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                    |                              |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_44545143  | Ca4                                     | 44545143                      | AATAT/AAT                                                          | TTTTCAGCCCATTCCTT<br>TTG     | TAATATGCAAGTGGAG<br>GCCC | 60.0                             | 910                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44555024  | Ca4                                     | 44555024                      | T/TGAGATGGAGA                                                      | TTTCTCAAGGATCAAAA<br>TGGG    | TGACCTGACCTATTCC<br>CACC | 59.0                             | 629                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44555673  | Ca4                                     | 44555673                      | TA/T                                                               | AGGTCAGACCAGGCTT<br>TGAA     | TAAGTTAGGCCGTCCG<br>TCAG | 59.8                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44561281  | Ca4                                     | 44561281                      | ATTTTTTT/ATTTTTTTT                                                 | TCAAATCAAGAATCAA<br>CAACAAAA | TTCGGTTAATTTTGCCA<br>GGA | 59.9                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44563494  | Ca4                                     | 44563494                      | CTTCTTTTT/CTTT                                                     | GGCAAATCACATGCTA<br>GGCT     | TCGTCCAATCTTGTGG<br>TTCA | 60.2                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44580709  | Ca4                                     | 44580709                      | TTAAT/TT                                                           | TGAGAGGTGTTGGGTT<br>CAAA     | CACAATATGTGGACGG<br>CAAG | 59.1                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44585709  | Ca4                                     | 44585709                      | GAATTAAATATAAATTAAATATA/GAA<br>TTAAATATAAATTAAATATAAATTAA<br>ATATA | TTTCTATTTGGGGCCT<br>AGCA     | TCTCATTGTCACCGTTG<br>CAT | 59.7                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44601700  | Ca4                                     | 44601700                      | TAAA/TAA                                                           | TGCAGGGATGAAATTC<br>AAAAA    | AGGACACGGATTCAAT<br>TGGA | 60.4                             | 380                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44603106  | Ca4                                     | 44603106                      | ATTTTTTT/ATTTTTT                                                   | TCAAAAACAATCAACAT<br>GGCTC   | CCGTCTCAGTTGCGAT<br>CTCT | 60.0                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44607011  | Ca4                                     | 44607011                      | ACTCT/ACT                                                          | GGGGAATGTAAGGGTA<br>GTATCG   | AATGCCAAACCTAAAG<br>CGTG | 58.8                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_44607037  | Ca4                                     | 44607037                      | ATTTT/ATTT                                                    | GGGGAATGTAAGGTA<br>GTATCG   | AATGCCAAACCTAAAG<br>CGTG   | 58.8                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44611506  | Ca4                                     | 44611506                      | TAAA/TAA                                                      | TTTTTGCCCCTATCACC<br>AAG    | TCCAATGAAGACGACA<br>ACGA   | 59.9                             | 807                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44613140  | Ca4                                     | 44613140                      | T/TA                                                          | CCATCGTTGAAACGTT<br>GTGAT   | TGCGAGTTTCTTTATCA<br>TTTCC | 60.8                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44613867  | Ca4                                     | 44613867                      | AACT/AACTGACT                                                 | TGATCAAGAAGTCACG<br>AGTTCAA | TTAATGTTTGGGGAAG<br>GCAA   | 59.9                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44622646  | Ca4                                     | 44622646                      | CT/CTGTGAGTTT                                                 | TGTTGAGTCGCCGTTA<br>AATG    | ACGCAAAGCACACACA<br>AGAG   | 59.7                             | 701                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44631148  | Ca4                                     | 44631148                      | GTCT/GT                                                       | CCCTATTTGGGTGCGT<br>CTTA    | CCACTTGACAAGACT<br>TGGA    | 60.0                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44631480  | Ca4                                     | 44631480                      | T/TTTA                                                        | TCCAAGTCTTGTCGAA<br>GTGG    | AGGGGTCTTTGGTGCA<br>AAAT   | 59.9                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44632456  | Ca4                                     | 44632456                      | GAAAAA/GAAAAAA                                                | CTTTTCGATTTTGCT<br>GACC     | GAAGGAGAGGAGGAG<br>GAGGA   | 59.7                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44632709  | Ca4                                     | 44632709                      | CAAA/CAA                                                      | TCCTCCTCCTCCTC<br>CTTC      | TTGAAACTTTAACGGTG<br>CCAT  | 59.9                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44661008  | Ca4                                     | 44661008                      | TAAAAA/TAAAAA                                                 | AACTGTTGACCCAAC<br>TACG     | CTCCTGGTTGCCATT<br>GTT     | 58.6                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_44661599  | Ca4                                     | 44661599                      | CAATAAT/CAATAATAAT                                            | AACAAATGGCAACCA<br>GGAG    | AAAATTGCGTTGAGTG<br>GTCC    | 60.0                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44662443  | Ca4                                     | 44662443                      | TAAAAAA/TAAAAA                                                | ACTCATTAGGTTGTT<br>GCCG    | CACATAGCACTTGCC<br>TTGA     | 60.0                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44662485  | Ca4                                     | 44662485                      | TAAAA/TAAAAA                                                  | ACTCATTAGGTTGTT<br>GCCG    | CACATAGCACTTGCC<br>TTGA     | 60.0                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44665101  | Ca4                                     | 44665101                      | ACCC/ACC                                                      | GGATATCCCAATTGA<br>GGCA    | GGTGTGAATTGCA<br>AGGG       | 59.7                             | 223                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44668816  | Ca4                                     | 44668816                      | TTGGAGAAA/TTGGAGAAAATGGAG<br>AAA                              | GTTCTCTATTGGCAC<br>ACCT    | TCAAGTTTCAAAATGCA<br>ACCC   | 60.0                             | 212                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44678377  | Ca4                                     | 44678377                      | TC/T                                                          | CATTTTGCCGATCAGA<br>GTCA   | GCAGGAACATGTGGGC<br>TAGT    | 59.8                             | 694                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44679413  | Ca4                                     | 44679413                      | CATA/CATATATA                                                 | AATCCTCTATGGATGC<br>CGTG   | TTGTGGGATTAAAAGT<br>CGAAAAA | 59.9                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44679485  | Ca4                                     | 44679485                      | TCATG/TCATGCATG                                               | AATCCTCTATGGATGC<br>CGTG   | TTGTGGGATTAAAAGT<br>CGAAAAA | 59.9                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44679748  | Ca4                                     | 44679748                      | ATTTTTTT/ATTTTTTTTT                                           | TTTTTGTTCGAATGGA<br>TAATCA | TACTCCGAGTCACCA<br>AAAG     | 59.4                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44681210  | Ca4                                     | 44681210                      | ATTTTT/ATTTTT                                                 | TTTGCAATTCACCACCA<br>CTC   | CGGCACATTACCCAAA<br>AGTT    | 59.5                             | 827                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_44681328  | Ca4                                     | 44681328                      | AAA/AAAGTTAA                                                  | TCTGATCCGTCTGTAC<br>CCCT    | CGGCACATTACCCAAA<br>AGTT | 59.5                             | 335                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44681450  | Ca4                                     | 44681450                      | TA/T                                                          | CCGTCTGTACCCCTTA<br>TCCA    | CGGCACATTACCCAAA<br>AGTT | 59.8                             | 329                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44681620  | Ca4                                     | 44681620                      | CTTTT/CTTTT                                                   | CCGTCTGTACCCCTTA<br>TCCA    | AAGTGGCTTGCTTTTG<br>CATT | 59.8                             | 811                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44685636  | Ca4                                     | 44685636                      | CTTT/CTTTT                                                    | TGTTCAAGCGATTATG<br>TCAAAGA | TATGTATGCAGGGAAG<br>CACG | 59.8                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44685700  | Ca4                                     | 44685700                      | T/TC                                                          | TTTCCACACTAAATCC<br>ACTTG   | TATGTATGCAGGGAAG<br>CACG | 59.0                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44688565  | Ca4                                     | 44688565                      | TAA/TA                                                        | CCTCTCACGACATTTT<br>CACA    | GGAGAGATCGCAGACT<br>TGCT | 59.7                             | 201                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44693876  | Ca4                                     | 44693876                      | TAAA/TAAAA                                                    | TGGGCTAGGCTTTAGC<br>TCTG    | TCATCAATGCAAGCTC<br>GTTC | 59.7                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44694609  | Ca4                                     | 44694609                      | AC/A                                                          | ATCAGCACTCCTGAAG<br>GGAA    | CCCAGATGATCGAATC<br>TGAA | 59.8                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44694688  | Ca4                                     | 44694688                      | TAGA/TAGAGA                                                   | GATTCGATCATCTGGG<br>GAAA    | AGGCTTCTGGTGCTGT<br>TCTT | 59.8                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44707356  | Ca4                                     | 44707356                      | A/AT                                                          | CGGAATCTGAGCCATG<br>TTTT    | AGACTCGGGTTACGAG<br>CAAA | 60.1                             | 394                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_44709686  | Ca4                                     | 44709686                      | TAAAAAAAAA/TAAAAAAAA                                          | TGTTGTTGGTGGAA<br>TGCT     | TTGACGGTTCAAATGC<br>AAAA    | 60.0                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44710249  | Ca4                                     | 44710249                      | AAAGATAAGATAA/AAAGATAA                                        | AGGAAGTGTGCGGTT<br>AAGA    | TTTTGTTGAATGGTGG<br>AAAT    | 59.9                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44710491  | Ca4                                     | 44710491                      | GTA/GTATCATTTTTA                                              | AGGAGTGGATGAGCCA<br>AAAA   | GGTGCTAAGTTCAAAC<br>ACACAAA | 59.7                             | 822                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44710559  | Ca4                                     | 44710559                      | GAAAAA/GAAAAAA                                                | AGGAGTGGATGAGCCA<br>AAAA   | GGTGCTAAGTTCAAAC<br>ACACAAA | 59.7                             | 822                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44711226  | Ca4                                     | 44711226                      | TT/TTAT                                                       | TTTGTTGTTTGAACCT<br>AGCACC | TCTCCCATCAACATCA<br>GTG     | 59.2                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44718587  | Ca4                                     | 44718587                      | GAAA/GAA                                                      | CAAAGATCGCGTCAAT<br>GAGA   | ATCTTCCTCCCAAAGC<br>CAT     | 59.9                             | 969                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44725573  | Ca4                                     | 44725573                      | AC/A                                                          | GGCTCAATTGGTCCAA<br>CCTA   | ATTGGTTGTGATGCCA<br>TGAA    | 59.9                             | 803                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44728647  | Ca4                                     | 44728647                      | T/TA                                                          | TTCACCACGAGATCAA<br>AATCA  | GCTTGTGAATTTCAA<br>CCAAA    | 59.1                             | 917                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44738537  | Ca4                                     | 44738537                      | ATTTTTTTTT/ATTTTTTT                                           | TCATGCACCAACGTGC<br>TTAT   | AAGAAATTCATGCAG<br>GTGG     | 60.1                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44738779  | Ca4                                     | 44738779                      | TT/TTAT                                                       | GGTTGCCTCTTTTACAT<br>GGG   | TCATGCATGGTTGGAA<br>AAGA    | 59.4                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_44739765  | Ca4                                     | 44739765                      | ATTT/ATTTT                                                    | ACTCCTTTCCTTCCCAC<br>GAT     | TCAAGGTCGTTTGTG<br>CTGT       | 59.9                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44742473  | Ca4                                     | 44742473                      | TAAAA/TAAAA                                                   | TGAAAGATGGCACATG<br>GAGA     | AGATTCATTTTGGGATG<br>CGA      | 60.2                             | 851                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44746122  | Ca4                                     | 44746122                      | ACC/AC                                                        | TGGCCCATACATC<br>TTCACA      | TTGCGTCGGTTACAAA<br>TGAA      | 60.4                             | 751                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44747851  | Ca4                                     | 44747851                      | ATTTTTT/ATTTTTTTTT                                            | TGGACTTGTAAGCAA<br>GCCT      | CTTCCCGTGTGCTT<br>ACAT        | 61.0                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44750498  | Ca4                                     | 44750498                      | TT/TTACATATAT                                                 | AACTTCAATCCGCAAC<br>AAGC     | TCATTTAGCCACTCGT<br>GTGAT     | 60.3                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44750857  | Ca4                                     | 44750857                      | TAAAAA/TAAAA                                                  | TCACACGAGTGGCTAA<br>ATGA     | AAAACCTTAATGTTTGAC<br>GAGTTGG | 57.8                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44764290  | Ca4                                     | 44764290                      | GTTTT/GTTT                                                    | TCTGTGCACGTGTAAA<br>TAGACAAA | ACGACTACCGAGTGAT<br>TGCC      | 59.7                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44764786  | Ca4                                     | 44764786                      | ATTTTT/ATTTTTT                                                | GGCAATCACTCGGTAG<br>TCGT     | AGGTTAGGCCATGCTT<br>TGAA      | 60.1                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44767237  | Ca4                                     | 44767237                      | CT/CTATT                                                      | GCTGAACAATGCCCTA<br>GCTC     | TGAGTGACAGAAAAAC<br>GGAGAA    | 60.0                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44771286  | Ca4                                     | 44771286                      | CT/C                                                          | ATCGGATGTAAAATTC<br>CCCC     | TTGCTTCAGTTGGTGC<br>ATTC      | 59.9                             | 411                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_44772447  | Ca4                                     | 44772447                      | AT/A                                                          | ACACCGCACGTAATGC<br>TATG     | CGAAATGTGTTTTGCTT<br>TCG  | 59.6                             | 149                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44773132  | Ca4                                     | 44773132                      | GAA/GA                                                        | TTGTTTCACTTTTTCCA<br>TTCCA   | TAGGGTTCCTTGATCCAT<br>CGC | 59.5                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44773439  | Ca4                                     | 44773439                      | ATTTTT/ATTTTTTT                                               | TTGTTTCACTTTTTCCA<br>TTCCA   | TAGGGTTCCTTGATCCAT<br>CGC | 59.5                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44773518  | Ca4                                     | 44773518                      | TAAAAAAAAA/TAAAAAAAA                                          | GACGATGACAATCTTTT<br>ATTGCAG | TAGGGTTCCTTGATCCAT<br>CGC | 60.0                             | 106                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44773874  | Ca4                                     | 44773874                      | G/GA                                                          | GCGATGGATCAAGAAC<br>CCTA     | GGATTTTGGCAACAGA<br>TGCT  | 60.0                             | 737                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44777732  | Ca4                                     | 44777732                      | TAAAA/TAA                                                     | GCTGGGTATGGTGATT<br>TTGC     | CCTTCTTAGATGCAAC<br>CCCA  | 60.3                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44780377  | Ca4                                     | 44780377                      | AC/A                                                          | AACCCCTCCTTCTCCTT<br>TGA     | AAGGCTCTCACGTGGA<br>ATTG  | 60.0                             | 562                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44781972  | Ca4                                     | 44781972                      | CTT/CTTT                                                      | AGCAGAAATGGTGGCA<br>GATT     | AATCCAAATGCCATAG<br>CTGC  | 59.7                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44782327  | Ca4                                     | 44782327                      | GT/GTT                                                        | TTTTGTGGCAGAAACA<br>ACGA     | AATCCAAATGCCATAG<br>CTGC  | 60.3                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44836604  | Ca4                                     | 44836604                      | A/AC                                                          | TGCATTAACCTGCCTC<br>CAAA     | GTTATTTTCTGCCTCC<br>CCG   | 59.3                             | 139                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_44837147  | Ca4                                     | 44837147                      | G/GAGAT                                                       | CGGGGAGGCAAGAAAA<br>TAAC     | TGCAATTTTACGTCCAA<br>ATCAT  | 60.8                             | 815                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44837783  | Ca4                                     | 44837783                      | GTTTTT/GTTTT                                                  | CATGTTATCAATAGCG<br>GTTTCG   | CTCAAACCATGCGTCA<br>AATG    | 58.2                             | 294                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44838015  | Ca4                                     | 44838015                      | CTT/CTTT                                                      | GTCATTTGACGCATGG<br>TTTG     | TTTCGTTGATAATTTT<br>GGCA    | 60.0                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44838352  | Ca4                                     | 44838352                      | GAAAAA/GAAAA                                                  | GTCATTTGACGCATGG<br>TTTG     | CCAAGATTGGTGTGA<br>AAAA     | 60.0                             | 875                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44843097  | Ca4                                     | 44843097                      | C/CCCG                                                        | TAGGGTTGTTTCATGG<br>CATT     | TTCCACACCACATTCCA<br>TTG    | 60.2                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44854235  | Ca4                                     | 44854235                      | ATTTTTTTTT/ATTTTTTTT                                          | GATGCGAGAATTGTAT<br>GCGA     | TGAAATGATTAAGTGG<br>CGAGTTC | 59.8                             | 865                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44854537  | Ca4                                     | 44854537                      | ATTTTTTT/ATTTTTTT                                             | CCAACTTTTTCATACAC<br>AAACACA | TGTTGCACTCGAACA<br>ACTCA    | 59.0                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44854776  | Ca4                                     | 44854776                      | ATTT/ATTTT                                                    | AACTCGCACTTAATC<br>ATTTCA    | TGTTGCACTCGAACA<br>ACTCA    | 58.8                             | 400                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44855429  | Ca4                                     | 44855429                      | TTAG/TTAGCTAG                                                 | CACGAAAAATCAAATTC<br>GGC     | TTTTGTTTTGCAACCAT<br>CCA    | 60.4                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44863007  | Ca4                                     | 44863007                      | GAAAAAA/GAAAAAA                                               | TGAGCATGCAAAGTCC<br>AATC     | CAACCTCCAGTTTC<br>ACAT      | 59.8                             | 285                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_44865492  | Ca4                                     | 44865492                      | TA/TAGA                                                       | TGACCATTGTGTGAAA<br>ATGAGA | TGGTCGTAAAGTGCAT<br>TGGA    | 59.0                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44878187  | Ca4                                     | 44878187                      | TG/TGG                                                        | CAATCGTGCAACAAT<br>TTGG    | ATGAAGCGATTGGTTG<br>GAAG    | 60.0                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44886483  | Ca4                                     | 44886483                      | TTCT/TT                                                       | TAATGGAGGGCAATTT<br>CGAG   | AAACACCCAACCCCT<br>TAAT     | 60.0                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44889469  | Ca4                                     | 44889469                      | AATT/A                                                        | AACCGATATGTGTGC<br>CCTT    | TCATCACATTGTAATCT<br>TGGAGG | 59.3                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44889516  | Ca4                                     | 44889516                      | ATT/ATTTGTT                                                   | AAACCGATATGTGTG<br>CCCT    | TTCAAAATAGCCCTCC<br>AAAAA   | 59.3                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44897539  | Ca4                                     | 44897539                      | T/TA                                                          | ATTTGTTGGAGGATGG<br>GTCA   | CACTCTTGTTCACGGC<br>AAAA    | 60.2                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44900080  | Ca4                                     | 44900080                      | T/TC                                                          | CCCCATTCGACCAAGA<br>TTTA   | AGAAAGTGGGAATGTG<br>GGGT    | 59.8                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44922267  | Ca4                                     | 44922267                      | CTTTTT/CTTTTTTT                                               | TGATTTGAGGGAGTTG<br>GAGTG  | CCCATAATGTCCCGAT<br>TCTG    | 60.1                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44922583  | Ca4                                     | 44922583                      | TTTTTT/TTTTTATTTTT                                            | CGCGAGAAATAAGTGC<br>ACAA   | ACAAAAAATGGACGG<br>AAGC     | 60.0                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44927225  | Ca4                                     | 44927225                      | TTT/TTTCTATTTTATT                                             | CGGGAGATACGTAGGA<br>GCAA   | GCTTGTGCATATCCCA<br>ACCT    | 60.2                             | 438                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_44934122  | Ca4                                     | 44934122                      | T/TCC                                                         | TCAAATCGTTGAAACAT<br>GAGAGA  | TCTCGTTCACCCATAGT<br>CCC    | 59.7                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44937033  | Ca4                                     | 44937033                      | TAAAAA/TAAAAA                                                 | TATCTCGCTCTTTCCTC<br>CCA     | GCTGTTTGATGGCTAT<br>GGGT    | 59.9                             | 888                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44937214  | Ca4                                     | 44937214                      | T/TA                                                          | CGTGTGTGGTATTCCA<br>ATTTGT   | GCTGTTTGATGGCTAT<br>GGGT    | 59.7                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44939636  | Ca4                                     | 44939636                      | TTA/TTATA                                                     | CTCGCTGAAATTGCCA<br>AAGT     | TTTTCTAAATAAACA<br>ACTCCCTG | 60.4                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44943130  | Ca4                                     | 44943130                      | TAAAA/TAAAAA                                                  | GCTAAACAGGGTGCA<br>AAGG      | AATAGCAACGCATTAC<br>GGCT    | 59.7                             | 798                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44949173  | Ca4                                     | 44949173                      | AA/AAATTA                                                     | TGACGTGTCCGTAAC<br>CTTT      | ATAAGCCCATGTTGCG<br>ACTC    | 60.4                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_44971582  | Ca4                                     | 44971582                      | TAAAAA/TAAAAA                                                 | AAATTGACTAAAAATCG<br>GGAAAAA | TTCGTCAACTCGCAAC<br>TCAC    | 59.3                             | 687                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45054175  | Ca4                                     | 45054175                      | AA/AACA                                                       | GCACTTCTTGCTGGTT<br>CCTC     | ATGGCATCACGTGAAT<br>GTGT    | 60.0                             | 933                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4505602   | Ca4                                     | 4505602                       | T/TA                                                          | CATTGAGAATTTGGGG<br>ACCA     | TCATGTTGAAGGCTCT<br>GTCG    | 60.7                             | 891                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45057895  | Ca4                                     | 45057895                      | CATGGA/CATGGATGGA                                             | GGATTGCGTATCAGTC<br>GTCA     | CGCGAAATGCAAAACA<br>ACTA    | 59.7                             | 344                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_45058561  | Ca4                                     | 45058561                      | AAACAA/AAA                                                    | ATACTTTTCGACCCG<br>TTCC    | TCACAGAAATGCTGGC<br>AGTC   | 60.2                             | 752                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_45062190  | Ca4                                     | 45062190                      | GAA/GAATAATAA                                                 | AAGGGACGTGGTGT<br>GAAG     | ACCCCGTTGGTAAAA<br>CTCC    | 60.0                             | 588                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_45064783  | Ca4                                     | 45064783                      | TAAA/TAA                                                      | GAACCACTTCACCTC<br>CCAA    | ATCGAGTTGAGTCGTG<br>GTCC   | 59.9                             | 737                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_45065586  | Ca4                                     | 45065586                      | TAAAA/TAAAAA                                                  | CGACTCAACTCGATCG<br>TCAA   | AAAACCTTAATCACCG<br>TGC    | 60.0                             | 500                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_45065685  | Ca4                                     | 45065685                      | ATGT/AT                                                       | GGCTCGAATGATGCCT<br>AAAA   | AAGATGTGATCGCAAG<br>GAATG  | 60.2                             | 899                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_4507561   | Ca4                                     | 4507561                       | AA/AAATA                                                      | TTGGGGACCAAACT<br>GAAG     | TCCGAGCAACCATACT<br>TTCA   | 59.9                             | 698                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_45076676  | Ca4                                     | 45076676                      | GTTT/GTTTT                                                    | CATTGACTTTCGGGCA<br>AGAT   | TCCACAAATAACAGGTT<br>TTCCC | 60.1                             | 741                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_45076892  | Ca4                                     | 45076892                      | CG/CGG                                                        | GGTCCAACATTCCTCC<br>TTGA   | TCCACAAATAACAGGTT<br>TTCCC | 59.9                             | 606                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_45093112  | Ca4                                     | 45093112                      | AAAAATAAAA/AAAAA                                              | CAACCCTTTTATCCAA<br>TAATGC | AGCACATGAATTGCAA<br>GCAG   | 58.8                             | 528                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_45098286  | Ca4                                     | 45098286                      | TAAAAA/TAAAAAA                                                | CCCAATTCAATCCTCC<br>AGA    | GAGGCGGGGTGTATCA<br>CTAA   | 59.9                             | 454                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_45100378  | Ca4                                     | 45100378                      | TTATATATATATATATATATA/TTATA<br>TATATATATATATATATATATATATA     | TTGCGTTGATCTTGTT<br>GGAA  | TTTGTGACTGGTTTG<br>GGA   | 60.2                             | 879                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45108878  | Ca4                                     | 45108878                      | CAAAAA/CAAAAA                                                 | AAACCCAACTTTTCA<br>TGGT   | GCTTTGGAGGTGGTT<br>TTGA  | 57.5                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45115420  | Ca4                                     | 45115420                      | TAAAAAAAAAAAAAAAA/TAAAAAAAAA<br>AAAA                          | TCGCAATGAGTTGATT<br>GTTCA | TCATCATCCGACTTTGC<br>TTG | 60.3                             | 701                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4512130   | Ca4                                     | 4512130                       | GAAAAAAAA/GAAAAAAAA                                           | TAGACTCAACTCTGCG<br>GGCT  | CCGGCGAGAATTTTC<br>AATA  | 60.2                             | 266                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45148376  | Ca4                                     | 45148376                      | TAAA/TAA                                                      | GGGGTTGGTTTGCTT<br>GTTA   | ATGCGGCTGTTTGT<br>CACT   | 59.8                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45150211  | Ca4                                     | 45150211                      | TTTCTTTTATT/TTT                                               | ACCATTGTGGTTGTGT<br>GCAT  | TGGTGGTGAAAGATGG<br>ATGA | 59.7                             | 831                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45168651  | Ca4                                     | 45168651                      | TAAAAA/TAAAAAAA                                               | TTGATGGCCTTCTCGA<br>AGAT  | ATGCAGCTTTTGGATG<br>TGTG | 59.8                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45169109  | Ca4                                     | 45169109                      | CATATATA/CATA                                                 | CACACATCCAAAAGCT<br>GCAT  | TCAAAGAAAATCGTCG<br>GAGG | 59.7                             | 632                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4517051   | Ca4                                     | 4517051                       | ATTT/ATTTT                                                    | AAATGCGTTTCACTC<br>GGAC   | GCACACTTGTGCTTGG<br>AAGA | 60.1                             | 304                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4517104   | Ca4                                     | 4517104                       | GATGAATTTATTAAT/GATGAATTTA<br>TTAATGAATTTATTAAT               | AAATGCGTTTCACTC<br>GGAC   | GCACACTTGTGCTTGG<br>AAGA | 60.1                             | 304                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_45174430  | Ca4                                     | 45174430                      | CTACGTAC/CTAC                                                 | GTCAAACCCCAATTC<br>AACG        | CAATGCTCATTGGTGC<br>TTCA       | 60.2                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45174707  | Ca4                                     | 45174707                      | AGTTGTT/AGTTGTTGTT                                            | GGCTGCAAAAAGTTCA<br>CGAC       | AGAAGGTCTAACCGCT<br>GCAA       | 60.8                             | 702                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45177041  | Ca4                                     | 45177041                      | ACCCCC/ACCCCC                                                 | CCAAGTTTTTGCAACC<br>CAGT       | TGTGTACCGGAAAAC<br>TCAAAA      | 60.0                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45177094  | Ca4                                     | 45177094                      | ATT/AT                                                        | CCAAGTTTTTGCAACC<br>CAGT       | TGTGTACCGGAAAAC<br>TCAAAA      | 60.0                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45178018  | Ca4                                     | 45178018                      | GAAAAA/GAAAAA                                                 | TGAAATGGGTTTGTA<br>TTTTCG      | CCATTGAGTGTTGT<br>GTTG         | 59.0                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45182355  | Ca4                                     | 45182355                      | AATATATATATATATATATAT/ATATATATATATATATATAT                    | TCATTGTCTTGGTCTTC<br>CCC       | GTGGTATTTAGTAAAT<br>GAATGTGTCA | 59.9                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45182772  | Ca4                                     | 45182772                      | AATATATATATATATAT/ATATATATAT                                  | TGAAAAATTAAATAAAA<br>AGCTGACGA | CAGTATTTATTCGGCG<br>GGAA       | 59.6                             | 629                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45182831  | Ca4                                     | 45182831                      | TTA/TTATGAAATA                                                | AAAATTAAATAAAAAGC<br>TGACGAAA  | CAGTATTTATTCGGCG<br>GGAA       | 57.1                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45183168  | Ca4                                     | 45183168                      | CTCACAATAAATATTATCACAATAAA<br>/CTCACAATAAA                    | TTCCCGCCGAATAAAT<br>ACTG       | AGGGCCCATCTTTTCA<br>CTCT       | 59.9                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45194041  | Ca4                                     | 45194041                      | CAATA/CA                                                      | GAGCGAGTCAAAACCG<br>AGTC       | GCAAGCAATCAAGTAA<br>AAATGG     | 60.0                             | 597                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_45196611  | Ca4                                     | 45196611                      | GATATATATATATA/GATATATATATA<br>TATATATA                       | CCAAGTTTTGTCCAAG<br>CAAA    | TAGTGTCATTCGTGG<br>TTGC      | 58.8                             | 662                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_4520382   | Ca4                                     | 4520382                       | CG/C                                                          | CATGCAATTGAACAATA<br>TCCG   | GTGGGCTTTCAAGTG<br>CCAT      | 58.9                             | 520                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_45205031  | Ca4                                     | 45205031                      | AG/AGGG                                                       | ACCCCATCTACCAAAC<br>CCTC    | TATTCCTCCTCCATT<br>TCC       | 60.1                             | 592                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_45205185  | Ca4                                     | 45205185                      | TC/T                                                          | GGAAATGGGAGGAGG<br>GAATA    | TCGTGTTTTGAATAAAC<br>AGGAAAA | 60.1                             | 300                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_45205721  | Ca4                                     | 45205721                      | ACC/AC                                                        | CGTATTTGGCTTAAAT<br>ATTCCAA | CCTCAACCCACTGAT<br>CCTA      | 59.7                             | 451                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_4521076   | Ca4                                     | 4521076                       | AATATATATATATATATA/AATATA<br>TATATATATA                       | CCACAGAAAATGTTGG<br>GCTT    | TCGTAAATAGTTGGC<br>CGGA      | 60.0                             | 568                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_45211328  | Ca4                                     | 45211328                      | CATATAT/CATATATAT                                             | GTTGGTTGGTGGCTTA<br>GCAT    | TCGTTTCGCAATGACTT<br>CTG     | 60.0                             | 552                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_4521903   | Ca4                                     | 4521903                       | ATTTTTTTTTT/ATTTTTTTTTT                                       | TGCTTGTATGTTTTAA<br>TACGGG  | AAACATAAAACACACA<br>GGACAAA  | 60.1                             | 690                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_45223304  | Ca4                                     | 45223304                      | ATTACT/ATGAATTACTTACT                                         | TGAAGAGGGGAAATAT<br>GCAA    | GAAAACGCTTTTATCAT<br>CATCCA  | 58.2                             | 442                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_4522341   | Ca4                                     | 4522341                       | ATTTTTTTTTT/ATTTTTTTTTT                                       | TTTGTCTGTGTTGTTT<br>TATGTTT | GGGCCGAAAATTTGTC<br>ATT      | 57.7                             | 276                                           | INTERGENIC                                           | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_45289876  | Ca4                                     | 45289876                      | GAAAAAAAAA/GAAAAAAAAA                                         | AAGCGAGCATCAGAGA<br>AAGC   | CTTGATGGCAAACCC<br>AAGT   | 59.9                             | 269                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45290418  | Ca4                                     | 45290418                      | GAAA/GAAAA                                                    | CTTGGGTTTTGCCATC<br>AAGT   | GAAGCAATCGTGTGTA<br>GCCA  | 60.0                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45295340  | Ca4                                     | 45295340                      | TAAAAAAAAA/TAAAAAAAAA                                         | GACGTATCCACTGTTC<br>TTTTCG | CGGACAGGTTCCACTC<br>CTAA  | 58.8                             | 737                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45296395  | Ca4                                     | 45296395                      | TAAAAA/TAAAAA                                                 | TTAAATTAAGCCGAAG<br>GCGA   | AAGATTCTCAAAGAG<br>GCAA   | 59.8                             | 800                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45297365  | Ca4                                     | 45297365                      | A/AT                                                          | CTTGTGCTCTCACAC<br>CGTCA   | ACCCTCGCCTTGATAC<br>ACAC  | 59.9                             | 343                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45297508  | Ca4                                     | 45297508                      | A/AGT                                                         | CAACAAGGTCGCTCAT<br>CGTA   | ACCCTCGCCTTGATAC<br>ACAC  | 59.9                             | 147                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45297724  | Ca4                                     | 45297724                      | TG/T                                                          | GTGTGTATCAAGGCGA<br>GGGT   | AGTTAAGAGAGCGCGT<br>GTCC  | 60.0                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45297957  | Ca4                                     | 45297957                      | TAAAAAAAAA/TAAAAAAAAA                                         | GTGTGTATCAAGGCGA<br>GGGT   | AGTTAAGAGAGCGCGT<br>GTCC  | 60.0                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45318040  | Ca4                                     | 45318040                      | CAA/CAAA                                                      | GCAAAACACAATATAT<br>GCAGCG | CAGGGGTAAGAGACGA<br>TTCAA | 60.7                             | 190                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45319208  | Ca4                                     | 45319208                      | T/TGATAAAACA                                                  | TGGTTCACGGAATAGA<br>GGAA   | AAAAGAAGGACCAACC<br>ACCA  | 58.1                             | 688                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_45334419  | Ca4                                     | 45334419                      | ATT/ATTT                                                      | TTTAATGTGGAAAGAG<br>AGACATGAA | AAACACATTGACCGC<br>CATT       | 59.2                             | 357                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45334674  | Ca4                                     | 45334674                      | TA/T                                                          | ATCATTCTTGAATGGC<br>GGTC      | CAAGACTTCGGGCACT<br>TTTC      | 59.9                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45334856  | Ca4                                     | 45334856                      | AACG/AACGACG                                                  | ATCATTCTTGAATGGC<br>GGTC      | AGAAGCCATGTGATCG<br>GAAC      | 59.9                             | 684                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45334966  | Ca4                                     | 45334966                      | ATT/ATTT                                                      | ATCATTCTTGAATGGC<br>GGTC      | AGAAGCCATGTGATCG<br>GAAC      | 59.9                             | 684                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45359294  | Ca4                                     | 45359294                      | A/AATGCG                                                      | TGACCGATAATCGTGA<br>CAAAA     | GGGGATCCAAAATAA<br>AGGC       | 59.0                             | 720                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45359395  | Ca4                                     | 45359395                      | AG/A                                                          | TCAGTTAGCAATGACC<br>CTCAAA    | GGGGATCCAAAATAA<br>AGGC       | 59.7                             | 429                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45368880  | Ca4                                     | 45368880                      | TA/TTAA                                                       | TGAATTGGTTGAGTGA<br>AAGGAA    | GAGTTATGTTAATTTTC<br>GAGTTTGA | 59.6                             | 120                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4537624   | Ca4                                     | 4537624                       | TAATAAAATAAAATAAAAT/TAATAAA<br>ATAAAATAAAATAAAAT              | TGCATCGCCCATATCA<br>ATAA      | TATTGGACCGACCCTG<br>AAAA      | 59.9                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45384926  | Ca4                                     | 45384926                      | CTCGACTCT/C                                                   | TCGATTGGTTGGTGAC<br>AAAA      | CAAAGTTCGTGTAGGA<br>GGGA      | 59.9                             | 205                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45385545  | Ca4                                     | 45385545                      | ACT/A                                                         | CACCCATAACTTTAT<br>GAGATGGAA  | CACAAATTAAGGGAAG<br>GCGA      | 59.6                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_45386230  | Ca4                                     | 45386230                      | ATATTTATTTATTTATT/ATATTTATT<br>TATTTATTTATT                   | CGCCTTCCCTTAATTT<br>GTGA | TACATTGAGATTGACC<br>GCCA | 60.1                             | 827                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45387909  | Ca4                                     | 45387909                      | CCT/CCTTCT                                                    | CTTCCTCCTCCAAATG<br>ACCA | AGGACCACTTGAAATG<br>CCAC | 60.0                             | 730                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45390678  | Ca4                                     | 45390678                      | ACCCC/ACCCCC                                                  | CTCGAAGTGATGGCAG<br>TCAA | CAGTAGGGTTTGGGAC<br>TCCA | 60.0                             | 791                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45391070  | Ca4                                     | 45391070                      | GAAAAA/GAAAAAA                                                | GGATTTCAACTTTGAG<br>GGCA | GAGCAGTAGCTCAGTG<br>TGGG | 60.1                             | 724                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45391856  | Ca4                                     | 45391856                      | CTTTTT/CTTTT                                                  | CCCACTGAGCTACTG<br>CTCC  | TCTCCGTGGGCTTAAC<br>AATC | 58.6                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45396716  | Ca4                                     | 45396716                      | ATT/AT                                                        | CGGAAAGGTTTTTGGT<br>TGTG | GTCACACTCACGTGAC<br>CCAC | 60.4                             | 748                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45397276  | Ca4                                     | 45397276                      | ATTTTTTT/ATTTTTTTT                                            | CACGTGAGTGTGACAT<br>GGTG | TAAATGGGAACGCAAA<br>AGGT | 59.6                             | 372                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45399331  | Ca4                                     | 45399331                      | ATTTTTTTTTTTTTTT/ATTTTTTTTTT                                  | ACCAC TTCACACAAG<br>AGGG | ATTCCGCTTTGCTGTCA<br>AAC | 60.0                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45401996  | Ca4                                     | 45401996                      | TAAAAA/TAAAAA                                                 | TTGATAGTGGCTGGCA<br>CAAA | GGGGTTTTGGTTTTGG<br>TTTT | 60.3                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4541237   | Ca4                                     | 4541237                       | ATTT/ATT                                                      | TATTCACAGCGCCAA<br>AGTG  | CCGCTACTTTCAACATC<br>CCT | 59.9                             | 964                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_45414589  | Ca4                                     | 45414589                      | CTT/CTTT                                                      | TGCATAAATGCACGAT<br>GAAAA     | GTTCAAACCGCAATG<br>TCTT   | 60.1                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4541506   | Ca4                                     | 4541506                       | TATACATACATACA/TATACATACA                                     | CACTATTTAAAGTATGT<br>CACGTCGC | GGACCACACTGCGGTA<br>ACTT  | 59.2                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45431315  | Ca4                                     | 45431315                      | CTT/CTTT                                                      | GAGGGCAAGACCAAGA<br>TCAA      | CCACCAAAAATCTCCCT<br>ATGA | 60.2                             | 248                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45431331  | Ca4                                     | 45431331                      | GATATAT/GAT                                                   | GAGGGCAAGACCAAGA<br>TCAA      | CCACCAAAAATCTCCCT<br>ATGA | 60.2                             | 248                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45432247  | Ca4                                     | 45432247                      | TTTGTT/TTT                                                    | TTTGTTGTGTGCATTCA<br>TGTC     | GGTAAACACATGACCC<br>GTCC  | 59.0                             | 746                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45433971  | Ca4                                     | 45433971                      | TTA/TTAATA                                                    | ATGGGATTGGGTATTG<br>TTGC      | TTAATCGCCCTCAAGG<br>TCAC  | 59.5                             | 406                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45434747  | Ca4                                     | 45434747                      | A/ATATAT                                                      | AGACCATGTTTGTATAA<br>CGCC     | GGTCCAATTTGCCTAC<br>CACA  | 59.0                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45436047  | Ca4                                     | 45436047                      | TAAAAAAAAAAAAA/TAAAAAAAAA                                     | TGTTTGCTTTTCACACA<br>TCA      | TCACATCATGCAAATCC<br>AATG | 60.1                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45436331  | Ca4                                     | 45436331                      | TT/TTCATAT                                                    | TGCTAATAACGTGTCA<br>CGCC      | CTCTCCCAACATATGAT<br>GCCT | 59.8                             | 819                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45436462  | Ca4                                     | 45436462                      | AC/A                                                          | AACCATGCACATGACT<br>CACAA     | CGAGCGTGACGAAATA<br>ATCA  | 60.0                             | 850                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_45437836  | Ca4                                     | 45437836                      | AA/AATA                                                       | TCAACTTGGCTTCATC<br>CTCC   | TTCGAAACGCACAATTA<br>ATCA      | 60.2                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45439383  | Ca4                                     | 45439383                      | GTTTTTTTTTTTT/GTTTTTTTTTTTT<br>TT                             | TTTGGATGTGGTTGTG<br>ATGAA  | ACCCTCGTAACTCCAA<br>GCCT       | 59.8                             | 338                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45440447  | Ca4                                     | 45440447                      | AT/A                                                          | GGAGGTCGAACTCGAG<br>AATG   | AAGTGGCGCTTAATCC<br>AAAA       | 59.8                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45441219  | Ca4                                     | 45441219                      | GTATATAT/GTAT                                                 | TTTGATTAAAGCGCCA<br>CTTT   | ATGGGTTTCATGTTGA<br>CCGT       | 59.7                             | 949                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45444757  | Ca4                                     | 45444757                      | ACTCTCTCTCTCTCTCTCTC/ACT<br>CTCTCTCTCTCTCTCTCTC               | TTGCTGGATAAAGTTG<br>GCAG   | GGACCTTTCTTCACGTT<br>TGC       | 58.9                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45488073  | Ca4                                     | 45488073                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATAT                   | TCGCCATTTTGAACCT<br>GAAT   | GGCGACTTTCCACATG<br>ATTT       | 60.6                             | 284                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45556140  | Ca4                                     | 45556140                      | AATAATATAATAT/AATAATATAATAT<br>AATAT                          | TCATAATCCACAATCG<br>CCCT   | TCTTTTAAGATGTCAGT<br>TGGAATACG | 60.3                             | 936                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45567618  | Ca4                                     | 45567618                      | TTATATATATATATATAT/TTATAT<br>ATATATATATAT                     | TCACAAATGGCAGTTTT<br>GTCTT | CCAATCCTAGCTTCTG<br>AAAATG     | 59.7                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45580465  | Ca4                                     | 45580465                      | CTTTTT/CT                                                     | GGAAGGAACGGTGCTT<br>CATA   | TGCCACATCACCTAA<br>ATCA        | 60.1                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45591547  | Ca4                                     | 45591547                      | CTTTTTTT/CTTTTTTTT                                            | TTTGGAAGGCAACTAA<br>TGTCAA | CGCCAAACGGTCTCTA<br>AAAA       | 59.6                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                              | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                            |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_45592829  | Ca4                                     | 45592829                      | ATTTTTTTTT/ATTTTTTTTTT                                                                                                     | TGCAAAGACATCATCT<br>CCCA  | GGCAATGTAGCATTTT<br>GGGT  | 60.2                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45645932  | Ca4                                     | 45645932                      | GT/G                                                                                                                       | AACTTGATGCCGAGTA<br>GCGT  | GCCGAATAAAACCCTC<br>ACAA  | 59.9                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45740702  | Ca4                                     | 45740702                      | TTATATATATATATATATATATATA<br>TATATA/TTATATATATATATATAT<br>ATATATATATATATA                                                  | TGTGATGCGGATTTAA<br>AACAA | AACAAAATACGCGTGC<br>ATGA  | 59.1                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45756786  | Ca4                                     | 45756786                      | GAAA/GAA                                                                                                                   | CAACTCCACCCCTC<br>TGTT    | ATCAGCAACATAACAC<br>CCA   | 60.0                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45844295  | Ca4                                     | 45844295                      | AAATAATAATAATAATAATAATA<br>ATAATAATAACAATAATAATAATA<br>AA/AAATAATAATAATAATAATA<br>TAATAATAATAATAACAATAATA<br>ATAATAATAA    | TTCACTGCAACACCCT<br>TCTG  | TCCAACACTTCTTTCCC<br>ATGT | 59.9                             | 847                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4589864   | Ca4                                     | 4589864                       | CTTT/CTT                                                                                                                   | TTTCGCTCAATGTGAAA<br>AGC  | AACGGAGGCAGTAATT<br>GTCG  | 59.0                             | 322                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4590029   | Ca4                                     | 4590029                       | C/CAT                                                                                                                      | TTTCGCTCAATGTGAAA<br>AGC  | CCACGATAACGATGTG<br>ATGC  | 59.0                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4591345   | Ca4                                     | 4591345                       | TAAAAAA/TAAAAAA                                                                                                            | TTGCATATCAATGGT<br>GAATTT | GTTGGTGTTCGACCTT<br>CCAG  | 59.3                             | 752                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4594832   | Ca4                                     | 4594832                       | GAAA/GAAAAATAA                                                                                                             | TATGAGTGGGGATGAT<br>GGGT  | CCTGTTTCCCGCACA<br>TAAT   | 60.0                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_45949230  | Ca4                                     | 45949230                      | AATTATTATTATTATTATTATTAT<br>TATTATTATGATTATTATTATTAT/AA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATGATTATTA<br>TTATTAT | TCGAAAGAACCTCGAC<br>TCGT  | TCAATATGAGGTCGCT<br>TCCC  | 60.0                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                    | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                  |                              |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_45959235  | Ca4                                     | 45959235                      | TTTATTATTATTATTATTATTAT/<br>TTTATTATTATTATTATTATTAT<br>AT                                        | GGCTATGGCCTAGCC<br>TACT      | ACGGCCTACCATAGGC<br>TTTT     | 59.7                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46001807  | Ca4                                     | 46001807                      | GATAATAATAATAATAATAATAA<br>TAATAATAATAATAATA/GATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATA | TTGCTCCTACGTATCC<br>CCAG     | CTCAATCGTGGGTGAC<br>CTTT     | 60.1                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46004838  | Ca4                                     | 46004838                      | TAAAAA/TAAAAA                                                                                    | TGATTCAATGAGAGG<br>ATTTTGT   | GCTCGATTGATGTTAA<br>GGGC     | 59.0                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46006002  | Ca4                                     | 46006002                      | TATATAATATA/TATATA                                                                               | TTTGTGTCCGGAATA<br>TATG      | GGTGAAATGAAAGGAC<br>CCAA     | 59.4                             | 793                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46035567  | Ca4                                     | 46035567                      | ATTTTTTTTT/ATTTTTTTTT                                                                            | GCAATCAATTATGAGT<br>GGGA     | CAACAAATCCTGTCAT<br>TGAAATC  | 59.8                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46040811  | Ca4                                     | 46040811                      | T/TG                                                                                             | TGCGCTTCTCATTAC<br>GTTG      | AGCAAGTTCTCCAAA<br>AGCA      | 60.0                             | 423                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46060270  | Ca4                                     | 46060270                      | CATATATATATATATATATATATA<br>TATATATATATAT/CATATATATATAT<br>ATATATATATATATATATAT                  | ATTTTAACGGATGTCG<br>CAGG     | TGTGGTGAATTTTCTT<br>CTTCTGA  | 60.0                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46189254  | Ca4                                     | 46189254                      | GTTATTATTATTATTATTATTATT<br>ATTATTATT/GTTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATT      | AACAACCTGATCCTATT<br>TTGGAGA | TTTTAGTTGAATCACC<br>GCC      | 58.3                             | 838                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46377594  | Ca4                                     | 46377594                      | TTTTACAT/TT                                                                                      | ATGGGAACCCACAAC<br>AATC      | CCACATGCTATTTTAAT<br>CTTTGGA | 59.5                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46384693  | Ca4                                     | 46384693                      | T/TCCCTATAAAAA                                                                                   | GAGGAGGGTGGAGAA<br>TGGAT     | GGGTGCCTGGTACAAA<br>ACTC     | 60.3                             | 708                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                             | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                           |                            |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_46493029  | Ca4                                     | 46493029                      | AATATATATATATATATATATATA/<br>AATATATATATATATATATATA                                                                       | GGGAAAGTGATATTGG<br>GGGT   | CAAAGCTCCTTCAATTG<br>TCTTG   | 59.9                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46493521  | Ca4                                     | 46493521                      | TAAAAAAAAAAAA/TAAAAAAAAAAAA<br>AA                                                                                         | CAAGACAATTGAAGGA<br>GCTTTG | CTTGTTTGAACCCATT<br>GCT      | 59.0                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46494987  | Ca4                                     | 46494987                      | TTGATGAT/TTGAT                                                                                                            | TGAATTCGACTTGATT<br>CCAA   | CTTGTTTGAACCCATT<br>GCT      | 58.2                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46495777  | Ca4                                     | 46495777                      | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>T/ATATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTAT | GAGGCTTCATTCTCT<br>CGTG    | TGAATTGGTGGATCAA<br>TGAAAA   | 60.0                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46508599  | Ca4                                     | 46508599                      | AATATATATATATATATATATA/AA<br>TATATATATATATATATA                                                                           | AAAGGGGAGTATTGT<br>TGGG    | CAAAGCTCTTTCATAAT<br>TGCTTGA | 60.0                             | 492                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46560817  | Ca4                                     | 46560817                      | CAAAAAAAAA/CAAAAAAAAA                                                                                                     | ACCATTTCCTGATTTT<br>GCG    | ATGAGGAGGATGTCAG<br>CCC      | 59.9                             | 838                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46581610  | Ca4                                     | 46581610                      | CAATAATAATAATAATAATAATA<br>ATAATAATAATAATA/CAATAATA<br>ATAATAATAATAATAATAATAAT<br>ATAATAATAATA                            | CGTCCTCGAACTAAG<br>AGGAAA  | TTTCGAAGAAGGCGAT<br>AACAA    | 59.9                             | 993                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46674801  | Ca4                                     | 46674801                      | A/AG                                                                                                                      | GGATGACTCGAAACGG<br>TGTT   | TTACCCAAACCCAAA<br>TCA       | 60.0                             | 667                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46683003  | Ca4                                     | 46683003                      | GAAGA/GAAGAGAAAGA                                                                                                         | GGTGGTGAATGAGGA<br>GAAA    | ATCACTTCTTGCCATGT<br>CCC     | 59.9                             | 106                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46708395  | Ca4                                     | 46708395                      | CAT/CATAT                                                                                                                 | CACACACACCACCA<br>CAAA     | CACAAAAATAGATGCCA<br>ACCA    | 59.9                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_46711628  | Ca4                                     | 46711628                      | GTTATAG/GTTATAGACTTATAG                                       | TCATTTACTCGTGCAT<br>GAAAGTT | ATGCTTTTTACCATCC<br>TCG    | 58.8                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46729372  | Ca4                                     | 46729372                      | ACTAATTCTAATTCTAATTCTAAT/AC<br>TAATTCTAATTCTAAT               | ATTGCGATGTGGTTAA<br>CGGT    | CCTCAAGTACGCATCT<br>GCAA   | 60.3                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46746914  | Ca4                                     | 46746914                      | GATTATTATTATTATTATTA/GATTAT<br>TATTATTA                       | ACAGTGCAACACAACA<br>AGGG    | TCGCTCCATCTTTTCCA<br>TTC   | 59.6                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46747194  | Ca4                                     | 46747194                      | AATATA/AATA                                                   | ACAGTGCAACACAACA<br>AGGG    | TCGCTCCATCTTTTCCA<br>TTC   | 59.6                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46753094  | Ca4                                     | 46753094                      | AT/ATT                                                        | AAACAATCAACACATCC<br>GCA    | CGAAAGAAGTTCAATC<br>AAACCC | 60.0                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46757820  | Ca4                                     | 46757820                      | ATTTTTTT/ATTTTTTTTT                                           | ATTTCTCAGGGAACA<br>ATCG     | TCATTCAACGGTAACTC<br>CCA   | 59.0                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46759694  | Ca4                                     | 46759694                      | AATA/AATATA                                                   | AGTTAAGGCACCGCAA<br>AAGA    | GGAATCACGCGGAAAT<br>TTTA   | 59.9                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46760540  | Ca4                                     | 46760540                      | T/TAA                                                         | TAAATTTCCGCGTGAT<br>TCC     | GCAAAGCAAAGGAAGA<br>TACACC | 59.9                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_46761044  | Ca4                                     | 46761044                      | CTTT/CTTTT                                                    | GGTGATCTTCCTTG<br>CTTTGC    | CATTCGTTACCCTCGC<br>TCTC   | 60.1                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_47185891  | Ca4                                     | 47185891                      | A/AG                                                          | CGAAACCCTAGCCACC<br>ATTA    | CTGCCACTTAGGCAAC<br>TTCC   | 60.0                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_47206093  | Ca4                                     | 47206093                      | TAAAAAAA/TAAAAAAA                                             | TCACCATTCAATCATTT<br>TTGG  | ATGCATGCTTGCCCTTT<br>TAT  | 58.3                             | 354                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_47206262  | Ca4                                     | 47206262                      | A/ATAT                                                        | TCACCATTCAATCATTT<br>TTGG  | CCCAGAGAAAGATTTTA<br>CGCA | 58.3                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_47206910  | Ca4                                     | 47206910                      | TATATATACATATATA/TATATATA                                     | TGCGTAAATCTTTCTC<br>GGG    | GGACCATAATGCCCTT<br>GCTA  | 60.2                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_47219947  | Ca4                                     | 47219947                      | TAAATAAAA/T                                                   | AAACTCCTCTCAAACG<br>GGGT   | CCATCGTGCTTCCAGA<br>AAAT  | 60.0                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_47230296  | Ca4                                     | 47230296                      | TG/TGG                                                        | GGAGCCCCACAAAATC<br>TATG   | CACCCATCTTGTGTTTG<br>ATT  | 59.4                             | 810                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_47232992  | Ca4                                     | 47232992                      | ATTTT/ATTTT                                                   | AGTGGTCATGTGTCGC<br>ATAAA  | TGTGAAACGTCACAAAT<br>TCAA | 59.1                             | 791                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_47238699  | Ca4                                     | 47238699                      | ATTT/ATT                                                      | TTTTGATCGAATCTGAC<br>CCA   | TCGGCCATTTTCTTCA<br>ATC   | 59.0                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_47238913  | Ca4                                     | 47238913                      | TAAA/TAA                                                      | GATTGAAGAAAAATGG<br>CCGA   | ATAATCCAAATGCGC<br>GAAG   | 60.0                             | 186                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_47240338  | Ca4                                     | 47240338                      | AATATATATATA/AATATATATA                                       | AAAGCTTAATTGTCGT<br>GCATCA | TAGTTTGGAGCGAGGA<br>GGAA  | 59.8                             | 352                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_47242175  | Ca4                                     | 47242175                      | AAATAATAATAATAATAATAA/AA<br>ATAATAATAATAATAATAA               | CGCTCCTAATCCCAC<br>ACAT    | TTTCTCGCATGCATTCT<br>CAC  | 60.0                             | 835                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                     |                             |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_47286913  | Ca4                                     | 47286913                      | ACCCCCCCC/ACCCCCCCCC                                                | GTTGTTGGTTTGAGCC<br>CAGT    | TGGAGATCACTTTCTC<br>CGCT    | 60.0                             | 619                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_47401934  | Ca4                                     | 47401934                      | TC/TCC                                                              | TTGGGGACCATAGTCT<br>TTCG    | CAGAGAACCAGCCTTT<br>GGAG    | 59.9                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_47457546  | Ca4                                     | 47457546                      | CATTATTATTATTATTATTA/CATTAT<br>TATTATTATTATTATTATTA                 | GGTTGGGATGAAACT<br>GGAA     | CCTGGAAAACATTAATT<br>CCCC   | 59.8                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_47685776  | Ca4                                     | 47685776                      | A/AGGTTTG                                                           | AGTCAGACGCTACTCG<br>GCAT    | CCGACGAAATAAGTCC<br>CTCA    | 60.0                             | 837                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_47685878  | Ca4                                     | 47685878                      | AATATATATATATATA/AATATATATA<br>TATATATATATATATA                     | AAATTAAAGTTTCAAAC<br>CACGG  | CCGACGAAATAAGTCC<br>CTCA    | 57.3                             | 667                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4769266   | Ca4                                     | 4769266                       | TTATATATATATATATAT/TTATAT<br>ATATATATATATATAT                       | ATACCGATGCAGTACC<br>CGAG    | TGTTTGCCAACCATATG<br>TGAA   | 60.0                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_47842857  | Ca4                                     | 47842857                      | GAAA/GAAAA                                                          | GGTTATCCCATTAATG<br>CATCTG  | TGTGTTCAATTGTTTTTC<br>GCTTT | 58.3                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48048628  | Ca4                                     | 48048628                      | CATATATATATATATATATATATA<br>TATATA/CATATATATATATATATATA<br>TATATATA | CGAAACCGTAACCCCTA<br>CGAA   | TTGTTAGTTTGACGAG<br>GGCA    | 60.0                             | 328                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48074355  | Ca4                                     | 48074355                      | TG/T                                                                | GGTCGACATGACATCA<br>CTAAATG | AGTGTCAAAGGGGGAG<br>GAAG    | 59.4                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48078751  | Ca4                                     | 48078751                      | AATATATATATATATATATAT/AA<br>TATATATATATATATATATATAT                 | TGGAATGTTCTCACCA<br>TTTTCA  | TGATTTCCACTCATGG<br>GGAT    | 60.3                             | 941                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_48115647  | Ca4                                     | 48115647                      | AATATATATATATATATATAT/AATAT<br>ATATATATATATAT                 | TCCTTCATATCCCACG<br>AACC   | TGGTGTGGAGTCATG<br>CTTT     | 59.8                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48202910  | Ca4                                     | 48202910                      | AAATAA/AAA                                                    | TCGTCCTTACACCGGA<br>AAAC   | CAAGTTTCGGTTGACT<br>ATACACG | 60.0                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48204434  | Ca4                                     | 48204434                      | CT/CTT                                                        | CTCGGCATCTCAAAGT<br>TTCTC  | CCTTTGCCCTCTTCCTC<br>TTT    | 59.1                             | 391                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48206793  | Ca4                                     | 48206793                      | CAT/CATAT                                                     | TATTTGGCCAACAGGA<br>AAGG   | AGAGCTGATTGGTTC<br>CTCG     | 59.9                             | 893                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48207152  | Ca4                                     | 48207152                      | CTTT/CTTTT                                                    | ATCGAATGTGCATCGT<br>GAAG   | CAATAAGGATAAGGGG<br>CGGT    | 59.7                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48208619  | Ca4                                     | 48208619                      | A/AG                                                          | GTAGACCGATTCTGAAG<br>GTCG  | GCGTAACGTGTAGTTC<br>AGTGC   | 59.7                             | 809                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48208929  | Ca4                                     | 48208929                      | TC/T                                                          | AAGTTTTTGAATACCGC<br>AAAAT | AAGCTGCGATGGGACA<br>ATAC    | 57.0                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48210066  | Ca4                                     | 48210066                      | AAAGTAA/AAA                                                   | AATTCACCTTGACGCGA<br>AACC  | TGGGTGTATCAGAGAC<br>CGAA    | 60.1                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48210310  | Ca4                                     | 48210310                      | TAA/TAAA                                                      | CCATAAGTCCACAACG<br>GACC   | TGGGTGTATCAGAGAC<br>CGAA    | 60.2                             | 400                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48211280  | Ca4                                     | 48211280                      | TA/T                                                          | TGATGTCCGATGAAC<br>TTGC    | CAAGTTATCGGCTGAG<br>AGGC    | 59.7                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_48212003  | Ca4                                     | 48212003                      | AATATATAT/AATATATATATAT                                       | GCCTCTCAGCCGATAA<br>CTTG     | ATTCCTTTACGGGGAA<br>AACG | 60.0                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48214681  | Ca4                                     | 48214681                      | TTTAT/TTTATTAT                                                | GAAATGACCCCTCGAA<br>CTCA     | ATGGATTGAAAGGCG<br>ATGA  | 60.1                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48214982  | Ca4                                     | 48214982                      | GAAT/GAATTAAT                                                 | ATGCTTTCAAACATC<br>GCC       | CCATCGGATAGGTCAG<br>AACC | 60.2                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48215838  | Ca4                                     | 48215838                      | TTCT/TT                                                       | AGTTCAAAGCAAAAGC<br>CCAA     | TCCTCCATACCCACATC<br>CAT | 59.9                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48217970  | Ca4                                     | 48217970                      | ATAT/A                                                        | AGTGCATACAGCTCAT<br>GGGG     | TGGCAGGATATGGTGG<br>ACTT | 61.1                             | 755                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48218216  | Ca4                                     | 48218216                      | TATTA/TATTAATTA                                               | CAACTTGAATTTGGTT<br>GGCT     | TCTGTCGGCAGATAAC<br>CCTT | 59.1                             | 885                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48223941  | Ca4                                     | 48223941                      | TTAT/TTATATTGAAAGGTGGCATAT                                    | TCTTGAATTGTTGCAAA<br>GAAACAT | CCAGCGAGAAGAAACC<br>TGTC | 60.0                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48230328  | Ca4                                     | 48230328                      | A/AC                                                          | TCCTTGAGGGACCAGG<br>ATAA     | ATTGTGGATTTTGTGTC<br>GCA | 59.5                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48278655  | Ca4                                     | 48278655                      | ATTTTTTTT/ATTTTTTTTTTT                                        | AATAGCAATGCCAGG<br>TTTG      | ACCAACGACGAGATAG<br>GGTG | 60.0                             | 297                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48279056  | Ca4                                     | 48279056                      | TAAAAA/TAAAAA                                                 | CACCTATCTCGTCGT<br>TGGT      | GTCTCGGGTGTGGAG<br>GATA  | 60.0                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_48280011  | Ca4                                     | 48280011                      | ATTT/ATT                                                      | TCCCAATAATCAAAATG<br>AGCG | GCCTCGTTGCTAGTTC<br>ACAA  | 59.9                             | 878                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48299604  | Ca4                                     | 48299604                      | A/AT                                                          | TCAATTGCACCAAGG<br>ATGA   | ATGAAAATCATGGCAG<br>ACCC  | 60.0                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48300219  | Ca4                                     | 48300219                      | TAAAAAA/TAAAAA                                                | ACTTATTTTGGGTCT<br>GCCA   | GCCATTGAGAAGCTCC<br>TTTG  | 59.4                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4830250   | Ca4                                     | 4830250                       | A/ATTATTATAGTTAT                                              | CAACATGGGCAACAAG<br>ACAC  | CCCTTCCCCTTCATCA<br>TTT   | 60.0                             | 273                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48306501  | Ca4                                     | 48306501                      | TAAAA/TA                                                      | TTCATTGGACTTTGGG<br>TTGA  | TTCCACAACGTTGAGT<br>TTCA  | 58.9                             | 835                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48307832  | Ca4                                     | 48307832                      | ATTTTT/ATTTTTT                                                | CTGCAGTCAATCGTCA<br>TCGT  | CGTTTATCTCTTCAATC<br>GCGT | 59.9                             | 203                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4830820   | Ca4                                     | 4830820                       | TTTATACATT/TTT                                                | AAATGATGAAGGGGAA<br>AGGG  | CAACGGTTTACATGAAT<br>TGGG | 60.1                             | 815                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48309328  | Ca4                                     | 48309328                      | AAAAGAAA/AAA                                                  | TTCGTAACCTGTTGAC<br>GTTGA | TAATGACGTTTGTGGA<br>GGCA  | 59.2                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48310812  | Ca4                                     | 48310812                      | GTTTT/GTTTTT                                                  | TCGAAAATTGGGGTT<br>TTGA   | ATGCAACATGCTGAA<br>GTGC   | 60.3                             | 773                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48316349  | Ca4                                     | 48316349                      | TAA/TA                                                        | ACGAGCACCAAGAGG<br>ACAT   | TTTTACCAGTTGCATC<br>CTAAA | 59.7                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_48335941  | Ca4                                     | 48335941                      | TA/TAAA                                                       | CATGCACTCCATGTTTT<br>TGG    | CAGTCATGTGAACCAC<br>CCAC   | 60.0                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48340280  | Ca4                                     | 48340280                      | T/TGATAATATTCGGCCCAA                                          | TCCAAACAAAGTGGAG<br>ATGC    | TTGGTCCCTGGTAGCT<br>TACG   | 58.7                             | 369                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48340605  | Ca4                                     | 48340605                      | GTTATTTTATTAT/GTTAT                                           | CGTAAGCTACCAGGGA<br>CCAA    | AAAAATGACACACCATT<br>TGACA | 60.1                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48341983  | Ca4                                     | 48341983                      | T/TTTATTTTTTA                                                 | CATTAGTGTGCTCCCC<br>ACCT    | AATGGGTATCAAAAAG<br>CCCC   | 60.0                             | 904                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48342297  | Ca4                                     | 48342297                      | GC/G                                                          | TAAAGACCGTCGCCAA<br>ATTC    | AATGGGTATCAAAAAG<br>CCCC   | 60.1                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48351278  | Ca4                                     | 48351278                      | TAATTCCAATTCCAATT/TAATTCCA<br>ATTCCAATTCCAATT                 | GACACGTGATGTCTCT<br>GTAATGG | AATGTATGTATCGAGA<br>GCGCC  | 59.5                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48368240  | Ca4                                     | 48368240                      | T/TC                                                          | TCACTTTTATTGCAAGT<br>GTTGGA | AACCTTGTCGGTTTCG<br>ATTG   | 59.7                             | 328                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48386323  | Ca4                                     | 48386323                      | ATTATTTTTATTTTTATTTTT/ATT<br>ATTTTTATTTTTATTTTTATTTTT<br>T    | ACACCACCCCATTTTG<br>TTGT    | TTGGTGATTGTGCCTT<br>GAGA   | 60.0                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48389863  | Ca4                                     | 48389863                      | TC/T                                                          | CCGTTTTCCACATTTTC<br>GAT    | CCATCAAATTCATCCAC<br>CAA   | 59.8                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48401392  | Ca4                                     | 48401392                      | GTTT/GT                                                       | GACCAAGGCAAGCAAG<br>AAAG    | GGAAAAGGAGTGCAGT<br>CACG   | 60.0                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_48404093  | Ca4                                     | 48404093                      | GATTAA/GATTAAATTAA                                            | TTTGTGGCCGAGAGTC<br>TTGA | GTGCATGGCAATTGAA<br>TGAT    | 59.6                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48404724  | Ca4                                     | 48404724                      | ACCCCC/ACCCCCC                                                | TTGCATGACTGCTTTT<br>GGAC | TTGTCATTGTTGCGGTT<br>TGT    | 59.8                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48404926  | Ca4                                     | 48404926                      | ATTTTTTT/ATTTTTT                                              | TTGCATGACTGCTTTT<br>GGAC | TTGTCATTGTTGCGGTT<br>TGT    | 59.8                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48404970  | Ca4                                     | 48404970                      | GTTTAATTT/GTTTAATTTTAATTT                                     | TTGCATGACTGCTTTT<br>GGAC | TTGTCATTGTTGCGGTT<br>TGT    | 59.8                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48405207  | Ca4                                     | 48405207                      | TTCTCTCTC/TTCTCTC                                             | ACAAACCGCAACAATG<br>ACAA | CTCACTCACCCGAAC<br>CATT     | 60.0                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48410108  | Ca4                                     | 48410108                      | CTAGATATATAGATATATAGA/CTAG<br>ATATATAGA                       | TTTGATTGTTTGGTG<br>GGTT  | GGCTGGCATATGGAGC<br>TTAT    | 60.1                             | 145                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48410907  | Ca4                                     | 48410907                      | ATTT/ATT                                                      | CACCGTCCAAATTATG<br>CCTC | TGAGAACGTGCGACCT<br>GTAG    | 60.3                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48411214  | Ca4                                     | 48411214                      | TG/T                                                          | CACCCCAAACTACAG<br>GTCG  | CCACTTTTCTACTTTTG<br>GCAGTT | 60.4                             | 104                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48414921  | Ca4                                     | 48414921                      | GTTT/GTTTT                                                    | TTGAATGTGAATGGGT<br>GCAT | AAACCGAACAATCAAT<br>GCC     | 59.8                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48431277  | Ca4                                     | 48431277                      | T/TAA                                                         | TTTGTTTTGTCCCATCC<br>CAT | TCGCCATACCTTTTCGA<br>ACTT   | 60.0                             | 762                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')          | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                                  |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_48434785  | Ca4                                     | 48434785                      | AG/A                                                          | GGTGAGAGTAGGTGG<br>GGACA     | TTCTTTCGAAATTCAC<br>TGCAA        | 60.0                             | 700                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48436603  | Ca4                                     | 48436603                      | AATA/AA                                                       | TGTGACCACCACCTTG<br>AAAA     | TGGAACCTCTGGTGCAA<br>GTCA        | 60.0                             | 383                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48440600  | Ca4                                     | 48440600                      | GTT/GT                                                        | TTTGTTTACAAGGTATT<br>CTTGCCA | GTCAATTGCACCTTTCC<br>CAT         | 59.9                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48443370  | Ca4                                     | 48443370                      | T/TA                                                          | CCCAACCATCCATCCT<br>ATTG     | TGATGATATGATATTCC<br>CATTAAATTTT | 60.0                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48445196  | Ca4                                     | 48445196                      | GAGAATTTAGAATTT/GAGAATTT                                      | GTAATAACGGCGGTGC<br>AAAT     | TCGCATGCAAAACTAA<br>CGTC         | 59.9                             | 838                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48445750  | Ca4                                     | 48445750                      | CTT/CT                                                        | GTAGTTGGTGGGGTG<br>GTGTC     | ATGAGGCCCAACAAC<br>TCAC          | 60.1                             | 280                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48446112  | Ca4                                     | 48446112                      | A/ATT                                                         | GTGAGTTTGTGGGCC<br>TCAT      | TTCCGACAATTCATTG<br>TGA          | 60.0                             | 764                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48446392  | Ca4                                     | 48446392                      | CTTTTT/CTTT                                                   | CGCCCTCATTATGGTA<br>TGCT     | GTGTTTTTCGAGTGAG<br>GGGA         | 59.9                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48447377  | Ca4                                     | 48447377                      | T/TA                                                          | GTTGAGGTCGCGTACT<br>GGTT     | CCATGATGCATTGTGG<br>ATTT         | 60.2                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48451241  | Ca4                                     | 48451241                      | TTTT/TTTTATCTTT                                               | TGTTTGGACCCCTAC<br>TGAC      | TTCGTCTCGCGGTATT<br>TATTG        | 59.8                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_48452771  | Ca4                                     | 48452771                      | CTTTT/CTTT                                                    | ACAAGCTTTCACCAAC<br>GGAA     | ATGGTAGTGGTGGTGG<br>TGGT     | 60.7                             | 926                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48453751  | Ca4                                     | 48453751                      | A/AT                                                          | GTTCCACCACCGCAAA<br>TATC     | GGTGGTGGTAGGAAAA<br>GCAA     | 60.2                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48481643  | Ca4                                     | 48481643                      | ATTTTT/ATTTT                                                  | TGACCAGTCATGACAA<br>AAATTAAA | GCTATTGGACTTCACCT<br>GTACCAC | 58.6                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4848593   | Ca4                                     | 4848593                       | ATTTTTTTTT/ATTTTTTTT                                          | TTTTGGCCCATGTCTTT<br>TGT     | TCAATTGTGAAAGTC<br>ACGATG    | 60.3                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4848650   | Ca4                                     | 4848650                       | GTTTTTTTT/GTTTTTTT                                            | TTTTGGCCCATGTCTTT<br>TGT     | TCAATTGTGAAAGTC<br>ACGATG    | 60.3                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48494467  | Ca4                                     | 48494467                      | TTTAATT/TTTAATTATGTTAATT                                      | TGGTTGACAAAACTG<br>CCAA      | ACTGGACCCCAAACCT<br>CTCT     | 60.1                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48494594  | Ca4                                     | 48494594                      | CA/CAA                                                        | GCATTCTGGCACAACA<br>AAGA     | ACTGGACCCCAAACCT<br>CTCT     | 59.8                             | 357                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48509401  | Ca4                                     | 48509401                      | GAAAA/GAAAAA                                                  | ACTGTCGAGCATAAAT<br>GGGG     | CGATCGACCCGAACTA<br>AAAC     | 60.0                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4851248   | Ca4                                     | 4851248                       | TAA/TA                                                        | GGAATGCATGGTATCC<br>AACC     | CAGCACTTCTCCCTTT<br>CCTT     | 60.0                             | 678                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48513254  | Ca4                                     | 48513254                      | CA/CAA                                                        | CGAAACTTTCACGCT<br>CTCC      | TTTGAAATTGCCCAAAG<br>GAC     | 60.0                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                     | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                   |                           |                           |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_48670468  | Ca4                                     | 48670468                      | GATA/GATAAAATCTTATA                                                                               | CTGTATTGTTAGTCGG<br>CGCA  | CCGACCCAACACGTTA<br>TGA   | 59.9                             | 620                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_48671006  | Ca4                                     | 48671006                      | ATTTTTTTT/ATTTTTTTTTTT                                                                            | GGTCGGCCCTGACTTT<br>AGAT  | TGACAATGTGGAATCG<br>GAAA  | 60.5                             | 198                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_4868200   | Ca4                                     | 4868200                       | TAAA/TAAAA                                                                                        | ATTGGTTTTGCTTTGAC<br>CCA  | CACCAATATTCCATTTC<br>CCG  | 60.3                             | 423                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_48690534  | Ca4                                     | 48690534                      | TCAA/TCAACAA                                                                                      | TCCAATTCCAAATCCCA<br>AAA  | TGTGGATATCAAGTGG<br>CTGG  | 60.1                             | 395                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_48694227  | Ca4                                     | 48694227                      | ATATTTT/AT                                                                                        | TGCTGCCACACCTAAA<br>CTTG  | TAATCCATTGGCCCAC<br>ATTT  | 59.9                             | 678                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_48721738  | Ca4                                     | 48721738                      | TTATATATATATATATATATATATA<br>TATATATATATATAT/TTATATATATA<br>TATATATATATATATATATATATAT<br>ATATATAT | GACTCTCAGCATCACA<br>CGGA  | AACTCCTCCTAATTTC<br>GTTCT | 60.0                             | 545                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_48723130  | Ca4                                     | 48723130                      | TTAATAATAATAATAATAATAA/TTAA<br>TAATAATAATAATAA                                                    | TTCTTGGGAAAGCGAC<br>ATCT  | GCAACTCCCTTTTATCG<br>TCAA | 59.8                             | 435                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_48723538  | Ca4                                     | 48723538                      | AATTATTATTA/AATTATTA                                                                              | TTGACGATAAAAGGGA<br>GTTGC | TCTTGAGAAGCGACC<br>TCTA   | 59.2                             | 580                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_48726209  | Ca4                                     | 48726209                      | GTTTTT/GTTTT                                                                                      | CCCAAAACAAGTTGTC<br>CCAG  | TGGAAGAAAAACGGAT<br>GAGG  | 60.4                             | 653                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_48739702  | Ca4                                     | 48739702                      | ATTTTTTTTT/ATTTTTTTTTTT                                                                           | ACACTCCACCAGCATC<br>AACA  | AGATTCTGCCAAATGC<br>CAAC  | 60.2                             | 577                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_48792373  | Ca4                                     | 48792373                      | ATCT/AT                                                       | AAACTGCGGGTATGAG<br>GATG    | AATGAGGGATCGTTTT<br>CACG | 60.0                             | 973                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48793555  | Ca4                                     | 48793555                      | TTCTCTCTCTCTCTCTCTC/TTCTCT<br>CTCTCTCTCTCTCTC                 | ACGGAGAGTTTGGGTG<br>TGAC    | GTTATTCCACCGCGAG<br>AAAA | 60.0                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48794099  | Ca4                                     | 48794099                      | TAA/TA                                                        | TTACGGTCGAAAATGA<br>AGGG    | TCGGGTAGCACAATCT<br>TCAA | 59.9                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48824681  | Ca4                                     | 48824681                      | ATTTTTTT/ATTTTTT                                              | TTTTGCTCGTTCTGTCA<br>TGG    | GAATTTGGGTCCGAAT<br>CTTG | 59.8                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48831208  | Ca4                                     | 48831208                      | GTATATA/GTATATATA                                             | TATTTCCAAGACCTC<br>GTGC     | ATGTGGTTGTTGTGC<br>CTGA  | 60.1                             | 255                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48837715  | Ca4                                     | 48837715                      | ATT/ATTT                                                      | TGTGTAACGGGTAAGA<br>AATACGG | CAAAATACATCATCACG<br>CGG | 60.2                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48847654  | Ca4                                     | 48847654                      | TTTGTT/TTT                                                    | GAAATTTGGACGAAAA<br>CGGA    | CAATGCGTTTTACCAAC<br>CCT | 59.9                             | 183                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48847771  | Ca4                                     | 48847771                      | ATTTTTTT/ATTTTTTTT                                            | GAAATTTGGACGAAAA<br>CGGA    | GTGTATATACGCGCAC<br>CCAA | 59.9                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48848304  | Ca4                                     | 48848304                      | AATAT/AAT                                                     | TTATATTAATTGGGTGC<br>GCGT   | TTTAGGGTGGAACAGT<br>TCGG | 59.4                             | 379                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_48942067  | Ca4                                     | 48942067                      | GTTTTTTTTT/GTTTTTTTTTT                                        | TGATCTTTCTGCAATGA<br>AACG   | GATGAAAAATGAAGGT<br>CCGA | 58.9                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_4899207   | Ca4                                     | 4899207                       | T/TATTTA                                                      | TTCCCAAACTGTCTG<br>CTCA   | CTCACGCGTTTGCTTA<br>ACTT   | 59.4                             | 810                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4903904   | Ca4                                     | 4903904                       | CTTTT/CTTTTTT                                                 | CCCTTGGATTGTTGT<br>GACC   | TGACACACCCTAACCA<br>TCCA   | 60.2                             | 684                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_49100863  | Ca4                                     | 49100863                      | GAAAAAAAA/GAAAAAAAAA                                          | TCATCAAATTCGTAACG<br>CAAA | GGAGGAAGGAGAGAG<br>GGAGA   | 59.2                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_49100951  | Ca4                                     | 49100951                      | GA/GAAGATA                                                    | TCATCAAATTCGTAACG<br>CAAA | GGAGGAAGGAGAGAG<br>GGAGA   | 59.2                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_49121831  | Ca4                                     | 49121831                      | TTATATATATATATAT/TTATATAT<br>ATATATATATAT                     | CCAAAAATCTGCCAAG<br>AACG  | TGGGGTGTAAGTG<br>TGGA      | 60.6                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_49137090  | Ca4                                     | 49137090                      | GTATATATATATATATATA/GTATA<br>TATATATATATATATA                 | AACATGCAGTTGGAGG<br>CTCT  | TTTCAACTGTAAACATC<br>CCGA  | 59.9                             | 298                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_49149348  | Ca4                                     | 49149348                      | TCC/TCCC                                                      | GCACCCTTGTATTTG<br>CTCC   | GGGAAAACCTGTGTAC<br>CGGA   | 59.6                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4917514   | Ca4                                     | 4917514                       | TAAAAAA/TAAAAA                                                | TCTTTCGCACAATTTT<br>GTCA  | GGACATGTTGTGATGA<br>CATTGA | 59.3                             | 851                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4941823   | Ca4                                     | 4941823                       | TAGACCATTAG/TAG                                               | GCCTCACGTTTGAAAA<br>CCAT  | CGCTTAAGATTGGACA<br>TTTCG  | 60.0                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_4943577   | Ca4                                     | 4943577                       | TAAAAAA/TAAAAA                                                | CCTCCTTTTCAAGCCA<br>ACAA  | ACAAACCGCAAGCTTC<br>ATTC   | 60.2                             | 940                                           | INTERGENIC                                        | --                                  | --                    | --  |





| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_5376318   | Ca4                                     | 5376318                       | GTTTTTTTTTTT/GTTTTTTTTTTT<br>T                                                | GCCGCCTTGATGTT<br>CATT   | ATACCAACACGAAGC<br>GGAC  | 60.0                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_5420471   | Ca4                                     | 5420471                       | TTATATATATATATATATATATATA<br>TATATATAT/TTATATATATATATATA<br>TATATATATATATATAT | CTTTAACGTGGCAGCC<br>TCTC | ACAACAGCGCTTGTC<br>ACTC  | 60.0                             | 299                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_548151    | Ca4                                     | 548151                        | AA/AATAATAATTA                                                                | GCTGATCTATTTTGCC<br>GCC  | TATGCCATTGCATGAC<br>CCTA | 59.8                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_5484877   | Ca4                                     | 5484877                       | GAAT/G                                                                        | TCGATCCACCACCACT<br>AACA | GGATACCCAAGTTGCT<br>GCAT | 60.0                             | 299                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_5546894   | Ca4                                     | 5546894                       | ATTT/ATT                                                                      | ATCACTCTGGCCTTG<br>TTGG  | AGCCATTAGTTTACTG<br>GCGG | 60.1                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_5701044   | Ca4                                     | 5701044                       | GAAAAA/GAAAAAA                                                                | GGAAATCAGGAATCT<br>GGCA  | TCCCACCCCTACCTTT<br>ACC  | 60.0                             | 222                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_5749738   | Ca4                                     | 5749738                       | ATTTTTTTTT/ATTTTTTTTTT                                                        | TGTCCGAGTTCAAGAT<br>CAGG | TGAGTTTGGGTGATG<br>GGTT  | 58.8                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_5798679   | Ca4                                     | 5798679                       | GTATA/GTATATA                                                                 | TGCACCATAGAATTG<br>GCCT  | TCGGAGGAAACAAAG<br>GGAA  | 60.5                             | 208                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_5818841   | Ca4                                     | 5818841                       | CATATATATATATATAT/CATATAT<br>ATATATATATATAT                                   | TTAATGCGGGGAGTAG<br>GTTG | TGGACTCTAAATCCAG<br>CACG | 60.0                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_5931184   | Ca4                                     | 5931184                       | ATTATTATTATT/ATTATTATTATT<br>TATTATTATT                                       | CCAGCCCAATTTACAT<br>GCTT | CCGCCCATTTCAACTTT<br>TTA | 60.0                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                           |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_5961971   | Ca4                                     | 5961971                       | T/TGTG                                                                                    | CCTCTAATATCGTCGC<br>TCCAA    | ATAATCGGTGCGATT<br>TCCT     | 59.3                             | 668                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_6091215   | Ca4                                     | 6091215                       | AATACAT/AAT                                                                               | GTGGTTTGTTACGGCC<br>ACTT     | GATTAATTGTTGGATGC<br>GACG   | 59.9                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_6146003   | Ca4                                     | 6146003                       | ATTTTTTTTT/ATTTTTTTTTT                                                                    | GCTCACATCTTCTTGC<br>CACA     | GGGAAAACGCACGTGT<br>AACT    | 60.0                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_6185177   | Ca4                                     | 6185177                       | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATATAT                                     | CCAAGCAGTGAAAGCA<br>CAAA     | AATCGGCGTAACGAAC<br>TTCA    | 60.0                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_6209314   | Ca4                                     | 6209314                       | TTATATATATATATATATATA/TTATA<br>TATATATATATATA                                             | AAACTGTTAGACTTTGC<br>AGGATGA | TCGCCCTTAAATTTGA<br>CAC     | 59.4                             | 205                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_626706    | Ca4                                     | 626706                        | CGAGAGAGAGAGAGAGAGAGAGAG<br>AGAGAGAGAGAGAGAGAGA/CGAG<br>AGAGAGAGAGAGAGAGAGAGAGAG<br>AGAGA | GAAGCTTAAAGTGATC<br>GCCG     | CCTTCATCTTCTTCTCC<br>CCC    | 60.0                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_630475    | Ca4                                     | 630475                        | TAAAAAAAAA/TAAAAAAAAA                                                                     | TTGGGATTAAGGGTGA<br>TGGA     | TCTCTCAAACCAATAA<br>TCGAACA | 60.1                             | 197                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_6324755   | Ca4                                     | 6324755                       | ATTAATAATTTAATAATTTAATAATT/<br>ATTAATAATTTAATAATT                                         | TGGGTGGAACATGACA<br>GAGA     | ATTTGCCATTTGGGAT<br>TGA     | 60.1                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_6371861   | Ca4                                     | 6371861                       | AAATAATAATAATAATAATAATA<br>ATA/AAATAATAATAATAATAATA<br>ATA                                | GCAAGTCGAAAATGCA<br>ATCA     | ATGGTGGGTTGTATGA<br>GGGA    | 59.8                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_6519306   | Ca4                                     | 6519306                       | TAAAAAAAAA/TAAAAAAAAA                                                                     | TGTGGAGTGATTTTGA<br>GGGA     | CCCTCGAAGTTACTAAA<br>GCGG   | 59.1                             | 720                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                 |                          |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_6528163   | Ca4                                     | 6528163                       | TG/T                                                            | TCCAAGTAAAGGATCG<br>TGGG | AAAAATTCGAATGAAGA<br>ATCAAAA | 59.9                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_6538330   | Ca4                                     | 6538330                       | ATTTTTTTTTTTT/ATTTTTTTTTTT                                      | ATGCGACCTCCTGAAG<br>AAGA | CGACCTAAACATACATT<br>TTGCG   | 60.0                             | 317                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_6542618   | Ca4                                     | 6542618                       | TAAAAAAAAA/TAAAAAAAAA                                           | CCACTTTGGTCTGCCA<br>TTCT | GCTCACGCGGTAAAG<br>ACTC      | 60.1                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_6609098   | Ca4                                     | 6609098                       | TTTATTATTATTATTATTATTATT<br>ATTATT/TTTATTATTATTATTAT<br>TATTATT | AGCAATAAATGGTCGC<br>ATCC | CGTTCCACTCCCAACA<br>ACTT     | 59.9                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_6796797   | Ca4                                     | 6796797                       | TGAGAGAGAGAGAGAGAGA/TGA<br>GAGAGAGAGAGAGAGAGAGA                 | AGTCAGTGCATATGGC<br>CTCC | GAACATGGCCACTTTC<br>AACA     | 60.1                             | 241                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_6899661   | Ca4                                     | 6899661                       | ATTTTTTTT/ATTTTTTTT                                             | AACCTTTGCAGAAATTC<br>CGA | AGAAATGTCCCACCATT<br>TCG     | 59.7                             | 395                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_690240    | Ca4                                     | 690240                        | AACTGAATGACT/AACT                                               | TGATGCCCTAAGGGAG<br>ACAT | GTGAAATGAGGGGAAA<br>GCAA     | 59.5                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_6907181   | Ca4                                     | 6907181                       | TTATATATATATATATAT/TTATATAT<br>ATATATAT                         | TTTGAAATGGCGACTT<br>CCTT | CCAAATGGCAACTTCC<br>AACT     | 59.7                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_6907343   | Ca4                                     | 6907343                       | TTATATATATATATATATAT/TTAT<br>ATATATATATATATAT                   | TTTGAAATGGCGACTT<br>CCTT | CCAAATGGCAACTTCC<br>AACT     | 59.7                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_7001379   | Ca4                                     | 7001379                       | ATTTCTTTTTTCTTTTTTCTTTT/A<br>TTCTTTTTTCTTTT                     | GGTACGATCTGCACAG<br>GGTC | CAGGTCAAACCTTCCTC<br>CCAA    | 60.5                             | 999                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)            | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                          |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_7007714   | Ca4                                     | 7007714                       | ATTTTTTTTTTTT/ATTTTTTTTTTT<br>TT                                         | ACGCCTCAAATCTGGA<br>AGAA  | CGACCCTTTGCATGGA<br>TATT    | 59.8                             | 421                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_7029739   | Ca4                                     | 7029739                       | AATATATATATATATATATATAT/ATATATATATATATATATATATATAT<br>TAT                | GCGAAAGTAGTCCCTC<br>CATTT | AATCAAATGCAAGGTG<br>TGGC    | 59.6                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_7031730   | Ca4                                     | 7031730                       | GATATATATATATATATA/GATATATA<br>TATATATATATA                              | GGATGTCGCTTGCAAG<br>AAGT  | TAAACTAACGTGTCGG<br>CGTG    | 60.4                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_7081636   | Ca4                                     | 7081636                       | AATATATATATATATATATATATA/ATATATATATATATATATATATATAT<br>ATATA             | AATTGGCCACACTTCTT<br>TCG  | GGCTTTGTGAAAAACG<br>AGGA    | 60.1                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_7089091   | Ca4                                     | 7089091                       | GA/GAACAAAAGAGATTCACA                                                    | CTTGCATACCCCTCT<br>CGAC   | TTGGGAGGATTGGTT<br>CAAG     | 59.7                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_7132134   | Ca4                                     | 7132134                       | TAAAAAAAAAAAAA/TAAAAAAAAAAAA<br>A                                        | CACACCAGGGGAGACT<br>CACT  | GTCTCCCTACCCAC<br>ATTT      | 60.2                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_7299840   | Ca4                                     | 7299840                       | T/TGTG                                                                   | AGCTCTGTCCTTTGCC<br>CATA  | GCATTGATACCGATT<br>ACCA     | 59.8                             | 276                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_7319426   | Ca4                                     | 7319426                       | TTATATATATATATATATATATATATAT<br>TAT/TTATATATATATATATATATATATAT<br>TAT    | TGGGAGTGAATGAAGG<br>GTTC  | TTTGAGTGGGCACAAA<br>TAAATG  | 59.9                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_7360660   | Ca4                                     | 7360660                       | TTTTATTTATTTATTTATTTATTTATTT<br>TATTTA/TTTTATTTATTTATTTATTTA<br>TTTATTTA | ACTACGAAAACGGTCA<br>TCCG  | CAAGCATGCTCTATCT<br>CTTTACG | 60.0                             | 380                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_7452921   | Ca4                                     | 7452921                       | C/CCTCAACTTATTTG                                                         | TGCCAACTCGATTGAA<br>CAAG  | GCACGCTAAAAGCCTG<br>AAAC    | 59.8                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                   |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_7638568   | Ca4                                     | 7638568                       | GTTTTTTTTT/GTTTTTTTT                                              | TAGGCCATCATCATTT<br>GGGT   | TTCATGCAACCCTCAAA<br>TAAAA | 60.2                             | 797                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_7638687   | Ca4                                     | 7638687                       | AATATATATATAT/AATATATATATAT<br>AT                                 | TAGGCCATCATCATTT<br>GGGT   | TTCGAATCAGGGATAA<br>GACGTT | 60.2                             | 896                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_7937193   | Ca4                                     | 7937193                       | TAAAAAAAAA/TAAAAAAAAA                                             | GCTCCGGTCAAACACA<br>ATTT   | GAAAATTGAAAGGCAT<br>GGGA   | 60.0                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_7938199   | Ca4                                     | 7938199                       | TTTTTATAA/TTTTTATAATTATTTTA<br>TAA                                | TGCAACACACAATTGC<br>AAAA   | TGAGGGGTGGAGTTTG<br>GTAG   | 59.7                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8003681   | Ca4                                     | 8003681                       | GTATATATATATATATATATATATAT/<br>GTATATATATATATATATATATATAT<br>ATAT | AATGTGTCCTCGCCGT<br>TAAA   | TAGGGGGATGATGTGG<br>AAAA   | 60.5                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_80132     | Ca4                                     | 80132                         | G/GA                                                              | CCGTTTGGATTGTCAG<br>GACT   | TCGTTGAAAGCTGGAG<br>GTCT   | 60.0                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8032351   | Ca4                                     | 8032351                       | GTTTTTTTT/GTTTTTTTTT                                              | CTATGATCCCTCGAAC<br>GGAA   | TCAACAAGAGCACGAG<br>CAAG   | 60.0                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8109855   | Ca4                                     | 8109855                       | GTTTTTT/GTTTTTTTT                                                 | GCGACCTTAAATTTTG<br>GGATT  | AAGTGATGCACTAAGA<br>CGGGA  | 59.3                             | 274                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8169626   | Ca4                                     | 8169626                       | TAAATAAAAA/TAAATAAAAAATAAAA<br>A                                  | TATGGCACCTCCAGTT<br>GAAA   | TGTTAAATCCTCCAGAC<br>GGC   | 59.1                             | 858                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8170540   | Ca4                                     | 8170540                       | TAAAAA/TAAAAA                                                     | TCAACCCCTTTGTAGTT<br>TCACA | CTGCCAACTCCAAAAG<br>ATACC  | 59.5                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_8172016   | Ca4                                     | 8172016                       | T/TC                                                          | CTAGTGTTTCGGCAACA<br>AACG   | GCCTCAATTGGAGTTT<br>GCTC | 59.4                             | 204                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8173963   | Ca4                                     | 8173963                       | TTAT/TTATAT                                                   | GAAGCTCGCTTTATCC<br>AACG    | TCCACGGAATTTTCTG<br>CTTC | 60.0                             | 147                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8183765   | Ca4                                     | 8183765                       | TA/TAA                                                        | AACTCAATCCAACCA<br>GCCA     | TCACCACACCAACCTC<br>AAAA | 60.5                             | 548                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8209527   | Ca4                                     | 8209527                       | ATTTTTTT/ATTTTTT                                              | TGGTACATCCGGTTT<br>CTTC     | GGGCCTCTCTCTTTG<br>GTCT  | 60.1                             | 779                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8209784   | Ca4                                     | 8209784                       | TAA/TA                                                        | TGAACCAGTGTTCCTC<br>TCTGTGA | GGGCCTCTCTCTTTG<br>GTCT  | 59.9                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8210483   | Ca4                                     | 8210483                       | GATAT/GATATAT                                                 | GGCCAGGAAATCAACT<br>TCAA    | ATGAATTGCATGCATG<br>GTGA | 60.1                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8210730   | Ca4                                     | 8210730                       | TCC/TC                                                        | GGGGATACTTGCCTCA<br>ATCA    | TGATGCTATTCATTTTG<br>CGG | 59.9                             | 814                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8211793   | Ca4                                     | 8211793                       | AG/A                                                          | CCAATATGTGATGGTT<br>GTTTGG  | CTACAATGGAATGAGG<br>CGCT | 60.0                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8214750   | Ca4                                     | 8214750                       | TAAAAAAAAAAAAA/TAAAAAAAAA                                     | AAAAGAAGGCGAGTGC<br>AGAG    | TTGGCTCTCTTCTTCAA<br>GGC | 59.8                             | 858                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8215117   | Ca4                                     | 8215117                       | GTAA/GTAATAA                                                  | TTTTTGTAAGGATAT<br>TTTGTCA  | CAATTGACGCAAAGGA<br>AACA | 57.1                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')         | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                 |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_8215566   | Ca4                                     | 8215566                       | CTTT/CTTTT                                                    | TTTCCTTTGCGTCAATT<br>GTG        | TGCTAATCTCGTGCATT<br>TTGA      | 59.7                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8217219   | Ca4                                     | 8217219                       | AG/A                                                          | ACCACATATTAAGCGG<br>GTCG        | ATGTTGGTGTGGTGG<br>AGGT        | 59.8                             | 781                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8237892   | Ca4                                     | 8237892                       | TAAAAAAAAA/TAAAAAAAAA                                         | TCCAATCCTCAACCTC<br>GTTC        | CTTGC GTGTCCCAATT<br>TTT       | 60.1                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8239012   | Ca4                                     | 8239012                       | CTTTT/CTTT                                                    | TTCTCGATCCACAAAA<br>CAAAA       | CAACCTCCTCAAATTG<br>GACA       | 59.6                             | 636                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8239700   | Ca4                                     | 8239700                       | GTTTTTTT/GTTTTTTT                                             | TGTCCAATTTGAGGAG<br>GTTG        | CATGGTCATAACCTCA<br>CTAATGC    | 58.5                             | 822                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8240019   | Ca4                                     | 8240019                       | TTTTTATTTAATTTTATTT/TTTTATT<br>T                              | CGTGGAAATATGATAAA<br>ATAAATCGAA | CCAACCCATTAAACATT<br>GCC       | 59.6                             | 313                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8281020   | Ca4                                     | 8281020                       | T/TA                                                          | TTGGTGTCATTGCCT<br>TTTT         | GGGAGACGGGTACAAG<br>AGTG       | 60.5                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8281041   | Ca4                                     | 8281041                       | ATTTTTTT/ATTTTTTTT                                            | TTTGGTGTCATTGCCT<br>TTTT        | TCGCAAGGATAATGGC<br>TTTT       | 60.5                             | 709                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8283120   | Ca4                                     | 8283120                       | TAAAAAAAAA/TAAAAAAAAA                                         | TTTTTGAGAAGCCATT<br>AATTTTT     | TTTTGTGTTCTGTTTATT<br>GTAACCAA | 57.7                             | 270                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8297213   | Ca4                                     | 8297213                       | TAAAAAAAAA/TAAAAAAAAA                                         | GGGTTTTGTTTGAAAA<br>ATTTGAT     | TGGTGCTAACATGTGG<br>CTAA       | 58.4                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_8307784   | Ca4                                     | 8307784                       | ATTT/ATT                                                      | TACACCCATTGACGTG<br>GCTA   | TCAATCATGTCTGCATA<br>CCG     | 60.0                             | 694                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8308503   | Ca4                                     | 8308503                       | GTTTTTT/GTTTTT                                                | TAACAGGTGAGGGCAT<br>GTCA   | TATGCAAACCCAATTGA<br>CCA     | 60.1                             | 321                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8309234   | Ca4                                     | 8309234                       | TCAACACAA/TCAACACAACACAA                                      | GAATTTAAGAGGAAGG<br>CGATGA | TTCACCCTAATTCGTAG<br>GCG     | 59.7                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8309498   | Ca4                                     | 8309498                       | A/ACC                                                         | CATCCCAGGATCAACA<br>CTCA   | TTCACCCTAATTCGTAG<br>GCG     | 59.5                             | 272                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8311787   | Ca4                                     | 8311787                       | A/AG                                                          | TTACTCCCTCCTTCCCA<br>TGA   | ATGGATGGGGGATAAA<br>AAGG     | 59.5                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8311844   | Ca4                                     | 8311844                       | TG/T                                                          | TTACTCCCTCCTTCCCA<br>TGA   | ATGGATGGGGGATAAA<br>AAGG     | 59.5                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8313290   | Ca4                                     | 8313290                       | ATTG/ATTGTTGTTG                                               | GGGTCACAGGGACAAG<br>GTAA   | CACAACAACCAAGTCCA<br>CCAG    | 59.8                             | 154                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8313629   | Ca4                                     | 8313629                       | ATTTTTTTTTTT/ATTTTTTTTTTT                                     | CTGGTGGAAGTGTGT<br>TGTA    | GGCAGACAGGAGAGG<br>GAGTA     | 60.0                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8315933   | Ca4                                     | 8315933                       | CTT/CTTATT                                                    | GGACCCGTGATGCTGT<br>TTAT   | TCTCGGTTGATGTCATT<br>ATGCT   | 59.8                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8316304   | Ca4                                     | 8316304                       | GTTTTTTT/GTTTTTTTTT                                           | GCATAATGACATCAAC<br>CGAGAG | AAAAGAAATGGTTGTTT<br>CTCGTTC | 59.6                             | 235                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_8318067   | Ca4                                     | 8318067                       | T/TA                                                          | GCATGGTAGCCAAAGA<br>AAGC  | TTCCGTTAAACTCAACT<br>TCCG | 59.9                             | 758                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8320140   | Ca4                                     | 8320140                       | C/CG                                                          | CTTTGCCCCCATCCAT<br>ATAA  | AGGCTGAAGACTTCGA<br>CGAG  | 59.6                             | 358                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8320682   | Ca4                                     | 8320682                       | AAGAGAGA/AAGA                                                 | AAATCTTCCGGTGTC<br>TCCA   | TTTCCCAAGTTGGAA<br>GTGG   | 59.5                             | 668                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8321099   | Ca4                                     | 8321099                       | A/ATTAATTCTT                                                  | CCACTTCCAAC TTGGG<br>AAAA | GGACAATGCCGTA AAA<br>CGTC | 59.9                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8325707   | Ca4                                     | 8325707                       | TA/T                                                          | ACGGGGCTGTTACTTT<br>ACCC  | TTCTCAATGGGTGCGT<br>ACAA  | 60.2                             | 739                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8326100   | Ca4                                     | 8326100                       | TAAAAAAA/TAAAAAA                                              | TGTACGCACCCATTGA<br>GAAA  | TAATGGCTGGTTTCGT<br>TTGG  | 60.1                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8326843   | Ca4                                     | 8326843                       | TTCT/TTCTCT                                                   | TAAAGAGCACGAATTG<br>CACG  | CCAATCCAAAACCCAT<br>ACG   | 60.0                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8332622   | Ca4                                     | 8332622                       | GTA/GTACCATA                                                  | GCCTTCTGATGTGGTT<br>TGGT  | TGTGCCAAACAAGTTA<br>GCGT  | 60.0                             | 916                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8333108   | Ca4                                     | 8333108                       | GAAA/GAAAA                                                    | TCCCACTTTCATGTCTC<br>CAA  | TGATCACCTTTGAAAAG<br>CCC  | 59.1                             | 147                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8333830   | Ca4                                     | 8333830                       | ATTTTTTTTT/ATTTTTTTTTT                                        | ACGTAGTGTTTTGGCA<br>AGGG  | TCACACATACCGCAA<br>ACTT   | 60.0                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_8362831   | Ca4                                     | 8362831                       | TT/TTAT                                                       | AGGTTCGAACGGATAT<br>GTCG | CCATGTGCAAACTAG<br>GAAAA   | 60.0                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8364920   | Ca4                                     | 8364920                       | GT/GTTGTCACGTGTTTGCT                                          | GCTGGAACCTGGTTAC<br>GAGG | TTAGCATGCATTGGGA<br>AACA   | 59.7                             | 378                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8376162   | Ca4                                     | 8376162                       | CT/CTT                                                        | TCGGGCTTGAGCTCTA<br>TCAT | TGGCCGAAATTGAGAG<br>AATC   | 59.9                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8376439   | Ca4                                     | 8376439                       | TA/TAA                                                        | GATTCTCTCAATTCG<br>GCCA  | TGCGATTGATTCAGTT<br>TTTG   | 60.2                             | 373                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8376670   | Ca4                                     | 8376670                       | CAAAAAAAAA/CAAAAAAAAA                                         | GATTCTCTCAATTCG<br>GCCA  | TGCCCCAAACACGTAC<br>ACTA   | 60.2                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8409923   | Ca4                                     | 8409923                       | AAGAG/AAG                                                     | CGCATCAATACGACGA<br>ACAA | ACCACCACCTTGTAGC<br>CACC   | 60.7                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8410561   | Ca4                                     | 8410561                       | ATTTTTTTT/ATTTTTTTT                                           | GGTGGCTACAAAGTGG<br>TGCT | ATAGCGTAAGGGCACA<br>TGCT   | 59.9                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8413764   | Ca4                                     | 8413764                       | TA/T                                                          | AATGGTGAACAAGGAG<br>CAGG | TCAAATATTAACCTCAA<br>GCGCA | 60.1                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8414626   | Ca4                                     | 8414626                       | C/CATT                                                        | TCTTGGTCAGAACCAT<br>GTGC | AAATGGCCAAATTGCAT<br>GAT   | 59.7                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8415263   | Ca4                                     | 8415263                       | T/TAA                                                         | CACCTGCACCGCTAAG<br>TTTT | TTGTGGAACCCACAT<br>GCT     | 60.3                             | 274                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')         | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|---------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                 |                                 |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_842960    | Ca4                                     | 842960                        | AATTATTATTATTATTATTATTAT<br>TATTATTATTA/AATTATTATTAT<br>TATTATTATTATTATTATTATTA | AACATCAACAACCTCTT<br>TTTGCC     | AGGCCTATTGGGCTGA<br>AAAT   | 59.6                             | 673                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8457992   | Ca4                                     | 8457992                       | ATTTTT/ATTTTT                                                                   | CATGTGTGCCTCTAAT<br>CCCA        | GAGCCCTTCAAAGAAC<br>TCACA  | 59.5                             | 457                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8458330   | Ca4                                     | 8458330                       | A/ATC                                                                           | GAGTTCTTTGAAGGC<br>TCACA        | TCCCTACCCAAAATTG<br>GAA    | 59.5                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8490694   | Ca4                                     | 8490694                       | TTATATATATATA/TTATATATATA<br>TATATATATA                                         | TATGCCTTAGCGTTT<br>TTGG         | GGTCCTTTGATCCAC<br>GTTA    | 60.1                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8491035   | Ca4                                     | 8491035                       | AAGA/AA                                                                         | TAACGTGGGATCAAAG<br>GACC        | ATATGAAACCACCAACC<br>CCA   | 59.8                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8491570   | Ca4                                     | 8491570                       | GTTTTTTTT/GTTTTTTTT                                                             | GCCAACGGTTGTTGT<br>TTTT         | TGAATGAGCCAACACG<br>TTTC   | 59.9                             | 344                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8504484   | Ca4                                     | 8504484                       | ATTTTT/ATTTTT                                                                   | TTTGGAGTCAAATGATA<br>AAAGTGG    | TTTCGAGTGCCGCTT<br>ACTT    | 59.4                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8576551   | Ca4                                     | 8576551                       | GTATATATATATATATATATATAT<br>ATATAT/GTATATATATATATATAT<br>ATATATAT               | AAATGAAAAATAATGAA<br>TTCTCGTGAT | TTGTATTTTTGTCTCC<br>CACTCA | 59.6                             | 607                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8576946   | Ca4                                     | 8576946                       | GTTTT/GTTTT                                                                     | TGCATAAAGAAACAATT<br>GGACG      | TTGCAGACTAACCAG<br>ATCG    | 57.7                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8609734   | Ca4                                     | 8609734                       | AGGGGG/AGGGG                                                                    | GTAGGAAGTCGCCATT<br>TGGA        | CACCAAATACCCCAT<br>TTG     | 60.1                             | 126                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_8612545   | Ca4                                     | 8612545                       | AA/AAATTAAAGGTGTA                                             | TTTCTTTCTGCTGCG<br>GCTT    | CATGCCATCCACTATG<br>TTGC    | 60.1                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8613689   | Ca4                                     | 8613689                       | TTTTTCT/TT                                                    | TGCATTTGGTTGAAAAT<br>GAAA  | TGGTGGGCCTACGAGT<br>AAAG    | 59.0                             | 374                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8616163   | Ca4                                     | 8616163                       | ATTTT/ATTTT                                                   | TTCAAAGGCCGTAGG<br>TTTC    | TAGTTTGAATGGTCG<br>CACA     | 59.2                             | 933                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8621719   | Ca4                                     | 8621719                       | GAATAATAATAATAATAA/G<br>AATAATAATAATAATAA                     | GTGCCTTTCTTGTCAG<br>GGAG   | TGGAAGCCCCATAAAG<br>ACTG    | 59.8                             | 765                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8626094   | Ca4                                     | 8626094                       | TTATA/T                                                       | GGTTTGAATGTCAACA<br>CCCT   | TGCATGTGTGTAACAA<br>CAACAAA | 57.3                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8633576   | Ca4                                     | 8633576                       | TAAAA/TAAA                                                    | TTGCACGAAAAATTGT<br>GAGC   | TAAATGGACGGAGTTG<br>GGAA    | 59.9                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8633989   | Ca4                                     | 8633989                       | CA/CAA                                                        | TTCCCAACTCCGTCCA<br>TTTA   | TTGATCAAACGCGCAA<br>ATTA    | 60.3                             | 271                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8636225   | Ca4                                     | 8636225                       | GTT/GTTT                                                      | GGGAAACCAAGGAGTG<br>TGAA   | GCATGCGATCGTAATT<br>CCTT    | 59.9                             | 771                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8636291   | Ca4                                     | 8636291                       | AAT/AATAT                                                     | GGGAAACCAAGGAGTG<br>TGAA   | GCATGCGATCGTAATT<br>CCTT    | 59.9                             | 771                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8644121   | Ca4                                     | 8644121                       | AATAT/AATATAT                                                 | TGAGAATATAGCATAC<br>CGACCG | GGGGGTTGAGTTTAGG<br>GTTC    | 59.1                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_8650892   | Ca4                                     | 8650892                       | AATATA/AATATATA                                               | TTTAAATTGAATGTGTT<br>CGCGT   | ACCACACATGATTCTG<br>CCA     | 59.5                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8679645   | Ca4                                     | 8679645                       | CAAAA/CAAAA                                                   | TAGTACCCGTACTGGG<br>CTGG     | GCGTTTTGGAATCTGC<br>ATT     | 60.0                             | 289                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8688751   | Ca4                                     | 8688751                       | AACA/AA                                                       | AGGACCCACAACATCC<br>ACAT     | ACCAATCCATGCACGC<br>TACT    | 60.1                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8689137   | Ca4                                     | 8689137                       | ATTTTT/ATTTTTT                                                | CCCATCTTGGGTGAAG<br>AAAG     | GGTGGTTTAGACGAAT<br>AGAGACG | 59.5                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8689670   | Ca4                                     | 8689670                       | A/ATCTC                                                       | TGCAAAATTTGGTGAA<br>ACAGA    | TGTCACATTTGCAGAA<br>GAAAA   | 59.2                             | 300                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8690768   | Ca4                                     | 8690768                       | TAAAAAA/TAAAAAAA                                              | GTTTTAATGCAAGCCAT<br>GTAGA   | GGTGTGTTTATGCGAA<br>GTGA    | 57.1                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8690798   | Ca4                                     | 8690798                       | G/GA                                                          | AATTCCAGATCACCGC<br>GA       | GGTGTGTTTATGCGAA<br>GTGA    | 60.2                             | 313                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8707105   | Ca4                                     | 8707105                       | AAAT/A                                                        | CGAGAGGTATTTATGC<br>TTCCTG   | ATCTCTCCGACCATGT<br>GGAA    | 58.1                             | 712                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8708859   | Ca4                                     | 8708859                       | A/AC                                                          | CAAAGCGAATTTAGGA<br>AAGTAAAA | GCATATTATGCCAC<br>CCAC      | 58.2                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8715030   | Ca4                                     | 8715030                       | ATTTTT/ATTTTTT                                                | GAGAGGCGTTGAAGAA<br>AACC     | AGTGGACCACATGACA<br>CCAA    | 58.9                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_8723077   | Ca4                                     | 8723077                       | T/TC                                                          | GCGTGTTTGGTTGAAA<br>GGAT  | GGTCGAGTCCAAATT<br>CCAA     | 60.0                             | 619                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8727347   | Ca4                                     | 8727347                       | TAAAAAAAAAAAAA/TAAAAAAAAA                                     | CGGGTCTCTTTGACTC<br>TTCG  | TCATCTTATTTTGGGCA<br>TTCA   | 60.0                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8727913   | Ca4                                     | 8727913                       | T/TCA                                                         | TGAATGCCCAAAATAA<br>GATGA | TCACCAATCCAGCTGG<br>TACA    | 58.1                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8727978   | Ca4                                     | 8727978                       | A/AG                                                          | TGAATGCCCAAAATAA<br>GATGA | TGATTGAAAGAGCGTT<br>GGATT   | 58.1                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8728353   | Ca4                                     | 8728353                       | TTTATT/TTTATTATT                                              | AATCCAACGCTCTTTCA<br>ATCA | GGAACCAAAACCAGCAT<br>GAAT   | 59.7                             | 343                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8741293   | Ca4                                     | 8741293                       | TAA/TA                                                        | TCTTCCTCTGTCAACCA<br>AACG | TCGGTTGAAAATGTTAC<br>TGCC   | 60.3                             | 106                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8744304   | Ca4                                     | 8744304                       | TA/TAA                                                        | TCTTTCCTTGGTCAGC<br>GTCT  | TTTGTCTGTGAAAATGCA<br>TTAGG | 60.0                             | 825                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8745750   | Ca4                                     | 8745750                       | C/CATT                                                        | ACTTGTCTCGTACCCG<br>CAGT  | TGCAACTTCTTATCAAT<br>TGCGT  | 59.8                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8748044   | Ca4                                     | 8748044                       | ACCCCC/ACCCCC                                                 | CACGATCCCATCAAAA<br>TGAA  | TCACAACATGAGAATG<br>GGACA   | 59.3                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8748580   | Ca4                                     | 8748580                       | GAAAAAAAAA/GAAAAAAAAA                                         | TGTCCCATTCTCATGTT<br>GTGA | CAAAATTGCATTCAAAG<br>TCCC   | 60.0                             | 424                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_8748930   | Ca4                                     | 8748930                       | TAAAAAAAA/TAA                                                 | GGGACTTTGAATGCAATTTTGT  | CGAGGATCTGTGACCAATCA    | 60.2                             | 482                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_8749252   | Ca4                                     | 8749252                       | T/TTA                                                         | ATACGGATTGGATGAGGTGC    | GGCGTAATTACTTCAAAGCAA   | 59.8                             | 376                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_8749651   | Ca4                                     | 8749651                       | ATATATTTAT/ATAT                                               | ATACGGATTGGATGAGGTGC    | CCGGCATTAAATTTGGAAAA    | 59.8                             | 878                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_8758399   | Ca4                                     | 8758399                       | TAA/TA                                                        | CATAGCAGCTTCGATGCAAA    | TCACAATTTGACAACCACTGG   | 60.1                             | 297                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_8766483   | Ca4                                     | 8766483                       | TAAG/TAAGAAG                                                  | GGTTGCGGTCGAAGTTACAT    | GATGGGCCAAACTGCTTTTA    | 60.0                             | 575                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_8766663   | Ca4                                     | 8766663                       | TAAAAAAAA/TAAAAAAAA                                           | GGTTGCGGTCGAAGTTACAT    | GATGGGCCAAACTGCTTTTA    | 60.0                             | 575                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_8780881   | Ca4                                     | 8780881                       | TTAT/TT                                                       | AACCCAGCAAACATCAAGA     | CGGGGCAGAGTAGAGCTATG    | 58.2                             | 881                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_8781421   | Ca4                                     | 8781421                       | GAAAAA/GAAAAAA                                                | CATAGCTCTACTCTGCCCG     | GCAAGTTTGCCGGTTATGTT    | 60.0                             | 114                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_8799497   | Ca4                                     | 8799497                       | TAATAGAGTTAAAA/TAA                                            | TCAAAGTGCGATACAGGAAGC   | TGGGTTTAATACATGAGATGG   | 60.4                             | 922                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca4_P4_8800933   | Ca4                                     | 8800933                       | TATAAGGACAAT/TAT                                              | TGATTGGCATCCATTTTCT     | TTAGAAACGTGTTGGAGGGG    | 60.3                             | 193                                           | INTERGENIC                                           | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_8810790   | Ca4                                     | 8810790                       | G/GTGA                                                        | AAAAATGGGTTATTAAG<br>TGAGGAAAA | TGTTACCGGAATTAGC<br>AAACG    | 59.6                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8812070   | Ca4                                     | 8812070                       | AT/ATGTT                                                      | TGGTGCACTTTTTGTG<br>TCCA       | TCAAACACACAATAATG<br>GCGA    | 61.2                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8812812   | Ca4                                     | 8812812                       | ATTTTTTTT/ATTTTTTTTT                                          | GTTTTTAATTCGCACCC<br>CAA       | GCAGTTTAAGCAATAAA<br>ATGATGC | 59.8                             | 427                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8816656   | Ca4                                     | 8816656                       | AT/A                                                          | ATCGTTGTCGTAGATT<br>GGGC       | TTGGATCAAATCTGAA<br>GCG      | 60.0                             | 789                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8828382   | Ca4                                     | 8828382                       | GTT/GTTT                                                      | GCGACTACCACATTTG<br>GGTT       | TGGCACTCCTTCTAAAT<br>GGG     | 59.9                             | 354                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8829389   | Ca4                                     | 8829389                       | C/CG                                                          | TTCTCTACCGATTGCG<br>CACA       | TGAAACATGTTGGTAC<br>GTGGA    | 59.3                             | 287                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8829890   | Ca4                                     | 8829890                       | ACTAAAAAATC/AC                                                | TCCACGTACCAACATG<br>TTTCA      | AAAGGCGCGGTTTAGA<br>TTTT     | 59.9                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8830201   | Ca4                                     | 8830201                       | AATATA/AATATATA                                               | AGAAAACTAAACCGC<br>GCCT        | TGGACTTTCTTATTTGC<br>CGC     | 60.2                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8836705   | Ca4                                     | 8836705                       | TTAAT/TTAATAAT                                                | AGCTTCGATTGGTGA<br>GGTG        | TGATGTATACCACAATG<br>ATTCCG  | 60.3                             | 444                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8836902   | Ca4                                     | 8836902                       | T/TG                                                          | AGCTTCGATTGGTGA<br>GGTG        | TTGAGTTTCAATATGGT<br>GATGTGA | 60.3                             | 854                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_8838334   | Ca4                                     | 8838334                       | ATTTATCAAATATTTTATCA/ATTTAT<br>CA                             | TTTTCACCCCTTCTTTC<br>CCA       | GAGGTTTGCAAATTGT<br>CGCT    | 59.5                             | 242                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8840917   | Ca4                                     | 8840917                       | GTT/GTTTTT                                                    | GATACTCTAAGAATAC<br>CTCCGACAAA | TTTTTGCGCACATATAT<br>AAAACA | 58.4                             | 174                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8864736   | Ca4                                     | 8864736                       | TGGGG/TGG                                                     | TTTTTGGCTTATGGGG<br>TGAG       | TCAGCGTATTGCGAAA<br>CAAC    | 59.9                             | 912                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8871044   | Ca4                                     | 8871044                       | CATAAAAT/CATAAAATTATAAAAT                                     | AAACATCGGAGTCCA<br>CGTC        | AATTTATTGCGGCAAA<br>TTC     | 60.0                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_887746    | Ca4                                     | 887746                        | ATTTTTT/ATTTTTT                                               | GCCGAATCAATTCAAA<br>TCAA       | ATGCACAACCAATTTCA<br>CCA    | 58.6                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8878932   | Ca4                                     | 8878932                       | CAATAATAATAATAAT/CAATAAT<br>AATAATAAT                         | ATGGACGGATTGGATG<br>GATA       | ATACGATGGTGGTTGG<br>TGGT    | 60.0                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8884777   | Ca4                                     | 8884777                       | TAAT/TAATATATAAAT                                             | ACACGTGGCTTGTGG<br>TGTA        | GTCGATCTCGCTCACT<br>CCAC    | 60.1                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8885675   | Ca4                                     | 8885675                       | A/ATTAC                                                       | TGCTACATAATCAAGT<br>GTTTTAGGC  | AAGAATGCAGATCAAT<br>CGCC    | 58.9                             | 744                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8885843   | Ca4                                     | 8885843                       | CTGT/CTGTGT                                                   | TGAGACCCCGTAAGAT<br>CCAA       | AAGAATGCAGATCAAT<br>CGCC    | 60.5                             | 194                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8887604   | Ca4                                     | 8887604                       | GTATTATT/GTATT                                                | GTTTCGTCCCTCGATCA<br>CAAT      | CCAACCACCCAAAATC<br>CAT     | 59.9                             | 308                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_8889782   | Ca4                                     | 8889782                       | A/AG                                                          | TTAAGAAGTATCACGC<br>GGGC | TCCTTTCTCCGTGGTG<br>AGTT    | 60.2                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8890585   | Ca4                                     | 8890585                       | GTA/GTATA                                                     | CATGCCTCGTTAGAGT<br>GCAA | TCCACCACACACTCCT<br>CAAA    | 60.0                             | 256                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8894416   | Ca4                                     | 8894416                       | CTATATATATATAT/CTATATATATAT<br>ATATATAT                       | TGATATCCGGTTTGGG<br>TGTT | CTCCCGTTATCCGAAA<br>CAGA    | 60.1                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8897355   | Ca4                                     | 8897355                       | TA/T                                                          | GATCCACTCAGGGTCG<br>TGTT | ACTTTTGCATCTGGATG<br>GCT    | 60.0                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8904309   | Ca4                                     | 8904309                       | CTTTTATATTTTCATTTTTTTTATA<br>TTTTTATT/CTTTTATATTTTCATT        | AAGAAAACCCACCACA<br>CTCG | CAACCCATAGAACAAAA<br>ATCCC  | 60.0                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_8946430   | Ca4                                     | 8946430                       | TGAGAGAGAGAGAGA/TGAGAGAGA<br>GAGAGAGA                         | ACAGCAACCGAAACTG<br>CTTT | GGGGAGCATTGGTCAC<br>TAAA    | 59.9                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9028821   | Ca4                                     | 9028821                       | TTATATATATATATATAT/TTATAT<br>ATATATATATATATAT                 | ATGGAACAATCGGACA<br>CCAT | CTGTCAACTCACTCATC<br>AAATCG | 60.1                             | 422                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9066423   | Ca4                                     | 9066423                       | ACC/AC                                                        | GCAACCCGTAGGTGTA<br>GGAA | TGTGCGTTGGTAGTCA<br>ATGTG   | 60.0                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9066518   | Ca4                                     | 9066518                       | ATTTTTTTT/ATTTTTTTT                                           | GCAACCCGTAGGTGTA<br>GGAA | TGTGCGTTGGTAGTCA<br>ATGTG   | 60.0                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9078995   | Ca4                                     | 9078995                       | TAAAAAAAAA/TAAAAAAAAA                                         | GTTATTTTGCCCACT<br>ACCG  | ATTTTCTTTGGCGACTT<br>CCA    | 59.3                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                    | Forward primers (5'-3')        | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                  |                                |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_9229798   | Ca4                                     | 9229798                       | TGGG/TGGGG                                                                                                                                       | AAGGCTCAACATGCAA<br>AACC       | TGCCAATTCGATTGGA<br>ATAA   | 60.1                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9230116   | Ca4                                     | 9230116                       | TA/T                                                                                                                                             | GTTGCGAAAAATGGGT<br>TTGT       | ACCAGGAAAAGAAGAA<br>GGGC   | 59.8                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9371255   | Ca4                                     | 9371255                       | GAAAAAAAA/GAAAAAAAA                                                                                                                              | GGAGCATATGCCTCGT<br>TGTT       | TGGAAATCAACTTTTT<br>GGACA  | 60.1                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9386505   | Ca4                                     | 9386505                       | AATATATATATATATATAT/AAAT<br>ATATATATATATATATAT                                                                                                   | TTTGCAATTGTGGCAA<br>GTGT       | CGTGGACAAAGATCGT<br>GATG   | 60.2                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9453892   | Ca4                                     | 9453892                       | GTATATATATATATATATATA/GTA<br>TATATATATATATATATATA                                                                                                | TTGATGGTGCTAGGAG<br>AAGACA     | AAACCCACAATTCATCA<br>GGTT  | 59.9                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9504124   | Ca4                                     | 9504124                       | CTACTATTA/CTA                                                                                                                                    | TTGTTGAGTATAAGGTT<br>GTCTTG TG | GACTGGAACGCTTCGT<br>CTTC   | 57.5                             | 791                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9574784   | Ca4                                     | 9574784                       | TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTA/TTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTA | ATTGACAAAAGTTGGA<br>GGCG       | TGCATGCTAATTTGCG<br>CTAT   | 60.1                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9586747   | Ca4                                     | 9586747                       | CTTTTT/CTTGTATATTTTTTTT                                                                                                                          | AATTAAGTACGACGGC<br>ACGG       | CGTTCATAAAGATTTCG<br>CCA   | 60.1                             | 827                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9625757   | Ca4                                     | 9625757                       | ATATTATTATTATTATTATTATTA<br>TTATT/ATATTATTATTATTATTATTA<br>TTATTATTATTATT                                                                        | ATGTGCGAGAAAGGGA<br>GAGA       | CACTTCGGTCATTCTCT<br>TCAAA | 60.0                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9629867   | Ca4                                     | 9629867                       | ATTTTTTTTT/ATTTTTTTT                                                                                                                             | CAACCGTAAACAAACC<br>AAAAA      | CAACCGAAGATTTGTTT<br>GGAA  | 57.7                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_9630152   | Ca4                                     | 9630152                       | GAA/GA                                                        | CCTCTTCCAAACAAATC<br>TTCG | TCAAAATATGGCATGT<br>GGGA   | 58.8                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9630289   | Ca4                                     | 9630289                       | ATTAGTTAGTT/ATTAGTTAGTTAGT<br>T                               | CCTCTTCCAAACAAATC<br>TTCG | CCAGCTCATCAAAGCC<br>ATT    | 58.8                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9631458   | Ca4                                     | 9631458                       | GTTTCCTCCTCCGTCCTT/GTTTCCT<br>CCTCCGTCCTTCTCCTCCGTCCTT        | TTCTTCATCTTCTCTCT<br>CCG  | TTATCGGATGTATGGG<br>AGGG   | 59.4                             | 148                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9632653   | Ca4                                     | 9632653                       | TG/T                                                          | TGGATTGTCGTGATCT<br>CAAA  | CACACCGTACTCAGC<br>ATTG    | 57.6                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9633059   | Ca4                                     | 9633059                       | TAAAAAAAAA/TAAAAAAAAA                                         | CAATGCTGAGTACGGG<br>TGTG  | AACACAAGGAGGCCAT<br>GTTC   | 60.2                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9658674   | Ca4                                     | 9658674                       | TAAAAAAA/TAAAA                                                | TGCAATTTGATACCGA<br>GCCT  | TCCCTTCTTTGAGGG<br>ATT     | 60.6                             | 914                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9677869   | Ca4                                     | 9677869                       | CATATATATATATATATATA/CATATA<br>TATATATATATATATA               | TTGCACATTTTGAATGC<br>TGA  | ATGCGATCCATTGAATT<br>TGA   | 58.8                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9736707   | Ca4                                     | 9736707                       | ATCTCTCTCTCTCTCTCTCTCT/AT<br>TCTCTCTCTCTCTCTCTCTCT            | CACTTCACCCACCTTC<br>CCTA  | ATCCAACAATCTGGGG<br>ACAA   | 60.0                             | 256                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9764739   | Ca4                                     | 9764739                       | GTTTTTTT/GTTTTTTT                                             | TCAGGCGGGTTTTATA<br>GACA  | CTCTGCTCACAACCCA<br>ACAA   | 58.2                             | 701                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca4_P4_9857350   | Ca4                                     | 9857350                       | TGTGCGAGTGCGAGTGCGAGT/TGT<br>GCGAGTGCGAGT                     | TGAGACGTTTTTCACA<br>CCCA  | CTGCAACAATGAATCTT<br>GAAGT | 60.1                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                          | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                        |                               |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_9967472   | Ca4                                     | 9967472                       | ATTTTT/ATTTTT                                                                                                          | CCCCTTTTATGAAATG<br>GTTGAA    | TGAGACTGAAATCGGG<br>TCTTTT | 60.0                             | 945                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_1000531   | Ca5                                     | 1000531                       | AATATATATATATATATAT/AATATAT<br>ATATATATATATAT                                                                          | GGGTTTTGGAAGGAGG<br>AATG      | CTTGTGTTGATACGC<br>ATCAT   | 60.7                             | 874                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10191815  | Ca5                                     | 10191815                      | ATATTATTATTATTATTATTATTA<br>TTATT/ATATTATTATTATTATTATTA<br>TTATTATT                                                    | AGCACACACGCAAA<br>AATG        | TGGGAAAGGACATTTG<br>CAT    | 60.8                             | 409                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_1020806   | Ca5                                     | 1020806                       | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATT/TTTATT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATT            | AATTATGCTCCGACTTC<br>CCC      | GAAGCCGAGAAAACGA<br>CTTG   | 60.3                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10213713  | Ca5                                     | 10213713                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATT/TTTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTAT              | AGAGGCAAAACAAGAAC<br>CGAA     | TGTGCGTTTGACTGTG<br>TTGA   | 59.9                             | 209                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10270439  | Ca5                                     | 10270439                      | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATATA<br>TATAT                                                      | CCATGTTCCCATCATAT<br>ATCATTTT | CTAAGGCATTACCCAC<br>TGCC   | 60.1                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10305520  | Ca5                                     | 10305520                      | ATTTTT/ATTTTT                                                                                                          | CGAACCTGAGACCCTA<br>CCAA      | ACATACTGTTCTCACC<br>GCC    | 60.1                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10311736  | Ca5                                     | 10311736                      | CGAGAGAGAGAGAGAGAGAGAGAG<br>AGAGAGAGAGAGAGAGAGAG/CG<br>AGAGAGAGAGAGAGAGAGAGAGAG<br>AGAGAGAGAGAGAGAGAGAGAGAG<br>AGAGAGA | ACACGACAAACACTTT<br>CGCA      | GCACACTTTTCTTCAT<br>TCGTC  | 60.3                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10420287  | Ca5                                     | 10420287                      | GTTTTTTTT/GTTTTTTTT                                                                                                    | GGTACAATTGTTGCAC<br>CACG      | TTTGGGAGTAGGCCTT<br>CCTT   | 59.9                             | 702                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10420664  | Ca5                                     | 10420664                      | AATATATATATATATATATA/AATA<br>TATATATATATATATATATA                                                                      | AAGGAAGGCCTACTCC<br>CAAA      | TACCAAGGCGTCGTCA<br>AAAT   | 60.1                             | 597                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                     |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_10513256  | Ca5                                     | 10513256                      | AATATATATATATATATA/AATATA<br>TATATATATATATA                         | TTGACCGACACCAATC<br>AGAA    | CTTGCATCCACAGGA<br>AAAT     | 60.1                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_105147    | Ca5                                     | 105147                        | AATATATATATATATATATATATAT<br>ATATA/AATATATATATATATATAT<br>ATATATATA | CAGAACAAACACGAGA<br>GCCA    | TTTGATCCCGAGGTTAT<br>CCG    | 60.0                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10572522  | Ca5                                     | 10572522                      | AATATATATATATATATATATATA/<br>ATATATATATATATATAT                     | CGTGGACAAAGATCGT<br>GATG    | TCATTGTAAAGAGCG<br>GTGC     | 60.1                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10634338  | Ca5                                     | 10634338                      | AC/ACC                                                              | AATTTTTCAGTCCCGT<br>GTCG    | ATCCCTCAAAGGGCTA<br>CTGC    | 60.0                             | 229                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10686981  | Ca5                                     | 10686981                      | TAAAAAAAA/TAAAAAAAAA                                                | GCTCCTTCTGCATCAA<br>CACA    | TGCCCCACATTTTAGA<br>CCTC    | 60.0                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10687869  | Ca5                                     | 10687869                      | TAAAAAAAA/TAAAAAAAAA                                                | CGAGGAACGACAAGG<br>GTAAA    | TGAGTTGAGTTAAAAC<br>CAGCAGA | 60.1                             | 673                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10688557  | Ca5                                     | 10688557                      | AGTTGTT/AGTT                                                        | TCCATCAAACCTGATCCT<br>AAGGG | TGGGTTTAGATGATG<br>GCTC     | 60.3                             | 179                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10689001  | Ca5                                     | 10689001                      | GAAA/GAAAAA                                                         | GAGCCATCATCTAAAC<br>CCCA    | TGCCAAAGAAAAAGGT<br>TTCG    | 59.9                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10689102  | Ca5                                     | 10689102                      | TAAAA/TAA                                                           | ATGGGCCACCTATTGA<br>GACA    | TGCCAAAGAAAAAGGT<br>TTCG    | 60.3                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10689236  | Ca5                                     | 10689236                      | ATT/ATTT                                                            | TTTCCGAATTCCAAGT<br>TGA     | GGATTGTCCTTCATT<br>GGTG     | 58.2                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_10689622  | Ca5                                     | 10689622                      | AGAAGCATG/AG                                                  | CGAAACCTTTTCTTTG<br>GCA      | AACGGATTGTCCCTTC<br>ATTG    | 60.2                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10693789  | Ca5                                     | 10693789                      | CTTGTGATTGTTTTGTTGTGATTG/C<br>TTGTGATTG                       | CCAATTTGAATTGTCC<br>GTCC     | TTGCAAAAGCTGGGTC<br>AAGT    | 60.2                             | 406                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_1083059   | Ca5                                     | 1083059                       | ATTTTTTTTTTTTT/ATTTTTTTTTT<br>T                               | TCAATCCGAACAAAC<br>ATGAA     | CGATGATCTTCTTCTTC<br>ACCC   | 59.0                             | 338                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10852097  | Ca5                                     | 10852097                      | AATATATATATAT/AATATATATAT                                     | CACAGTTGTCCACGTA<br>CGAAA    | AAATGGAGGTTTCAATT<br>GCG    | 59.7                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10854983  | Ca5                                     | 10854983                      | AA/AATA                                                       | TGGATTGACATTAATGA<br>GTGATTG | GGATGTGATCCTTATG<br>CGCT    | 58.9                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_10931505  | Ca5                                     | 10931505                      | AG/A                                                          | TTGATGAATTTGATGTC<br>GTTGA   | AAATACCTTACGCGGT<br>CCCT    | 59.0                             | 344                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11093470  | Ca5                                     | 11093470                      | TTATATATATATATATAT/TTATAT<br>ATATATATATATATAT                 | CAGCGCTTGCTAAACA<br>CAAG     | TCAAAACAGAACAGATC<br>ATGTGG | 59.8                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11132723  | Ca5                                     | 11132723                      | TTTATTATTATTATTATTA/TTATTA<br>TTATTATTA                       | AAAAACCAACAATCTCC<br>CCC     | TGTTTTCTGCCTTTTTG<br>CCT    | 60.0                             | 262                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11138840  | Ca5                                     | 11138840                      | GT/G                                                          | TCGACTTGCAATCGC<br>TTTG      | TCGCATTAACACGAAC<br>GCA     | 60.0                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11167847  | Ca5                                     | 11167847                      | CAAAAAAAAAAAAA/CAAAAAAAAA                                     | GGTGGACTCGAGCAAG<br>TAGC     | AAAGCATCAGTCCGT<br>TTGAA    | 60.0                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_11168411  | Ca5                                     | 11168411                      | AATA/AA                                                                 | TTCAAACGGAACGTAT<br>GCTTT  | TTGGTTGGGGGAGTTA<br>TTGA  | 59.7                             | 954                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11168800  | Ca5                                     | 11168800                      | CACTATTAG/C                                                             | TCGTTGAGGAAAAACA<br>AACAAA | TTGGTTGGGGGAGTTA<br>TTGA  | 59.6                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11168904  | Ca5                                     | 11168904                      | GTCTCTCT/GTCTCT                                                         | TCAATAACTCCCCAA<br>CCAA    | TCACAATTGGGTTTGG<br>ATCA  | 60.2                             | 227                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11169035  | Ca5                                     | 11169035                      | CG/C                                                                    | TCAATAACTCCCCAA<br>CCAA    | TGACGCCGTGAAAAAC<br>ATTA  | 60.2                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_111805    | Ca5                                     | 111805                        | TTAT/TTATAT                                                             | CAACGACGGCATGACT<br>CTAA   | ATTTATCATTCAACCG<br>CCA   | 59.9                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11233017  | Ca5                                     | 11233017                      | TAAAAA/TAAA                                                             | ATTGGACGTATCCCGA<br>GTTG   | GTTGTGGGATGAACTG<br>ACCC  | 59.8                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11324561  | Ca5                                     | 11324561                      | T/TTGCTCAG                                                              | GCCATGAAATAGAGGT<br>TGGC   | TATTGCTGGCTGACAA<br>ACCA  | 59.5                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11376503  | Ca5                                     | 11376503                      | AATATATATATATATATATATATAT<br>ATATATA/AATATATATATATATATAT<br>ATATATATATA | CGAACTCGTGATTCTC<br>CACA   | TAAAAAGCGTCGCACT<br>CAGA  | 59.8                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11414411  | Ca5                                     | 11414411                      | A/AACCT                                                                 | TCTGAATCGGAGTACC<br>CCAC   | AATGGCTTTCCCTTCGT<br>GATG | 59.9                             | 770                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11424234  | Ca5                                     | 11424234                      | CAAAAAA/CAAAAAA                                                         | TAAACCGGATCCAAA<br>TCCA    | GAGGTCTATGAACCC<br>CTCC   | 60.1                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_11438610  | Ca5                                     | 11438610                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATAT             | GCCAAAACCCTCAGAA<br>ACAA   | ACTTTTGATTGAACGA<br>GGG  | 60.1                             | 773                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11505972  | Ca5                                     | 11505972                      | TTTCTTC/TTTC                                                  | GGACCTAAATTTTGCA<br>ACAACA | GAACGCGAGATATTGG<br>GTGT | 59.0                             | 199                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11551348  | Ca5                                     | 11551348                      | ATTT/ATT                                                      | TTGACGGTTGAGATTG<br>ATTGA  | TAGGGTTTATGCTCCAT<br>CGC | 59.1                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11582454  | Ca5                                     | 11582454                      | TT/TTTAT                                                      | TGACTCATCAATTCGAA<br>CGC   | GAATGCCACCAGGAAA<br>AGAA | 59.8                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11658471  | Ca5                                     | 11658471                      | GAAAAAAAAA/GAAAAAAAAA                                         | CTAGGTGCGGTGTTCA<br>TGTG   | TTGTGGTGAACCGGGA<br>TAAT | 60.2                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11729570  | Ca5                                     | 11729570                      | AAATAATAATAA/AAATAATAA                                        | CACGGTCCCTAGAGCC<br>AATA   | CGGGAGATACGTAGGA<br>GCAA | 60.1                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_11879108  | Ca5                                     | 11879108                      | TAA/TAAA                                                      | AAGATTTCTCCCTCCT<br>CCA    | CTTTAACATGCGTTTCC<br>GGT | 60.0                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_12095777  | Ca5                                     | 12095777                      | CAAAAAAAAA/CAAAAAA                                            | CTCTTTAAGACGTTTC<br>GCGG   | TGCTCGCCTAATTTTCG<br>AGT | 60.0                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_12161825  | Ca5                                     | 12161825                      | CAA/CA                                                        | GCGGATAATCAATTC<br>CCAA    | CCTTGTTGTTTTGGCT<br>GGT  | 59.7                             | 247                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_12161940  | Ca5                                     | 12161940                      | AG/A                                                          | GCGGATAATCAATTC<br>CCAA    | CCTTGTTGTTTTGGCT<br>GGT  | 59.7                             | 247                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                           |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_1230643   | Ca5                                     | 1230643                       | TT/TTCCGT                                                                                 | ACGAAATCGAAGAGAA<br>GCGA   | TCCAGGACACAAACA<br>TCCA      | 60.1                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_12325595  | Ca5                                     | 12325595                      | GTA/G                                                                                     | ATGTATTGGGCCAGTC<br>CTGA   | GGCGCCGCTAATTAAA<br>GTTAT    | 60.3                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_1239625   | Ca5                                     | 1239625                       | AATATATATATATATATATA/AATA<br>TATATATATATATATATA                                           | GGTTGATTTTGAATAG<br>GTGTCG | ATTAAATTAAGGGGCC<br>GCAG     | 58.5                             | 107                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_12532663  | Ca5                                     | 12532663                      | A/AT                                                                                      | TGCAATTGGTTGGAAT<br>GTGT   | CCAATGAGTTTGAGCC<br>TTCC     | 59.8                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_12544184  | Ca5                                     | 12544184                      | AATATATATATATATATATATATAT<br>ATATATATATATA/AATATATATAT<br>ATATATATATATATATATATATA<br>TATA | TCTTCCACCATCCATC<br>CTTC   | GGCGATTTTACGTGTA<br>TATGTGAG | 59.9                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_12672542  | Ca5                                     | 12672542                      | AATATATATATATATATAT/AATATAT<br>ATATATATATATATAT                                           | AATGGAGGAAGGAGG<br>GAGAA   | CTTGGGAACTGGAGAG<br>CAAG     | 60.0                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_131876    | Ca5                                     | 131876                        | GTTTT/GTTTT                                                                               | ATCCAAGTATCCAACG<br>GCTG   | CACCTCTGCCCACTTC<br>ATTT     | 60.0                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_132937    | Ca5                                     | 132937                        | CAA/CAAA                                                                                  | CCAAAGACACAGCAAA<br>GCAA   | CACTTCCACCAAGTTGC<br>AAAA    | 60.0                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_133061    | Ca5                                     | 133061                        | GGTG/GG                                                                                   | GCCATGGAGTGCTGGT<br>TATT   | GCGTTGTGAAAACAGG<br>ACAA     | 60.0                             | 709                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_133085    | Ca5                                     | 133085                        | ACC/AC                                                                                    | GCCATGGAGTGCTGGT<br>TATT   | GCGTTGTGAAAACAGG<br>ACAA     | 60.0                             | 709                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                  | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_133283    | Ca5                                     | 133283                        | AATATAT/AATAT                                                                                  | ACCTTTACATGGTGCC<br>AAGC  | GCGTTGTGAAAACAGG<br>ACAA | 60.0                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_133428    | Ca5                                     | 133428                        | GAACA/GAACAATTTTATAATAACA                                                                      | ACCTTTACATGGTGCC<br>AAGC  | GCGTTGTGAAAACAGG<br>ACAA | 60.0                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_133648    | Ca5                                     | 133648                        | GAAAAA/GAAAA                                                                                   | TTGTCCTGTTTTCACAA<br>CGC  | TCAACAATTGTGGGC<br>TTCA  | 59.7                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_133972    | Ca5                                     | 133972                        | CAAAAA/CAAAAA                                                                                  | TTGTCCTGTTTTCACAA<br>CGC  | TCAACAATTGTGGGC<br>TTCA  | 59.7                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_135216    | Ca5                                     | 135216                        | GTTCTT/GTTCTTCTT                                                                               | CCATCATTGGTTTGTG<br>GTGA  | AAATCCTAATCATGGC<br>GCAG | 60.2                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_13624288  | Ca5                                     | 13624288                      | ATTTT/ATTTTTT                                                                                  | TGAAATGTTGTTGGT<br>AGTGGC | CGACGGTGCCAATTT<br>CTAT  | 59.9                             | 948                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_136326    | Ca5                                     | 136326                        | A/AT                                                                                           | TCGAATGTCAACAAAC<br>AAGCA | ATTCTGCACACCACTT<br>TCC  | 60.3                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_13636401  | Ca5                                     | 13636401                      | A/AC                                                                                           | ATCGACAAACCAACAT<br>GCAA  | GGGAAACTCACTTGCG<br>GTTA | 60.0                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_13636921  | Ca5                                     | 13636921                      | CTGT/CT                                                                                        | TAACCGCAAGTGAGTT<br>TCCC  | GCGGTGGCTGAGTTTC<br>TTAC | 60.1                             | 387                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_13754064  | Ca5                                     | 13754064                      | CATTATTATTATTATTATTATTAT<br>TATTATTATTATTAT/CATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTAT | TCGATTTTGGCTTTAAC<br>CAG  | CCCACACCTTAAAAGC<br>CACT | 57.9                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                 |                             |                           |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_1377883   | Ca5                                     | 1377883                       | TCC/TC                                                          | GACTCTTTCATAGCG<br>TGCC     | CACCTTGTAGCCAACG<br>GTTT  | 59.8                             | 720                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_13801981  | Ca5                                     | 13801981                      | TAA/TAAGACCTCTCCACCGAA                                          | TTTGCTCATGTGCTTTT<br>TGC    | TTCTCATTTGTGTTGGG<br>TGAA | 60.0                             | 538                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_1390115   | Ca5                                     | 1390115                       | CATATATATATATATATATAT/CATAT<br>ATATATATATATAT                   | AGGCTCAAACGTCGAA<br>GAAA    | TGAGTTGAGTGCAAAC<br>CTGG  | 60.0                             | 792                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_13970765  | Ca5                                     | 13970765                      | TA/TGA                                                          | TATTTGGACAAACGAA<br>GGGC    | CCCCTTTTGCTTGTTG<br>GTTA  | 59.9                             | 282                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_13971864  | Ca5                                     | 13971864                      | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>ATATA | ATGGAGACTTTCTGCA<br>GCGT    | TCCTCCGGCTGCTAAA<br>TAAA  | 60.0                             | 691                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_14022502  | Ca5                                     | 14022502                      | ATTT/ATTTT                                                      | GGAAATGGATGTCTGC<br>CAAT    | TTGCAATCTCATCAACT<br>CGG  | 59.8                             | 318                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_14263455  | Ca5                                     | 14263455                      | AATATATATATATATATATATA/AA<br>TATATATATATATATATATATATA           | ACTTGCAGCAATTTCC<br>ATCC    | GGATGCTTCCATAAT<br>CTGC   | 60.1                             | 716                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_14300751  | Ca5                                     | 14300751                      | G/GA                                                            | TTTGC GTTACGAATTTG<br>ATGA  | AAATGAACGAATTTGCA<br>CTCG | 59.2                             | 595                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_14316093  | Ca5                                     | 14316093                      | TTATATATATA/TTATATATATATATA<br>TATATATATATA                     | TTTACGGAGGCCCTA<br>ATTC     | TGAAGAGGGATTGGTA<br>TGCC  | 60.3                             | 627                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_14330970  | Ca5                                     | 14330970                      | ATTTTTTTTT/ATTTTTTTTTT                                          | TGATTAAGAAGTTTTGA<br>TTTGCG | GGTTTGACAATCTGC<br>CTTG   | 58.5                             | 795                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_14394852  | Ca5                                     | 14394852                      | CTTTTT/CTTTT                                                            | TCTTCCACCCAGTTTT<br>ACC  | TTGAGGGCTATGTTTT<br>CGG  | 59.9                             | 337                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_1453148   | Ca5                                     | 1453148                       | CATATATATATATATATATAT/CATAT<br>ATATATATATATATATAT                       | AGGAAGAGTGGAGTTG<br>CGAA | TGCGTTACGGTGAAAT<br>GGTA | 60.0                             | 368                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_15176756  | Ca5                                     | 15176756                      | AATATATATATATATATATATATAT<br>AT/AATATATATATATATATATATA<br>TATATATATATAT | ACATTTAGGGCCACTT<br>GGTG | GTTGGTCCCTAGCAC<br>CGTA  | 59.9                             | 725                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_1521350   | Ca5                                     | 1521350                       | TT/TTAT                                                                 | TTGGCCAAGTCCCTGT<br>TTAC | CTCTCATCTGAGGCA<br>AAGC  | 60.0                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_152255    | Ca5                                     | 152255                        | CATATATATATATATATAT/CATATAT<br>ATATATATAT                               | TTTTGGCCCCTAAGAC<br>ACAC | TTTAATTGCACGCTCAC<br>GTC | 60.0                             | 331                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_15339602  | Ca5                                     | 15339602                      | GAAAAAAAAA/GAAAAAAAAA                                                   | AGGAGAGAAAAAGGGG<br>GAAA | GGGAAACCCACCTCTT<br>GATT | 59.1                             | 211                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_153461    | Ca5                                     | 153461                        | GTTTAATTTA/GTTTA                                                        | GCCTCGCAATTCCTGA<br>AAGT | ATCCGGAACTTTTGC<br>CTTT  | 61.6                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_15462644  | Ca5                                     | 15462644                      | CAAAAAAAAA/CAAAAAAAAA                                                   | CTTGAAATGGTGCTGC<br>AAGA | GGGGGAGTCTTGCTGT<br>GTTA | 60.0                             | 733                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_15481624  | Ca5                                     | 15481624                      | CTTTTTTTTTTT/CTTTTTTTTTTT                                               | TTTTGACACGCAGTAG<br>GCAC | AGTCGGGAGTCACGT<br>ATGG  | 59.9                             | 781                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_155187    | Ca5                                     | 155187                        | AA/AATA                                                                 | TGTGACGTGGGAGGAT<br>TGTA | GAGGCTGCAGCATGTT<br>CATA | 60.0                             | 355                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)                  | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                 |                          |                             |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_15543535  | Ca5                                     | 15543535                      | CATATATATATATATATATATATA<br>TATATATATATATATAT/CATATATAT<br>ATATATATATATATATATAT | AATCCGGTAAAATCTC<br>CGCT | GTTTTCTTCCTTTGGGC<br>CTT    | 59.9                             | 731                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_1558914   | Ca5                                     | 1558914                       | TAAAAAAAA/TAAAAAAAAA                                                            | TCAAGATTGCAAACCT<br>GCAT | TCTTCAGGTTCAGCA<br>AACC     | 59.3                             | 452                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_15716362  | Ca5                                     | 15716362                      | CTTTTTTTTT/CTTTTTTTTT                                                           | TTTGTCGACTGCGT<br>TTGT   | TTGATAAGTGGCGGA<br>GAAAA    | 60.5                             | 327                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_15716555  | Ca5                                     | 15716555                      | ATTTTTTTTTTT/ATTTTTTTTTTT<br>T                                                  | TTTGTCGACTGCGT<br>TTGT   | TTGCAATGTCAACAACA<br>GAGG   | 60.5                             | 859                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_15756736  | Ca5                                     | 15756736                      | GACAC/GAC                                                                       | GCGCGATTTACCAAAA<br>ATGT | TTTGAGTGGTGGGTTG<br>TGAA    | 60.0                             | 431                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_15772842  | Ca5                                     | 15772842                      | AT/ATATCT                                                                       | GCCTTAAATTTGGCA<br>ATGG  | CCCTTAAACCAATAA<br>AAGAAACA | 59.4                             | 231                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_158353    | Ca5                                     | 158353                        | AT/ATT                                                                          | TTTTGCATACCAAAACA<br>CCC | ATGTCCATGACGCATC<br>AAAA    | 58.4                             | 463                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_15835478  | Ca5                                     | 15835478                      | CAAA/CAAA                                                                       | TGCATGATTCCAGAATT<br>CCA | AGCGGTGAGGAGAACT<br>CTGA    | 60.0                             | 690                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_1586054   | Ca5                                     | 1586054                       | TAAAA/TAAA                                                                      | CTGTTTTCTACCCCCA<br>CCCT | AGCGTTGTAAAAGATG<br>CGCT    | 60.2                             | 727                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_15877436  | Ca5                                     | 15877436                      | GC/G                                                                            | GGGCTACATCCAGTCC<br>TCAC | TTTGGCTGTAGAGGTT<br>CCAAA   | 59.5                             | 474                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                              | Forward primers (5'-3')      | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------|------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                            |                              |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_158794    | Ca5                                     | 158794                        | TAAAAA/TAAAA                                                                                                               | TGATGCGTCATGGACA<br>TAAA     | TTTAAAAATGTCCATT<br>TACACCG   | 58.5                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_159164    | Ca5                                     | 159164                        | TA/TAAA                                                                                                                    | TCAAAATTGTTTATTTA<br>CCGGTGT | TTGGGAACAAAAAGTG<br>GGAG      | 58.8                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_15918981  | Ca5                                     | 15918981                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT/TT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATT | CCTCCCCCATTTGTCT<br>TCTT     | GCCTGATGTTCGAATTT<br>TTCA     | 60.3                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_15929247  | Ca5                                     | 15929247                      | AACCAC/AAC                                                                                                                 | TGATGACGAAGACGAA<br>GACG     | AACACATCCGGGATCC<br>ATTA      | 60.0                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_15929348  | Ca5                                     | 15929348                      | ACCC/ACC                                                                                                                   | TGATGACGAAGACGAA<br>GACG     | AACACATCCGGGATCC<br>ATTA      | 60.0                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_15993780  | Ca5                                     | 15993780                      | TTATATATATATATATATATATATA<br>TATATAT/TTATATATATATATATATA<br>TATATAT                                                        | AGGAAGAGTGGAGTTG<br>CGAA     | ACCCCCGTTCCCTTGTA<br>AATC     | 60.0                             | 716                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_16029850  | Ca5                                     | 16029850                      | AAATAATAATAATAATAATAATA<br>ATGATAATAATAAT/AAATAATAATAA<br>TAATAATAATAATAATGATAATA<br>ATAAT                                 | TTGAACAACCGAACTT<br>CAAAGA   | CAATATTGTGATGACAT<br>TGGTATGA | 59.8                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_160572    | Ca5                                     | 160572                        | TAAAAAAAA/TAAAAAAAA                                                                                                        | AATCCAATGGCTTTCAA<br>TCAA    | CACACGACAAAGTGGA<br>GTATCAG   | 59.4                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_16083320  | Ca5                                     | 16083320                      | CAATTAATTAATTAAT/CAATTAATTA<br>ATTAATTAAT                                                                                  | TGAATGGAGACGTGAA<br>GCTG     | ACGCAGTGTAACCCC<br>CAAT       | 60.0                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_161153    | Ca5                                     | 161153                        | CTT/CTTAAATT                                                                                                               | CTGATACTCCACTTTGT<br>CGTGTG  | GCATAATCCGCTCACC<br>CTAA      | 59.7                             | 819                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                       | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                     |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_161487    | Ca5                                     | 161487                        | GTTTTTTT/GTTTTTTTTT                                                                 | ACGTGCAACGTATCCC<br>AAAT  | GCATAATCCGCTCACC<br>CTAA | 60.3                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_16319965  | Ca5                                     | 16319965                      | TGGG/TGGGG                                                                          | TTGTGTGCAGGATCCA<br>CATT  | TTGACCATTGCACGAA<br>ACAT | 60.0                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_164139    | Ca5                                     | 164139                        | A/ATAAATGG                                                                          | GGTAAAAGAGACTCGC<br>GTGG  | CTGATGTGCTCGTTGT<br>TGCT | 59.9                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_16469239  | Ca5                                     | 16469239                      | GTATATATATATATATATATATAT<br>ATAT/GTATATATATATATATATAT<br>ATAT                       | TCGGTGTCAAATGAAG<br>ACCTC | CGATTTGACAACATCAC<br>GCT | 60.1                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_16519732  | Ca5                                     | 16519732                      | ATTTTTTT/ATTTT                                                                      | ATCTGAATTTTGTGGC<br>GGT   | GGACCAAATTGACAAC<br>GACA | 59.4                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_16522289  | Ca5                                     | 16522289                      | TTATATATATATATATAT/TTATAT<br>ATATATATATATATAT                                       | CTTTCCCTCTCGAGC<br>TCAT   | ATCCTTTGCATGTCCCA<br>CTC | 58.6                             | 238                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_16523502  | Ca5                                     | 16523502                      | CTATATATATATATATATATAT/CT<br>ATATATATATATATATATATATAT                               | GCATGCCACTTAGCTT<br>CCAT  | GGGGAGGTTAAAGGAT<br>CCAA | 60.2                             | 296                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_16557774  | Ca5                                     | 16557774                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTA/TTTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA | GTGCTCCTCCCTTCTT<br>CCTT  | TGTCCCTGATTCCGTTT<br>TTC | 59.8                             | 331                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_16637694  | Ca5                                     | 16637694                      | AATA/AATATA                                                                         | GACACGTCCTGCCTT<br>TATT   | ACAAGAAATTGGGAG<br>GGAG  | 60.0                             | 284                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_16650628  | Ca5                                     | 16650628                      | GTTTTTT/GTTTTTTTT                                                                   | CCCGAAAGTCCTCCAA<br>AAAT  | CCAAGTTCCCAGAGT<br>CAAA  | 60.3                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_16715155  | Ca5                                     | 16715155                      | CTTTTTTTTT/CTTTTTTTTT                                         | TGGGTTACCCCAAT<br>TAAA    | TCATCAAATCCGTAACG<br>CAA    | 60.0                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_16715406  | Ca5                                     | 16715406                      | GAAAAAAAA/GAAAAAAAA                                           | TTGCGTTACGGATTG<br>ATGA   | GCTAAATTACATTCTGTG<br>GTCCC | 60.1                             | 240                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_1678181   | Ca5                                     | 1678181                       | TTATATATATAT/TTATATATATAT<br>AT                               | CGGTGAATCCTTTACG<br>GAGA  | AGGAAGAGTGGAGTTG<br>CGAA    | 60.1                             | 384                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_16881029  | Ca5                                     | 16881029                      | GGTTGTTGTTGTTGTT/GGTTGTTG<br>TTGTTGTTGTT                      | TGCATGCTTAATTGAC<br>AGTGA | TGATTTAACGGTTGTGA<br>TTGATT | 59.4                             | 779                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_16948578  | Ca5                                     | 16948578                      | CATATATATATATATAT/CATATAT<br>ATATATATATATAT                   | GTTTTCGAATCAACGA<br>GGGA  | GCTCAGAGGCTTTTTA<br>GCCA    | 60.1                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_17007480  | Ca5                                     | 17007480                      | AATATATATATATATATA/AATATATA<br>TATATATATATA                   | TGCAATCAATTTTGAG<br>CCA   | TGGTGGTTGTTGTCTC<br>CTCA    | 60.2                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_17020837  | Ca5                                     | 17020837                      | TAGAGAGA/TAGAGA                                               | CCTACGGATGACCTCT<br>CTCG  | GGTTTAACATCCCCAC<br>AAGC    | 59.8                             | 773                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_17048541  | Ca5                                     | 17048541                      | AATATATATATATATATATAT/AAT<br>ATATATATATATATATATAT             | GGTCAGCATTTACCCC<br>ATGA  | TTTCTCACCTTCCTTG<br>GTG     | 60.7                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_17120322  | Ca5                                     | 17120322                      | AATATATATATATATAT/AATATATAT<br>ATATATATATAT                   | CGGTCACCATCGACAC<br>TATG  | TCCCTGCTCCTCGTCT<br>TCTA    | 60.0                             | 816                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_17244450  | Ca5                                     | 17244450                      | AG/A                                                          | GTACCCTCCTCCTCG<br>TCTC   | TTGTGTTTCAACAAC<br>CTCAA    | 60.1                             | 729                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                           |                            |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_17314539  | Ca5                                     | 17314539                      | TAAAAAAAAA/TAAAAAAAAA                                                     | TCGATTATGCGTAGGG<br>AAGG   | TTGCGACAACTTGGTG<br>ATTC      | 60.1                             | 824                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_17448710  | Ca5                                     | 17448710                      | CACTATACAA/CACTATACAACTATA<br>CAA                                         | TGTGGATGTTCAAGGG<br>ACAA   | ACAAATGGCGTATGCC<br>TCTC      | 59.9                             | 864                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_17494887  | Ca5                                     | 17494887                      | CTGA/CTGACCTCCTATATGTGA                                                   | CTACGCCAAGAACTG<br>CTCC    | GTACGCGTCCAGACAT<br>AGCA      | 60.0                             | 245                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_17526738  | Ca5                                     | 17526738                      | T/TG                                                                      | GATTGGGGGAAGATGA<br>GGAT   | TTTGC GTTACGAATTTG<br>ATGA    | 60.1                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_17534242  | Ca5                                     | 17534242                      | AATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATATA<br>TATATATATATAT | TCATTGAGGATGTTCC<br>AAAGTT | ACAAAAGGCATCTCTG<br>GTCTG     | 58.6                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_17549591  | Ca5                                     | 17549591                      | TTATATATATATATATAT/TTATATAT<br>ATATATATATATAT                             | GTGGGGGTGCAATGTA<br>AAAT   | TTGCATAAACTACACAA<br>TGGAAAAA | 59.6                             | 357                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_17733319  | Ca5                                     | 17733319                      | A/ATCGGTTTCAGC                                                            | CGCGATGTCGTCTAAA<br>GTGA   | GAGGGGAGGGTTTTTG<br>CTAC      | 60.0                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_17760753  | Ca5                                     | 17760753                      | TAATAAAATAAAATAAAATAAA/<br>TAATAAAATAAAATAAAATAAA<br>ATAAAA               | TGAAACCGCGTTTGAT<br>TGTA   | GGTTGGGACCACTTCT<br>CAAA      | 60.1                             | 168                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_17876530  | Ca5                                     | 17876530                      | CAA/CAAA                                                                  | TTTCATCCATCACCGA<br>CAAA   | CTCAACGAATGCCTGA<br>AACA      | 59.9                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_17876692  | Ca5                                     | 17876692                      | ACAC/A                                                                    | TGTTTCAGGCATTTCGT<br>TGAG  | TCAATACCATTTTCACC<br>GCA      | 59.8                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                           | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                         |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_17876974  | Ca5                                     | 17876974                      | ATTTTT/ATTTTTTT                                                                                         | TGTTTCAGGCATTCGT<br>TGAG   | TCAATACCATTTTCACC<br>GCA   | 59.8                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_1794712   | Ca5                                     | 1794712                       | AATTATTATTATTATTATTATTATT<br>TATTATTATTATTATTATTATT/AATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATT | GAGAAGGCGAGAAGG<br>AAGGT   | GCAAGGTTTAGGTGGG<br>TCAA   | 60.0                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_18049660  | Ca5                                     | 18049660                      | CATATATATATAT/CATATATATAT                                                                               | GCACGTTGTAAAGAGT<br>GGACTG | AAAAGGCCCAACAAGAG<br>TTGA  | 59.8                             | 694                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_18072367  | Ca5                                     | 18072367                      | TAAAAAAAAA/TAAAAAAAAA                                                                                   | CGAAAAGAAAATGGTG<br>CAGTT  | GTTCAACTGACGGGGA<br>GAAA   | 59.3                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_18136111  | Ca5                                     | 18136111                      | CTTTTTTTTT/CTTTTTTTTT                                                                                   | CGGGTCATTTTCTTTCT<br>CCA   | TTGTGGTCCTTTAAGAT<br>GGTTG | 60.0                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_18179865  | Ca5                                     | 18179865                      | CAAAAAAAAA/CAAAAAAAAA                                                                                   | GGCAAAATATCTTTTCAT<br>TCCG | TCTGAACAGTGTTGCC<br>ACAGA  | 58.6                             | 352                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_18589694  | Ca5                                     | 18589694                      | TATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATAA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAA  | CACAAGCATCTTGTTT<br>GTCC   | TGTGGTTTTGCTAATTG<br>GGG   | 59.3                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_18593873  | Ca5                                     | 18593873                      | TTA/T                                                                                                   | GGTCTGTCCAATCAGA<br>CCGT   | TCCATTAAGCCCCCTCAA<br>CAA  | 60.0                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_18686080  | Ca5                                     | 18686080                      | G/GACAAATAAATCCT                                                                                        | GTCAGGTCGACCCACA<br>AGAT   | AGGTAAGGGCTCCTTC<br>CAAA   | 60.0                             | 808                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_18808476  | Ca5                                     | 18808476                      | TATAAATAAATAAATAAATAA<br>TAAATAAA/TATAAATAAATAA<br>TAAATAA                                              | CAACGTTGATGCAAAA<br>ATAGG  | CAAATTGCAAGGAAAC<br>CACA   | 58.2                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                  | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                |                          |                             |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_18944656  | Ca5                                     | 18944656                      | CAAAA/CAA                                                                                      | TCCTGTCATGTGCTTT<br>GAGC | CTAACCTCCCAGGACC<br>CAAT    | 60.0                             | 131                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_18962064  | Ca5                                     | 18962064                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAA/AAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAA | GCCCTCTCCTCGTGTT<br>ACAA | CCGAAAATAGCGATGA<br>GAGC    | 60.3                             | 394                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_1903216   | Ca5                                     | 1903216                       | GA/GAA                                                                                         | TGCATAGGCCTCTTGT<br>CCTT | AGTTCCGCGCTAGATT<br>TCAA    | 59.8                             | 553                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_191284    | Ca5                                     | 191284                        | GAATTCCAAATTCCAAATCCAAAT<br>CCAAATTC/GAATTCCAAATTC<br>ATTCC                                    | GCAAGTGATGATGTAG<br>CGGA | GCTCCAAAGTGCAAGT<br>GTGA    | 59.8                             | 605                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_191704    | Ca5                                     | 191704                        | CGGA/C                                                                                         | TCACACTGCACTTTG<br>GAGC  | TTGTTGGGATCCCTGA<br>AGAG    | 60.0                             | 484                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_19591188  | Ca5                                     | 19591188                      | CATATATATATATATATATATATA<br>TATATAT/CATATATATATATATAT<br>ATATATATATATATATATATATAT              | CCACAGCTTCAACAAA<br>AGCA | TGGATGATTTGATGTCA<br>CATAGG | 60.0                             | 525                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_19705316  | Ca5                                     | 19705316                      | TA/TACA                                                                                        | TTGGAAGGAGCCCTTA<br>CCTT | CTGCCACGTCACCCTT<br>TTAT    | 60.1                             | 742                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_19725939  | Ca5                                     | 19725939                      | CTGA/CTGATGA                                                                                   | GCCCAGGAAAAAGAAA<br>GGAC | TCGGTATTTGCCATGA<br>GACA    | 60.1                             | 405                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_19762990  | Ca5                                     | 19762990                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAA/AAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAA | TCAGTCTGCCCTGACC<br>TTTT | GGCCAATGGCATGATC<br>TACT    | 59.8                             | 598                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_19778378  | Ca5                                     | 19778378                      | A/AAGAGAGTTAGTAGT                                                                              | ATCAAGTTTTTGGCGC<br>TGTT | CATACTCGCCGAGGGT<br>ACAT    | 59.8                             | 393                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_19815812  | Ca5                                     | 19815812                      | A/AC                                                          | TTTGGGTTGGGATGA<br>CATT     | ACCAGGAAAAGAAGAA<br>GGGC    | 60.0                             | 378                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_19816092  | Ca5                                     | 19816092                      | CATATA/CATATATATA                                             | TTTGGGTTGGGATGA<br>CATT     | TGTCGATTTTAATAGGG<br>CGG    | 60.0                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_19914483  | Ca5                                     | 19914483                      | TTA/TTTAGATTGACTA                                             | TGTTCCCAATCAACA<br>CCAA     | GCCCTCTATGGGTTGA<br>AACA    | 59.8                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_1995521   | Ca5                                     | 1995521                       | ATGTT/ATGTTGTT                                                | TCTTCGTTTGCAGTCA<br>AACTT   | TCTTCGTTTATGGTTT<br>TATTCA  | 59.1                             | 279                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_19959975  | Ca5                                     | 19959975                      | TAAAAAAA/TAAAAAAA                                             | CAATGACAAATTTTTGT<br>TTCGTG | TTGTTGGGTCATTAGC<br>GATG    | 59.4                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_2000745   | Ca5                                     | 2000745                       | T/TGC                                                         | TATGAAAATCGCCCGA<br>AAAG    | TTCTGGGTCCTCGATT<br>TCAC    | 60.0                             | 380                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_2008256   | Ca5                                     | 2008256                       | G/GC                                                          | GGTCCTCGATTTCATC<br>TGGA    | TAGGCTTCAAGGAAGC<br>TGGA    | 60.0                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_20107894  | Ca5                                     | 20107894                      | ATTTTTTTTT/ATTTTTTTTTT                                        | TTTGAAGCCATTGAGT<br>CGTG    | CTCACCCACCTTCACC<br>ATTT    | 59.8                             | 207                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_20438947  | Ca5                                     | 20438947                      | AT/A                                                          | AGTTTGGAACCAAGCC<br>ACTG    | TAAGCCGTGGAACGT<br>TAAG     | 60.1                             | 343                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_20531337  | Ca5                                     | 20531337                      | ATTTTTTTTT/ATTTTTTTTTT                                        | AGTCGCTGAAAATTCG<br>GTTG    | TGATTCAATGTCATAAG<br>TGACGG | 60.2                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_20547334  | Ca5                                     | 20547334                      | AACCAACACCAACACCAACA/AACC<br>AACACCAACACCAACACCAACA           | AGGAGATGGAGCGTTG<br>TTTG     | TTGGTTAGCGTGCATC<br>TGAG   | 60.3                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_20717387  | Ca5                                     | 20717387                      | TAAAAAAAA/TAAAAAAAAA                                          | CGTCGTTAAAGTGGAG<br>ACCAA    | TGAGTTCACGTGTTGA<br>GATGCT | 60.2                             | 804                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_20740792  | Ca5                                     | 20740792                      | GAAAAAAAA/GAAAAAAAAA                                          | TCTCACAACACTCCAAA<br>ATAAACA | ATTCCGTGGCTGAGCT<br>AAAA   | 58.7                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_208132    | Ca5                                     | 208132                        | TAATGAATGAATGAA/TAATGAATGA<br>ATGAATGAA                       | TGTTTGGGGAAC TTGC<br>TTTC    | GCCAACATGCGACTCT<br>GTTA   | 60.1                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_20910377  | Ca5                                     | 20910377                      | AATATATATATATATATATATATATA<br>ATA/AATATATATATATATATATATA      | CTGGGATACAGTGGT<br>GCCT      | AAATGGAGGAAGGAGG<br>GAGA   | 60.0                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_21005933  | Ca5                                     | 21005933                      | CAAAAAAAAA/CAAAAAAAAAA                                        | GCTTCCAAGCAAAGCA<br>AATC     | CCTTCATTCCTCTCC<br>CTC     | 60.0                             | 151                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_2100607   | Ca5                                     | 2100607                       | ATTTTTTT/ATTTTTTTTTT                                          | TGGACACGACGGTGAA<br>ATAA     | TTCGGTCTTTGTTGCC<br>TCT    | 60.0                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_21085449  | Ca5                                     | 21085449                      | A/AT                                                          | TTAGGCGACCACTGTA<br>TCCC     | TGAGCCACTTTGATCA<br>GCAC   | 60.0                             | 758                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_21176907  | Ca5                                     | 21176907                      | AT/ATTTT                                                      | AGGCTCGACTTG TAGC<br>CAAA    | CACGGTGTGTAATCGG<br>AAC    | 60.0                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_212468    | Ca5                                     | 212468                        | CCTCCCCTCTC/CC                                                | TGTTTCGACGCTTTGTT<br>GAAG    | CCCAACCAAGTTTGT<br>GTAAA   | 60.0                             | 922                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                            | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                          |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_21289753  | Ca5                                     | 21289753                      | CTATATATATATATATATATATAT<br>ATATA/CTATATATATATATATATA<br>TATATATA                                        | GGTACCGCGAGTAATT<br>CCAA | TGTGGAAATTGTGGG<br>TGAA   | 60.0                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_21290533  | Ca5                                     | 21290533                      | ATT/ATTT                                                                                                 | GTGCAGGTGTCTGTCG<br>AGAA | TGGATGAACTACATTG<br>CCCA  | 60.0                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_21458602  | Ca5                                     | 21458602                      | GATATATATATATATATATATATA<br>TATATATATAT/GATATATATATAT<br>ATATATATATATATATATATATATA<br>T                  | AAATCAGAATGGCCC<br>TTGA  | TGGACATTTGGTTTCA<br>TTGAG | 59.5                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_21460979  | Ca5                                     | 21460979                      | AATATATATATATATATATATAT<br>A/AATATATATATATATATATATA                                                      | TGAGGTTTGTATTATC<br>GCCC | CAACTTTAGGCTTGTC<br>CCTCA | 59.9                             | 390                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_21503150  | Ca5                                     | 21503150                      | AT/A                                                                                                     | CCTCTGTTCTGCGTT<br>AAGG  | AAAGTGGATGGCACA<br>CACA   | 59.9                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_21598205  | Ca5                                     | 21598205                      | TA/TAA                                                                                                   | TTGGTGTGGATTGTGC<br>ATTG | GGGGAAATCGATTGAA<br>TGAA  | 60.4                             | 953                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_21623515  | Ca5                                     | 21623515                      | AAATTAATT/AAATT                                                                                          | AGGTCATTTTCATCCAC<br>CCA | ACACACCTATGGGATG<br>CACA  | 60.2                             | 678                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_21754940  | Ca5                                     | 21754940                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATA/AAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATA | TAAACATGTGTTGCATC<br>CGC | TTGCAGCAAAACAAG<br>CAAC   | 60.5                             | 396                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_21759113  | Ca5                                     | 21759113                      | AATATATATATATATATATAT/AA<br>TATATATATATATATATATAT                                                        | AATGACAAAAAGGGG<br>AGAAA | TTGTCTCGCGTATGAA<br>CTGG  | 59.8                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_218483    | Ca5                                     | 218483                        | ATCTCTC/ATCTCTCTC                                                                                        | TAGCGTGGTGGTGTG<br>TGAT  | CCTTTCAAGGTCAGCC<br>ACAT  | 60.0                             | 739                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                              |                              |                            |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_2185075   | Ca5                                     | 2185075                       | ATTCC/ATTCCTTTCC                                                                             | TTGGGGGAATGGAGGT<br>AAAT     | TCCCCAAAACCCCTAAA<br>TTC   | 60.4                             | 677                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_218592    | Ca5                                     | 218592                        | TATAATAATAATAATA/TATAATA<br>ATAATAATAATAATA                                                  | TAGCGTGGTGGTGTG<br>TGAT      | CCTTCAAGGTCAGCC<br>ACAT    | 60.0                             | 739                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_21866481  | Ca5                                     | 21866481                      | GA/GAA                                                                                       | TCCGATTGGATTTCA<br>GGAC      | GCTTCGTTCTCGTTCT<br>TCG    | 59.9                             | 437                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_21899576  | Ca5                                     | 21899576                      | TAAAAAAAAAAAA/TAAAAAAAAAAAA                                                                  | TGACCTGACCTGGCCT<br>ATTG     | CCCAACAAAGCCTTAT<br>GGA    | 60.1                             | 519                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_21953528  | Ca5                                     | 21953528                      | TATAATAATAA/TATAATAA                                                                         | AAGTTGCCGATGGA<br>AATG       | TTGCAAAAGTCAAAC<br>CTCTT   | 59.9                             | 513                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_21965060  | Ca5                                     | 21965060                      | AG/AGG                                                                                       | ACGCTCAGAGTTCAC<br>GGGT      | GGCAATCGATTGGAC<br>AAGT    | 59.9                             | 365                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_22101626  | Ca5                                     | 22101626                      | TTATATATAT/TTATATATATATAT<br>ATAT                                                            | TTTTGCGGTTGTAGT<br>CCTC      | GGTGACGGATCGAAAA<br>ACAT   | 60.1                             | 717                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_22105938  | Ca5                                     | 22105938                      | CTATTTATTTATTTAT/CTATTT<br>ATTTATTTATTTATTTAT                                                | CACGCCACTAATGTAA<br>ATAATGTT | TCGCTCAAGTAATTTT<br>GAATTT | 57.4                             | 549                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_22149309  | Ca5                                     | 22149309                      | TAAAAAAAA/TAAAAAAAA                                                                          | TGTGGTGCGGTAGTG<br>ATTA      | CAAACTGCGATCCAA<br>AAGT    | 60.0                             | 440                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_22150301  | Ca5                                     | 22150301                      | GTATATATATATATATATATATAT<br>ATATATATATAT/GTATATATATAT<br>ATATATATATATATATATATATAT<br>TATATAT | CTCAACCGTACATACA<br>CGAGC    | TGGCAAGACAAAATGA<br>CTGTT  | 58.3                             | 345                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                    | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                  |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_222234    | Ca5                                     | 222234                        | TT/TTAAT                                                                                         | ACCGCTTTACAGAACA<br>ACCG    | GGTGAGGACAAAACAT<br>GGCT    | 60.2                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_22232670  | Ca5                                     | 22232670                      | TAAAAAAA/TAAAAAAA                                                                                | AAAGTGGGGTCCTTAT<br>CATTTTT | CAGTTTTCTGGGACCT<br>CCTG    | 59.2                             | 930                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_22362053  | Ca5                                     | 22362053                      | G/GA                                                                                             | CATGCGCAACTTCTTG<br>GTAA    | CGTATGCGACAACGAA<br>TCAC    | 59.9                             | 948                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_22389657  | Ca5                                     | 22389657                      | AT/ATT                                                                                           | TGCCTTTGCTAAGTCC<br>CACT    | TAAATAGCACCTGCGG<br>TTCC    | 59.9                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_22485566  | Ca5                                     | 22485566                      | TAATAAATAAATAAATAAT/TAATAA<br>ATAAATAAATAAATAAT                                                  | TTTTCTGGGTTTGAA<br>CTCG     | CCCACAAAACAAAGGA<br>GGAA    | 60.1                             | 624                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_22604396  | Ca5                                     | 22604396                      | AC/A                                                                                             | GTTTTCGCCGTATTTG<br>ATCG    | TATCAGAGTTCTCCCC<br>ACCG    | 60.5                             | 803                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_22659444  | Ca5                                     | 22659444                      | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATATAT<br>ATATATATATATA                        | CCAAGTTTGAAATGCC<br>GATT    | GCTGCATGTTCTTATG<br>CTCG    | 59.9                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_22693454  | Ca5                                     | 22693454                      | CGGG/CGGGG                                                                                       | CCTGCTTTGTTTTAGCT<br>CCG    | TGGGATGGATACCCGT<br>TAAA    | 60.0                             | 387                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_22734448  | Ca5                                     | 22734448                      | TATA/TATACATA                                                                                    | CCAACTTTTCTGCCCC<br>ATAA    | TCATGTTTTTACCCCTA<br>AGTCCA | 60.1                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_22735708  | Ca5                                     | 22735708                      | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTAT/ATATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTAT | GCAACTTGCAATACC<br>CCAA     | TGGTGGATACATTGAT<br>GGGA    | 60.9                             | 379                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_2277714   | Ca5                                     | 2277714                       | ATTTTTTTTTTT/ATTTTTTTTTT                                      | TTTTCGGGAGAAGCCA<br>CTTA   | TCGATTCACGAAATTG<br>GTCAT   | 59.8                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_22788346  | Ca5                                     | 22788346                      | ATACTA/ATA                                                    | TGATTGACATTTTTCAA<br>TTGGT | CAGCAAATAAATATCA<br>TCTGCAA | 57.0                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_22918447  | Ca5                                     | 22918447                      | T/TG                                                          | TTATCGGCCTTATCCA<br>CTGC   | GGATTCCACCAAATTCA<br>GGA    | 60.1                             | 721                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_22918526  | Ca5                                     | 22918526                      | AT/ATT                                                        | TTATCGGCCTTATCCA<br>CTGC   | TGAAATCCATGAACC<br>GTGA     | 60.1                             | 915                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_22970811  | Ca5                                     | 22970811                      | GATATATATATATA/GATATATATATA                                   | AATGTGAATCCACCA<br>GGAA    | CAAGCGCTATGTGACC<br>CTTT    | 60.2                             | 833                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_23081226  | Ca5                                     | 23081226                      | ATTTT/ATTTT                                                   | CATTTTAACGTTGGGG<br>CAGT   | ACCAGCAACCATAAAAA<br>CGC    | 59.9                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_23111759  | Ca5                                     | 23111759                      | ACCCCC/ACCCCC                                                 | TCTCACGGTTGTGAGG<br>ACTG   | TAGAGAAGTGTGCACC<br>GTGG    | 59.9                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_23166274  | Ca5                                     | 23166274                      | AA/AAC TAGTA                                                  | GAGAAGCGAAAGCGAA<br>GAGA   | GATATTAGGGGCAACT<br>CGCA    | 60.0                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_23184362  | Ca5                                     | 23184362                      | AATTATTATTATTATTATTATTA/AAT<br>TATTATTATTATTATTATTATTA        | GAAAAAGCGCTGTAA<br>TGCC    | ATCCCAACCAACAAGA<br>CAAA    | 59.9                             | 725                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_2323461   | Ca5                                     | 2323461                       | GAAAA/GAAAAA                                                  | GCGCCAGATTTCAAAC<br>ACTA   | ACCAGCAGACCAAAAT<br>GGAC    | 58.9                             | 262                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_2323758   | Ca5                                     | 2323758                       | TGA/TGGAGGA                                                   | GTCCATTTTGGTCTGCTGGT    | TCCCTGTCTCGATTTCATC     | 60.0                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_2327252   | Ca5                                     | 2327252                       | TAA/TAAA                                                      | TCGAAATGAAATCGAGGACC    | ACAGACGAGGGCTAGGGATT    | 60.0                             | 721                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_23275268  | Ca5                                     | 23275268                      | TAAAAAAAA/TAAAAAAAAA                                          | AAGCCTAATTCAGCCAGCA     | TGATAGCCTCCAACGACAAA    | 60.0                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_23557611  | Ca5                                     | 23557611                      | GGCCAGCCAGCC/GGCCAGCCAGCC                                     | GTGACTGGGGACTGGTGACT    | CTGTGACTAGGGAAGGCTCG    | 60.0                             | 122                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_236073    | Ca5                                     | 236073                        | CGAAGAAAA/CGAAGAAAAATGAAGAAAATGAAGAAAAAT                      | TTGAATTGACCGGAGGAATC    | GGGATAGGGAGGGTTGTGTT    | 59.9                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_23643411  | Ca5                                     | 23643411                      | ATTTTTTT/ATTTTTTTT                                            | AAGCAATCAACGCATTACACA   | TTGACTCTCGAAATGTCCTCC   | 60.3                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_23663124  | Ca5                                     | 23663124                      | C/CGA                                                         | GAGGGTTTTGGGTCAGTGAA    | AGTTTTCAAGGGTAGCGGGT    | 59.9                             | 789                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_23664574  | Ca5                                     | 23664574                      | TT/TTCCAAT                                                    | CAAGAAGGAACGAGGTGCTC    | TAGCCTAGAGCAGGGGTGAA    | 60.0                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_23675051  | Ca5                                     | 23675051                      | GT/G                                                          | TCCATGCACATTGCTCTCTC    | TGGGTTATTTTCATGGCTT     | 60.0                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_236894    | Ca5                                     | 236894                        | CCACA/CCA                                                     | CCCTCACAAATTACAATCCCA   | CCAACAAATGCATGTCATC     | 59.7                             | 763                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                           |                         |                         |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_237162    | Ca5                                     | 237162                        | TGCATTTGTTGGACG/TG                                                                        | TCGTCTGATATTTTGGATTGA   | TGCAACATTATATTTCCCGGT   | 58.0                             | 143                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_237297    | Ca5                                     | 237297                        | CTGTCAT/CTGTCATGTCAT                                                                      | TCATTGCAATACCGGGAAAT    | TGAATTTGGATAGGTGCCAAAAA | 60.2                             | 233                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_23770283  | Ca5                                     | 23770283                      | ATTTTT/ATTTTTT                                                                            | TTGGCCTTCCTTTTACATGTC   | CCATCAAGCGTCTGTTGAGA    | 60.1                             | 882                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_238011    | Ca5                                     | 238011                        | GTTTTT/GTTTTT                                                                             | CATGCACGATTCACACATGA    | GTGTCGTCCAACCTCTCCAT    | 60.1                             | 486                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_23841713  | Ca5                                     | 23841713                      | GA/G                                                                                      | TTTTCTCCCATCGTTGACAT    | TTCTCAGCTATTCATCCGGG    | 58.0                             | 712                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_23893834  | Ca5                                     | 23893834                      | AATATATATATATATATATATATATATATATATATA/AATATATATATATATATATATATATATATATATATATATATATATATATATA | CCAAATTTTACCTTCATCCACA  | TGGATGCGATAAACCAACTTT   | 58.9                             | 242                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_239546    | Ca5                                     | 239546                        | AATA/AATATA                                                                               | CTCAACGCTGCCACAATAGA    | TGGATTCCCAAACACTAGCC    | 60.0                             | 473                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_23976521  | Ca5                                     | 23976521                      | GT/GTT                                                                                    | TTGGTGAAAAGATTTTGTGCG   | TTCAATGACAAAGGGGAGAGA   | 59.7                             | 759                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_23995501  | Ca5                                     | 23995501                      | CATATATATATATATATATATA/CATATATATATATATATA                                                 | TTGCGAGCATGAGAAGTTGT    | AAAAACCACCTAATCGCTCA    | 59.6                             | 714                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca5_P4_240288    | Ca5                                     | 240288                        | AAAAAAAAAAAA/AAAAAAAAAAAAATAAAAA                                                          | GGCTAGTGTTTGGGAATCCA    | ACGGTGTGTTGGGTTAAGG     | 59.9                             | 820                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                          | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                        |                             |                               |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_24054306  | Ca5                                     | 24054306                      | CTATTATTATTATTATTATTATTATTA<br>TTATTATTAT/CTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT | TCAATAGAAGGTCGCA<br>TCCC    | TCGCACATCTACCTAAA<br>CGC      | 60.0                             | 759                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_240662    | Ca5                                     | 240662                        | T/TCAATCCA                                                                             | CCTTTAACCCAACACA<br>CCGT    | TTGGTGCCTACAACAT<br>ATTTTCC   | 59.8                             | 268                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_241183    | Ca5                                     | 241183                        | ATTTTTTT/ATTTTTTTT                                                                     | AAAACACAACCCTTCAA<br>GAGACA | GGGACGTCTTCGCATA<br>CATT      | 60.1                             | 129                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_24297832  | Ca5                                     | 24297832                      | AATATATATATATATA/AATATATATA<br>TATATATA                                                | CCCAAGTTTTAAATGG<br>GCAA    | GGAGGCCACCTTCAAC<br>ATTA      | 59.8                             | 556                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_243143    | Ca5                                     | 243143                        | GAT/GATAT                                                                              | CAGAAAGTAAACGGGC<br>CAAG    | TGAAAATATACAACACC<br>CATGAAAA | 59.7                             | 241                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_244132    | Ca5                                     | 244132                        | TAAAAAAAA/TAAAAAAAA                                                                    | TTTTGCGCGAGAATTG<br>ATAA    | TTTCAGAGGTTTGTTG<br>CATTTTT   | 59.4                             | 360                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_244256    | Ca5                                     | 244256                        | CAAAAAA/CAAAAAA                                                                        | TTTTGCGCGAGAATTG<br>ATAA    | TCGCTTTTTATTTT<br>CAGAGGTTTG  | 59.4                             | 370                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_244348    | Ca5                                     | 244348                        | TA/TAATACAAA                                                                           | TTTTGCGCGAGAATTG<br>ATAA    | GCACCTACCACCGCTC<br>TCTT      | 59.4                             | 918                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_2444633   | Ca5                                     | 2444633                       | GACTAACTAA/GACTAA                                                                      | GAAGCATCCAAATGG<br>GAGA     | GTGAGTTTCATGATGC<br>CACG      | 60.0                             | 737                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_244612    | Ca5                                     | 244612                        | ATT/ATTT                                                                               | AAAAATGCAACAAACCT<br>CTGAAA | GCACCTACCACCGCTC<br>TCTT      | 60.0                             | 581                                           | INTERGENIC                                           | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                   | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                 |                               |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_25027142  | Ca5                                     | 25027142                      | TAAAAAAAAAAAAA/TAAAAAAAAA                                                                                                       | AAATGGAATAACTTTGA<br>AAATGGAA | CTCCATCGCACACTTT<br>CTCA    | 59.2                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_25132630  | Ca5                                     | 25132630                      | CTATATATATATATATATATATAT/<br>CTATATATATATATATATATAT                                                                             | GCAAAAAGGAAGTTTG<br>TCCC      | TGCATGCATATTTGGAA<br>CATC   | 58.7                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_25232481  | Ca5                                     | 25232481                      | T/TC                                                                                                                            | CCACCCTGATTTTGG<br>AGAA       | AAATCCAACAATCTCC<br>CCC     | 59.9                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_25381692  | Ca5                                     | 25381692                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTA/TTATTATTATTATTATTATT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTA | ACGCGACTCAGCCAAG<br>TAAT      | AACCAATGATATGCAT<br>CACG    | 59.9                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_2550837   | Ca5                                     | 2550837                       | AC/ACC                                                                                                                          | TGAGACGTGGCATTGA<br>TGAT      | CGAACTCGTCTAGCCC<br>TTTG    | 60.1                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_25544088  | Ca5                                     | 25544088                      | TAAAAAAAAA/TAAAAAAAAA                                                                                                           | TTCAACAACATTCAATT<br>CCAA     | TGGTTATGCATGTTTCG<br>TCGT   | 58.9                             | 175                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_25574427  | Ca5                                     | 25574427                      | CATATATATATATATATATATATA<br>TAT/CATATATATATATATATATAT<br>ATATATAT                                                               | TTTTTGCAATCCACTCT<br>TGAA     | GATTGTTACACAATTCT<br>TCACGC | 58.4                             | 301                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_25624396  | Ca5                                     | 25624396                      | CATATATATATATATATATATATA<br>TATA/CATATATATATATATATATA<br>TATA                                                                   | GGGTTGGACAACACTT<br>GGTT      | CGACGGGAGTTAACAC<br>CATA    | 59.7                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_25656601  | Ca5                                     | 25656601                      | TCTT/TCTTACTT                                                                                                                   | CTACCCAAAAAGCCAC<br>GAAA      | TGGGGCAACCTATCAA<br>AGAG    | 60.1                             | 317                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_25657788  | Ca5                                     | 25657788                      | CAAA/CAAAA                                                                                                                      | GACTCGCAATCGTCTT<br>CACA      | AGATTCTCGAGTTTC<br>CCGT     | 60.0                             | 343                                           | INTERGENIC                                        | --                                  | --                    | --  |





| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                 | Forward primers (5'-3')        | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------|--------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                               |                                |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_26141778  | Ca5                                     | 26141778                      | AG/AGG                                                                                        | ATGGGTAGGGTAAAA<br>CCCG        | TCTTTCCCCACCCTCCT<br>ACT  | 59.9                             | 767                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_26159871  | Ca5                                     | 26159871                      | TATAATAATAATAATAATAATA<br>TAATAATAATAATAATAATAATA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAA | TCCCAATGAATTCGTT<br>TTAGA      | TGGATTAAACCAACTGT<br>CCCA | 58.6                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_26280416  | Ca5                                     | 26280416                      | CTTTTTTTTT/CTTTTTTTTTT                                                                        | GGGGAAAAAGGTACAA<br>GCCT       | AGCGACCTCCTACTTG<br>GTGA  | 59.5                             | 251                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_2628560   | Ca5                                     | 2628560                       | AT/ATATATT                                                                                    | TTGTTTCTCCCAGTTT<br>TGG        | TTTAGCATTGACCGCT<br>CCT   | 59.9                             | 357                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_26325634  | Ca5                                     | 26325634                      | T/TATATATAC                                                                                   | CACTTCCTCTCCTTG<br>CTCA        | ATATAAGCGGCGCTAT<br>CCCT  | 60.5                             | 164                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_26398930  | Ca5                                     | 26398930                      | AGAAATTG/AGAAATTGAAATTG                                                                       | TCGGTGGAGTGATGAC<br>AAAA       | CCACCACTTAGAACCTT<br>CGG  | 60.1                             | 366                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_26457056  | Ca5                                     | 26457056                      | AG/AGTAACATGGG                                                                                | GCACTAGGCTTCAAC<br>AGGC        | CACATTCCTGCACGGT<br>TCAT  | 60.0                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_26537164  | Ca5                                     | 26537164                      | AC/A                                                                                          | CAGAGCTGGGTGCAGT<br>CATA       | TCGTCCATATTCGGTA<br>GCC   | 60.0                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_26856153  | Ca5                                     | 26856153                      | AATATATATATATATATATATAT<br>ATA/AATATATATATATATATATAT<br>ATATATATATA                           | AAAAAGTTCATCTTCG<br>AAATGTTAGT | TTACCCGACGACAAAA<br>GTCC  | 59.8                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_26862103  | Ca5                                     | 26862103                      | AT/ATTGTT                                                                                     | GAAAGTGAAAAGAAGA<br>AAAAGGAAA  | CCATGGTAATGCATCG<br>TGAG  | 58.6                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_26889455  | Ca5                                     | 26889455                      | T/TTA                                                         | TCATCGCAGGTGTACC<br>ATGT | GCGCTGACATGATCCC<br>TATT | 60.0                             | 792                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_26989148  | Ca5                                     | 26989148                      | AG/A                                                          | CCAAAGCAAGCCAGAA<br>AGAC | GCGAGGTGGAACCACA<br>CTAT | 60.0                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_26996806  | Ca5                                     | 26996806                      | A/AAAAGCAAATTA                                                | TCGTTTTGGGTGAATT<br>GTGA | TGCCTCCTCGTTCCTTT<br>TTA | 59.9                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_26998600  | Ca5                                     | 26998600                      | CGGGGGG/CGGGGGGG                                              | TCAGTCGATACAGAG<br>TGCG  | ATGTTTGATGCTTCTTG<br>GGG | 60.0                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_26999969  | Ca5                                     | 26999969                      | GA/G                                                          | ATCCTGGCTTTTCCAC<br>CTTT | CGAGCACTATTCACTG<br>CCAA | 59.9                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27000123  | Ca5                                     | 27000123                      | ATCTCTCTC/ATCTC                                               | ATCCTGGCTTTTCCAC<br>CTTT | CGAGCACTATTCACTG<br>CCAA | 59.9                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27000261  | Ca5                                     | 27000261                      | A/AG                                                          | ATCCTGGCTTTTCCAC<br>CTTT | CGAGCACTATTCACTG<br>CCAA | 59.9                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27000469  | Ca5                                     | 27000469                      | T/TATC                                                        | TTGGCACTGAATAGTG<br>CTCG | TCGAAGCTGTGCTAAT<br>GGTG | 60.0                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27000513  | Ca5                                     | 27000513                      | A/AGTCG                                                       | TTGGCACTGAATAGTG<br>CTCG | TCGAAGCTGTGCTAAT<br>GGTG | 60.0                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27000752  | Ca5                                     | 27000752                      | CTTTTTTTTTTTTT/CTTTTTTTTTT<br>TTT                             | TTGGCACTGAATAGTG<br>CTCG | CGTCCCGAATAGACGA<br>ACAT | 60.0                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_27000834  | Ca5                                     | 27000834                      | ATCTCT/ATCT                                                             | TTGGCACTGAATAGT<br>CTCG   | CTCAGCGGGTAGAGTA<br>TCGC | 60.0                             | 940                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27103158  | Ca5                                     | 27103158                      | ANNNNNNNNN/ANNNNN                                                       | CAAGTGGAGCTTGCCA<br>ATTT  | CAGAGCGAAAATCAAG<br>GAGG | 60.2                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_2719069   | Ca5                                     | 2719069                       | GTTTTTTTTTTTT/GTTTTTTTTT<br>T                                           | TGAACTGCCGTTTGGT<br>TAGA  | TTTACCTCTTCGTTCC<br>CCT  | 59.3                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27225961  | Ca5                                     | 27225961                      | TG/T                                                                    | ACTCATTTTCTGCGCAA<br>TCA  | TGTGGAGGCACATACG<br>ACAT | 59.4                             | 880                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27389155  | Ca5                                     | 27389155                      | A/AAAAAAT                                                               | CACGAGCTTCAAGAGA<br>GCCT  | ATGAGATCGTTGTGG<br>GAGC  | 59.9                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27397872  | Ca5                                     | 27397872                      | AATATATATATATATA/AATATATA<br>TATATATATATA                               | CCTGCAACAATTTAC<br>CAAA   | TTCGTCGTGTTGCGTC<br>TAAC | 59.6                             | 885                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27458530  | Ca5                                     | 27458530                      | TTATATATATATATATATATATATA<br>TATAT/TTATATATATATATATATA<br>TATATATATATAT | CAATTGGTCGGCAGAG<br>TTTT  | CCCACAACCATGCAAT<br>AGAA | 60.1                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27472549  | Ca5                                     | 27472549                      | AG/A                                                                    | GCATTATGCCGTCATC<br>ATTTT | TTCGCATTCAAATTGT<br>TGTT | 59.8                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27510424  | Ca5                                     | 27510424                      | AATATATATATATATAT/AATATAT<br>ATATATATATATAT                             | CCAACACGGCAAAAAG<br>AGAT  | GCCATTTGGAATGACG<br>ACTT | 60.1                             | 799                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27718024  | Ca5                                     | 27718024                      | TAAAAAAA/TAAAAAAA                                                       | TGGCAACAGAAACCAA<br>ACAA  | TTCTTTTAGCCCGTTGC<br>TGT | 60.1                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                             | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                           |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_27759321  | Ca5                                     | 27759321                      | TATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAA<br>TAATAATAATAATAATAA                                                    | AGCCCAACTAAGCTGG<br>AAAA   | TCACCCCTCTTCATGCC<br>AAT | 59.0                             | 702                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27776620  | Ca5                                     | 27776620                      | ATTTTTTTTT/ATTTTTTTTT                                                                                                     | TCCAACTTGGGTTGG<br>TTTC    | CATGAGCATGCAAGAT<br>GGAT | 59.8                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27779493  | Ca5                                     | 27779493                      | GTTATATA/GTTATATATTATATA                                                                                                  | CATACTCCACGTCGTC<br>GCTA   | TTACAATTGTCACCGC<br>CTCA | 59.9                             | 278                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27784195  | Ca5                                     | 27784195                      | AATATATATATATATATATATAT<br>/AATATATATATATATATATATAT<br>TATATAT                                                            | TCATGTCATGTTGGTT<br>CATCA  | GAGTGTTGGTGGCAAT<br>TGTG | 58.3                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27800920  | Ca5                                     | 27800920                      | AC/A                                                                                                                      | TCTCAACAAGCACAATT<br>GCC   | TTTATTTGAGCCAAGG<br>GGTG | 59.8                             | 112                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27906217  | Ca5                                     | 27906217                      | AATATATATATATATATATATAT<br>/AATATATATATATATATATATAT                                                                       | TCCAACAACATCAAATT<br>CATCA | TGCTCACTCTCCAGC<br>ACCA  | 58.9                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27953689  | Ca5                                     | 27953689                      | TA/T                                                                                                                      | AACAACAGCCCCAATG<br>TAGC   | ACGCTTTTCAACAAAC<br>GCT  | 60.0                             | 794                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_27964664  | Ca5                                     | 27964664                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTAT/<br>TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTAT                     | GGGGTGTGATGTTCA<br>CTCT    | AACATGTCATTGCCTC<br>CCTC | 60.0                             | 400                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_28061616  | Ca5                                     | 28061616                      | TTATATATATATATATATATAT/<br>TTATATATATATATATATATAT                                                                         | TAGGGGGATCAAACT<br>GCAA    | GTCAGACCCGTTCAAT<br>TGCT | 60.4                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_28101883  | Ca5                                     | 28101883                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT/<br>AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAAT | TTGAGGAAGCGACTTA<br>TAACGA | CGTGTGATTGGTAATG<br>TGGC | 59.0                             | 829                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                              |                               |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_28187994  | Ca5                                     | 28187994                      | AATATATATATATAT/AATATATATAT<br>ATATATAT                                                                                      | CAAGAAAAGTAACCAT<br>CGTAATGA  | TGTGGATTCATGATCCT<br>TGTG   | 57.5                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_28188039  | Ca5                                     | 28188039                      | T/TC                                                                                                                         | CAAGAAAAGTAACCAT<br>CGTAATGA  | TGTGGATTCATGATCCT<br>TGTG   | 57.5                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_28192036  | Ca5                                     | 28192036                      | CATATATATATATATATATAT/CAT<br>ATATATATATATATATATAT                                                                            | CCACATGCTCATTGTG<br>TGACT     | CCATTCTCCTTCACCCA<br>GAC    | 59.6                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_28243344  | Ca5                                     | 28243344                      | CG/CTGCGTATTTCTGAG                                                                                                           | GCCTAATGGGTACGAA<br>AAGGA     | GGTTGGGATCCCTTTG<br>TTTT    | 60.3                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_28291153  | Ca5                                     | 28291153                      | CAAAAAAAAA/CAAAAAAAAA                                                                                                        | CACGTCCTAACATTTT<br>GCC       | TGTTCTGATATTTTGC<br>CGA     | 60.4                             | 400                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_28305464  | Ca5                                     | 28305464                      | GTGTATATATG/GTGTATATATGTAT<br>ATATG                                                                                          | AATATGTGGCGATTAAT<br>CTATTGTT | TGGTTGATCATTTTCGT<br>AGTACG | 57.3                             | 960                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_28310357  | Ca5                                     | 28310357                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAAT/AAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAAT | CCAACATGTGGGATAA<br>CTTG TG   | TGGCCTGACCTATTCT<br>CACC    | 60.1                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_28370910  | Ca5                                     | 28370910                      | TTATATATATATATATATATATATA<br>TATAT/TTATATATATATATATATA<br>TATATATAT                                                          | CTAGTTCGTAACCCGT<br>GCGT      | AGGCATGGTGTGGAG<br>TCAT     | 60.2                             | 260                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_28399764  | Ca5                                     | 28399764                      | GT/GTACTAGCATCCT                                                                                                             | AGAGTCGCCAGCTGAA<br>CAAT      | TGATTCTCCATAGCAC<br>CGA     | 60.0                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_28413401  | Ca5                                     | 28413401                      | A/AT                                                                                                                         | TTCTCCTTGAAGCTGT<br>CGGT      | ATTGCCAACATTCCG<br>GTAG     | 60.0                             | 252                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                           |                             |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_28463884  | Ca5                                     | 28463884                      | TAAAAAAAA/TAAAAAAAAA                                                    | TGTTTCCTTCGACACA<br>TTGA  | TGTTGAGCCCAAATA<br>CAAGG    | 59.2                             | 590                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_28483546  | Ca5                                     | 28483546                      | ATTTTTTTTT/ATTTTTTTTT                                                   | TGAAGCGTATGGAACA<br>ATCG  | TGAATCATTGAATTG<br>CACG     | 59.7                             | 674                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_28588926  | Ca5                                     | 28588926                      | TGGG/TGG                                                                | CAACTGCTCCTGTTCT<br>CCAA  | CTAGGAGCATGTCGCT<br>CTCC    | 59.0                             | 412                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_286593    | Ca5                                     | 286593                        | AGTTTTCGT/AGTTTTCGTGTTGC<br>GT                                          | CACACTCCCATTTTCC<br>ACC   | TACGTGTATCCAACGG<br>GGTT    | 60.2                             | 573                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_28734209  | Ca5                                     | 28734209                      | TTATATATATATATATATATATATA<br>TATAT/TTATATATATATATATATATA<br>TATATATATAT | TGTGGGATTCTTTCCC<br>CATA  | TTTGTATGATTGACG<br>GTTC     | 60.1                             | 785                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_28869871  | Ca5                                     | 28869871                      | TAAAA/TAAAAA                                                            | TGCTGGTGAACCTGGT<br>GGTA  | AAGTGGTCGACCGTCA<br>TTTC    | 60.2                             | 912                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_28977874  | Ca5                                     | 28977874                      | CAATGCAGAA/CAATGCAGAATAAT<br>GCAGAA                                     | TGCAGAACCAGAACAA<br>GCAC  | TCTGGATTTTGATGTG<br>CTGC    | 60.0                             | 137                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_29001853  | Ca5                                     | 29001853                      | TAAAAAAAA/TAAAAAAAAA                                                    | TGCACGGATAATGAAG<br>TCGT  | TCTCACATTTTATGCAC<br>ACAACC | 59.2                             | 897                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_29097154  | Ca5                                     | 29097154                      | ATTTTTTTTT/ATTTTTTTTT                                                   | GCTGCATGCGTTACGA<br>GATA  | AAATTCACGGTGTCAT<br>CTTCG   | 60.0                             | 271                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_29098754  | Ca5                                     | 29098754                      | ATTTTTTTTT/ATTTTTTTTT                                                   | CATCATGTTCAATGAAA<br>GCCA | CCATCCATTATCCAAC<br>CCA     | 59.5                             | 822                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                 | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                               |                               |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_29099232  | Ca5                                     | 29099232                      | CATTATTATTATTATTATTATTATT<br>TATTATTATTATTATTATTATTATT<br>TATT/CATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATT       | GGCATGACATGTGAAG<br>ATGG      | TAGCCCCACAACACAA<br>ACAA   | 59.9                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29144882  | Ca5                                     | 29144882                      | AATTATTATTATTATTATTATTATT<br>TATTATTATTATTATTATTATTATT<br>TATTATTATTATTATTATTATTATT<br>TATTATTATTATTATTATTATTATT<br>TATTATTATTATTATTATTATTATT | AGTGCTGATTGATATG<br>CCGT      | ATTAGGGCTGCACTTG<br>GACA   | 58.2                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29351977  | Ca5                                     | 29351977                      | CTATTATTATTATTATTATTATTATT<br>TTATTATTATT/CTATTATTATTATTATT<br>TTATTATTATTATTATTATTATT                                                        | GAGCCGAAAACGTATC<br>CTAA      | TTAGGCGCGTTTCAAG<br>AACT   | 57.0                             | 701                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29384323  | Ca5                                     | 29384323                      | CTTTTTTTTT/CTTTTTTTTT                                                                                                                         | CTTGGACAATTGAGGC<br>ATTTC     | ATAGACAAACGTCCGC<br>CTTC   | 59.6                             | 545                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29394828  | Ca5                                     | 29394828                      | ATTATATATATATATATATATATAT<br>ATATATATAT/AATATATATATATATA<br>TATATATAT                                                                         | GCGGTGAAACAATTCC<br>AAAT      | TGTTGCACACTCATTAT<br>CACCA | 59.8                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29418196  | Ca5                                     | 29418196                      | CAAAAAAAAA/CAAAAAAAAA                                                                                                                         | TGAAAAACACGGAGTC<br>AAACA     | CGTGACACTTCTAGCT<br>TGGA   | 59.2                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29462599  | Ca5                                     | 29462599                      | AATATATATATATATATATATATAT<br>AT/AATATATATATATATATATATA<br>T                                                                                   | ATTGCATCATGGCTAG<br>AGGG      | CACATGCAATCAACCT<br>CCAC   | 60.1                             | 702                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29515244  | Ca5                                     | 29515244                      | TAAAAAAAA/TAAAAAAAA                                                                                                                           | CAACTCCACAACACAA<br>CGCT      | CGGACAATTTCAACGT<br>CCTT   | 59.8                             | 673                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29614403  | Ca5                                     | 29614403                      | ATTTTTTT/ATTTTTTT                                                                                                                             | TGGAAGTTACAATCAC<br>GTGTAAAAA | CGTGTTCAGAAATTT<br>TGTTT   | 59.9                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29663443  | Ca5                                     | 29663443                      | AATATATATATATATATA/AATATATA<br>TATATATATATA                                                                                                   | CTCCTCCACTAAAAATA<br>ATTCCAA  | GGGGAGGAGCTTCCTA<br>TATCC  | 57.9                             | 756                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                               |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_29664249  | Ca5                                     | 29664249                      | GAAAAAAAAA/GAAAAAAAAA                                                         | ATTCATAAACACATGG<br>CCCC    | TAGGGTTAGGTGAGGG<br>GCTT | 59.5                             | 255                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29665140  | Ca5                                     | 29665140                      | ATCACATTTTCACATTTTCACATTT/AT<br>CACATTTTCACATTTTCACATTTTCACAT<br>TT           | TGGAAAGCGATTTATC<br>CTGG    | AGAGATCTTCTTGCGG<br>TGGA | 60.0                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29725622  | Ca5                                     | 29725622                      | TTATATATATATATATATATATATATA<br>TATATATATATAT/TTATATATATATA<br>TATATATATATATAT | AAGACATCGTCAAAAT<br>CCCG    | GAGATGAGAAATGAAG<br>CGGC | 59.9                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29725806  | Ca5                                     | 29725806                      | A/ATATAATAT                                                                   | AAGACATCGTCAAAAT<br>CCCG    | TCCACAGACGACGAGA<br>TGAG | 59.9                             | 687                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29778022  | Ca5                                     | 29778022                      | CAAAAAAAAAAAAA/CAAAAAAAAAAAAA<br>AAAAAA                                       | GCTGCTGGCACATCTA<br>CTCA    | TAAGTCAACAGATGG<br>TCGC  | 60.2                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29858771  | Ca5                                     | 29858771                      | ATTTTTTTTTTTT/ATTTTTTTTTTTT                                                   | TTTCAATTCTCTCACCG<br>TGCT   | CGCATCGAAAACAGTG<br>GTAA | 59.9                             | 789                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29858988  | Ca5                                     | 29858988                      | GATATATATATATATATATA/GATATA<br>TATATATATATATATATA                             | TTTTGCCACTTTATACA<br>CCAAAA | TCAGGCCATGTGAGTG<br>TGAT | 58.6                             | 878                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29904685  | Ca5                                     | 29904685                      | GAAAAAAAAA/GAAAAAAAAA                                                         | GCTTCCACGTTTGATT<br>GGT     | TGGGAAGATTACGCAC<br>TTCA | 60.0                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29920694  | Ca5                                     | 29920694                      | CTATATATATATATATATA/CTATATA<br>TATATATA                                       | AATTGTTTCATGCGACAT<br>TTG   | ATCTTCTCACTCCCA<br>CCT   | 57.1                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_29933647  | Ca5                                     | 29933647                      | GATATATATATATA/GATATATATATA<br>TATA                                           | GACCTTTTCAAAGGAT<br>GCATTA  | CGTGATGACAGACCA<br>CACC  | 58.3                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                  | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                |                            |                              |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_30106907  | Ca5                                     | 30106907                      | TAAAAAAAA/TAAAAAAAAA                                                                                                                           | GCCAGCAACCTCCAAT<br>TAAG   | TGCACATTGACCCAAAT<br>TGT     | 59.7                             | 779                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_30114759  | Ca5                                     | 30114759                      | TCGGCGG/TCGGCGGCGG                                                                                                                             | TTGCCTGAAACTCGAG<br>TAAAAA | ACGGGACTTTTTC AATT<br>CCG    | 59.1                             | 306                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_30121237  | Ca5                                     | 30121237                      | TTATATATATATATATATATATATA<br>TATATATA/TTATATATATATATATAT<br>ATATATATATATATATATATATATA                                                          | TTGCTTTTGAAAAATTG<br>TGGA  | TTGTGCAACCAAAAATG<br>GAA     | 58.3                             | 654                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_30121835  | Ca5                                     | 30121835                      | TTATATATATATATATATATATATA<br>TAT/TTATATATATATATATATATATA<br>TATATATATATATATAT                                                                  | CATGCGTGAATTGAT<br>CGTC    | AAACGCGTCACTTTAC<br>CTTCTC   | 60.1                             | 224                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_30126893  | Ca5                                     | 30126893                      | ATTTTTTTTT/ATTTTTTTTT                                                                                                                          | GTGGCTTCCAAGAGA<br>AACG    | TTCGGTACACAATTTTC<br>CCC     | 59.9                             | 612                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_30128968  | Ca5                                     | 30128968                      | GATTATAATTAATAA/GATTATAAT<br>TAAAAATAATTATAATTAAAAATA                                                                                          | TGTTTCTCTCTCGCT<br>CACA    | CCGCCGACTATACCTG<br>TTTT     | 59.7                             | 681                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_30131050  | Ca5                                     | 30131050                      | AATATATATATATATATATATA/AA<br>TATATATATATATATATA                                                                                                | CAAATTCGAGCAACA<br>ATGC    | AACACAAATGTTAAATT<br>GCGAAGA | 59.3                             | 571                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_30284983  | Ca5                                     | 30284983                      | ATATTATTATTATTATTATTATTA<br>TTATTATTATTGTTATTGTTATTATT<br>ATTATTAT/ATATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTGTTATTGTTATTATTATTATTAT | TGTTGTCACATGCTTT<br>GGGT   | TTGTGCACATTTTATTC<br>TTCAAA  | 60.0                             | 651                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_30337231  | Ca5                                     | 30337231                      | TTTGTGTTTAAATTGTGTTTAAAT<br>TGTGTT/TTTGTGTTTAAATTGTGT<br>T                                                                                     | TTGCCCAAGTTTTCAG<br>TTCG   | TCATACGATGTGGGG<br>TGTA      | 61.2                             | 679                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_30612967  | Ca5                                     | 30612967                      | TAAAAAAAA/TAAAAAAAAA                                                                                                                           | CGGCATATCATCACC<br>TTTT    | ACCCCCGAAAAAGTGC<br>TAGT     | 59.8                             | 378                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                 |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_30613533  | Ca5                                     | 30613533                      | CATATATATATATATATATATA/CA<br>TATATATATATATATATATATATA                                           | ACTAGCACTTTTTCGG<br>GGGT    | AAATCCATAATTGGTT<br>CACTCA | 60.0                             | 746                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_3063134   | Ca5                                     | 3063134                       | TAT/TATCAT                                                                                      | TTGTCTTCTTGTGGCC<br>GACT    | TTGAAGCCGAGAAAAC<br>GACT   | 60.8                             | 812                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_30712358  | Ca5                                     | 30712358                      | G/GGATAGAAA                                                                                     | TATTGGATTGGGCCAA<br>ACAT    | TTCTTTGGTTTGGGT<br>TCTC    | 60.0                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_30917049  | Ca5                                     | 30917049                      | CAAA/CAAAA                                                                                      | GTGCGCTAATGCTTCC<br>ATTT    | CTCTCCAAGGTTCTAC<br>CCCC   | 60.2                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_30990176  | Ca5                                     | 30990176                      | TTTTATTTATTTATTTATTTATTT<br>TATTTATTTATTTAT/TTTTATTTATTT<br>ATTTATTTATTTATTTATTTATTT<br>TATTTAT | GAATCCCCAAACAAA<br>CCCT     | CACACCACCAGCATTTT<br>GAC   | 60.0                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31051193  | Ca5                                     | 31051193                      | AATATATATATATATATATAT/AA<br>TATATATATATATATATATATAT                                             | GCCCGAAAACAATTAA<br>GACC    | GCAATTTCTCAGTCAAT<br>TTCAA | 58.6                             | 686                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_3106419   | Ca5                                     | 3106419                       | CACA/CACATAACTACA                                                                               | CAATTTTCGTGATGTG<br>GCAG    | TGAGTGATGCGAGTTG<br>TTCG   | 60.1                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31068432  | Ca5                                     | 31068432                      | TTTATTATTATTATTATTATTATT<br>ATT/TTTATTATTATTATTATTATT<br>TATTATTATT                             | AGCAAATTGATTAATCG<br>CAAA   | TTCAATAGGAGGTCGA<br>GTTTTT | 57.5                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31144433  | Ca5                                     | 31144433                      | CAA/CA                                                                                          | ATGGGAACACAAATCA<br>CCGT    | TTGGGAACCTCGTAAC<br>AGCA   | 60.1                             | 259                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31153866  | Ca5                                     | 31153866                      | ATTT/ATT                                                                                        | TGAACAATATTTCTCTT<br>CCAGCA | TTGTGTGGAGGTAAAA<br>GCC    | 58.9                             | 885                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_31154228  | Ca5                                     | 31154228                      | TTGTGTGT/TTGTGTGTGT                                           | GACCATACTTCAATTT<br>ATGCCAA | TTGTGTGGAGTAAAA<br>GCCC     | 59.3                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31154924  | Ca5                                     | 31154924                      | CAA/CA                                                        | GTGGGTGTACCGGAAC<br>AAAT    | GCCATATTCGAGTTCA<br>ACGG    | 59.6                             | 115                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_3115746   | Ca5                                     | 3115746                       | CAAAAAAAAA/CAAAAAAAAA                                         | GCAACATGGGATGATT<br>CAGA    | TCCAAGTCGTTCAGCT<br>TGTG    | 59.5                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31166296  | Ca5                                     | 31166296                      | TGAGAGAGAGAGAGA/TGAGAGAGA<br>GAGAGAGA                         | ATTGAAGGAGCAGAAG<br>CGAA    | GTCAACCTCTCTCTCG<br>CTGG    | 60.1                             | 144                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31187017  | Ca5                                     | 31187017                      | A/AAT                                                         | GTGTCCTTCGGTGGAG<br>GAAA    | TGACGTTGATAGAAAC<br>GAAGACA | 60.1                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31187958  | Ca5                                     | 31187958                      | AAATAATAATAAT/AAATAATAATAAT<br>AAT                            | CATTCCCCTTAAGCA<br>CGAG     | TTTCTCGCCTCGAACA<br>CTTT    | 59.7                             | 197                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31237915  | Ca5                                     | 31237915                      | TAAAAAAAA/TAAAAAAAA                                           | ACACAAATTCGCCAAA<br>ATCC    | CATCATGCCTCAAGAT<br>CACG    | 59.8                             | 768                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31291175  | Ca5                                     | 31291175                      | CTATTTATTTATTTATTTATTT/CTATTTATTTATTTATTT                     | GAGTTCTGATATTTGA<br>TGCCAA  | CCCACAACCTCCTACAA<br>CCC    | 58.3                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31324450  | Ca5                                     | 31324450                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                     | GAAATCAACGTGGATG<br>AGTCAA  | TAGCAAGCAAGCAGCA<br>AAAA    | 60.0                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31342028  | Ca5                                     | 31342028                      | TTATATATATATATATATATAT/TTATATATATATATATATATATAT               | TTTCCCGGCTCAAAAC<br>TTTA    | CGATCACAATTGAAAG<br>GGGT    | 59.7                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                     |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_31420220  | Ca5                                     | 31420220                      | ATTTTTTTTT/ATTTTTTTTT                                               | TTGCTTGCTGGCTTCT<br>TTTT    | ATTTCTCCTCCATTCT<br>CCC   | 60.1                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31599333  | Ca5                                     | 31599333                      | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATAT               | CACAGTATGAAACGTC<br>ACCCA   | ATATGCCTCTGACGGA<br>CGAC  | 59.5                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31621509  | Ca5                                     | 31621509                      | CT/CTGTATATCTACTTT                                                  | ATCCGAGTTTGCGTAT<br>GTCC    | GGGACGTGGAGATTGT<br>TGAT  | 60.0                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31663882  | Ca5                                     | 31663882                      | GATATATATATATATATA/GATATA<br>TATATATATATATATA                       | TCGATCATGATGGGAA<br>GACA    | GTTTCATGATGGTGAC<br>CAAA  | 60.0                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_317066    | Ca5                                     | 317066                        | TAAA/TAAAA                                                          | GAGCATTGATCCGGAT<br>TGTA    | TTTGACGATGCAACGG<br>TTTA  | 59.9                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31790895  | Ca5                                     | 31790895                      | GTTTTTTTTTTTT/GTTTTTTTTTTTT<br>T                                    | TGAACAAAATAACGTC<br>GAACTCA | ACTTGAGTCTGGCGCC<br>TTAG  | 59.7                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31821908  | Ca5                                     | 31821908                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                           | TGGGTGGTATCCAAGA<br>AAGC    | TGCTCTTTGCGACCCT<br>TACT  | 59.9                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31835054  | Ca5                                     | 31835054                      | CTTT/CTTTCCTTTTTTT                                                  | GCAAGGAACAAGGTAA<br>CCCA    | CCAACAAAAGAGGGG<br>AGTT   | 60.0                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31858708  | Ca5                                     | 31858708                      | GTCAA/G                                                             | CTCCAGCTTTTGGGGA<br>CATA    | TCTTCTGCTTGAGAC<br>AAAACA | 60.1                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_31941021  | Ca5                                     | 31941021                      | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATAT<br>ATATATATA | CGTAAACAAGGCCAA<br>ACAC     | GCCCCCTTCAATAATC<br>CAT   | 60.4                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_31961640  | Ca5                                     | 31961640                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATATAT                 | AAAAATCACGGCAAAT<br>CAAA  | TAAGATGTGCATGGGA<br>TGGA  | 59.5                             | 549                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_32095261  | Ca5                                     | 32095261                      | GAAAAAAAA/GAAAAAAAA                                           | CTCTCAAGTTCAACCA<br>CGCC  | ACTGAAGAGTGACGCC<br>AACA  | 60.8                             | 677                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_32139547  | Ca5                                     | 32139547                      | ATTAT/A                                                       | GCGACTTCGCAATGTG<br>TAGA  | GTTAAGGAAGTCCGCG<br>TTTG  | 60.0                             | 531                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_32290531  | Ca5                                     | 32290531                      | ACCCCC/ACCCCCC                                                | TTGGAAATGGGCCAC<br>TTAG   | CACCACGTCAGATTT<br>TCCT   | 59.9                             | 545                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_32299791  | Ca5                                     | 32299791                      | ATTTTTTTTT/ATTTTTTTTTT                                        | CAAGCAAAACCCTCAA<br>AAGC  | GGCGGATCAACTCTTT<br>GTGT  | 59.9                             | 364                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_32302712  | Ca5                                     | 32302712                      | AATATATATATATATATATA/AA<br>TATATATATATATATATA                 | CCATCATCTTTTCGTCC<br>GAT  | GTGCTCAGCAATTCAG<br>GGA   | 59.9                             | 263                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_323043    | Ca5                                     | 323043                        | CTTTATTTATTTAT/CTTTATTTATTT<br>ATTTAT                         | ATGGTCTCAAAGATGC<br>AGGG  | TGTGGCGAAAAACAAA<br>TCAA  | 60.1                             | 795                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_32364771  | Ca5                                     | 32364771                      | TAAAAAAAA/TAAAAAAAA                                           | TCCTCAGTTTCGAAG<br>AGGA   | CCC GCCATCACTCACT<br>ATTT | 59.9                             | 760                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_32396570  | Ca5                                     | 32396570                      | TATAATAATAATAAT/TATAATAA<br>TAATAAT                           | CAGCTGTT CAGATCCG<br>GTTT | TGGATCGAGAAGAAAG<br>TGCC  | 60.3                             | 810                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_32471582  | Ca5                                     | 32471582                      | ACAACCT/A                                                     | AGTCGCCATTGAAAC<br>TTGG   | AATGCATTTTGGCCTG<br>AGAA  | 60.1                             | 560                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_32522095  | Ca5                                     | 32522095                      | TTATATATATATATA/TTATATATATA<br>TA                                       | GCTGTTATGTTTGGTT<br>CGCA | GGGTTTTGCCTTCTCC<br>ACTC  | 59.7                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_32605650  | Ca5                                     | 32605650                      | TAAAAAAAAA/TAAAAAAAAA                                                   | TCAATCACAAATCAGG<br>GTGC | ATCCAGATCCAATACG<br>ACGG  | 59.5                             | 874                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_32610734  | Ca5                                     | 32610734                      | TAAAAAAAAA/TAAAAAAAAA                                                   | ATCCAGCCGTAAAAAC<br>AACG | GCTGGGGTTTGAAAA<br>TCCT   | 60.0                             | 832                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_32649227  | Ca5                                     | 32649227                      | ATTTTTTTTT/ATTTTTTTTT                                                   | TTCTTCTGCTCGATT<br>TTT   | TTGTTTTGCTAACTTG<br>TCCGA | 60.0                             | 279                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_32739425  | Ca5                                     | 32739425                      | GTTTTTTTTTTTT/TTTTTTTTTT<br>TTT                                         | TTGGCGTGTGAGACAG<br>AAAA | AATCCGCACGAGCATA<br>ATTC  | 60.4                             | 307                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_32739512  | Ca5                                     | 32739512                      | ATTTTTTT/ATTTTTTTTT                                                     | TTGGCGTGTGAGACAG<br>AAAA | AATCCGCACGAGCATA<br>ATTC  | 60.4                             | 307                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_32745764  | Ca5                                     | 32745764                      | TAAA/TAAAA                                                              | AGGCATCACATTGAGG<br>GACT | CCTCGGTGACCCTGAA<br>TAAA  | 59.5                             | 148                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_32769672  | Ca5                                     | 32769672                      | GATATATATATATATATATATATA<br>TATATATA/GATATATATATATATATA<br>TATATATATATA | CATGGCGTGAGTGAGT<br>GAGT | TCACGGTCCATGAAG<br>AACA   | 59.9                             | 760                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_32771430  | Ca5                                     | 32771430                      | ATTTTTTTTT/ATTTTTTTTT                                                   | GGGACAGTAGGGTTCC<br>CAAT | GGAGACCTTTACATC<br>GCTC   | 60.1                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_32771738  | Ca5                                     | 32771738                      | AT/ATT                                                                  | GAGCGCTGTAAAAGAC<br>CACC | CGTTGTAAAAGGATTG<br>CGCT  | 59.9                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                      | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                    |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_32849143  | Ca5                                     | 32849143                      | TAAAAAAAAA/TAAAAAAAAA                                                                                              | CCCAGTTAACAAAGG<br>GGAA    | TCACCGTATGCAAGA<br>CGAG     | 58.9                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_32849892  | Ca5                                     | 32849892                      | TTATATATATATATATAT/TTATAT<br>ATATATATATATATAT                                                                      | GATGTACCAAGACATC<br>GCCA   | TCGAATAAGGGATGAA<br>TAACAGG | 59.5                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_32879637  | Ca5                                     | 32879637                      | AGTAAACAATGTAAACAA/AGTAAAC<br>AA                                                                                   | TCCTGCTAAAGATGGT<br>CATTCA | TTGTTGTAGGATGGAT<br>GGAGTG  | 59.7                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_32912336  | Ca5                                     | 32912336                      | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATA<br>TATATATATATAT                                            | ACCCCTCACCTCCTT<br>ATTG    | TTTTCTTGCCTCACTTG<br>TTGA   | 60.2                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_32950457  | Ca5                                     | 32950457                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT/<br>AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>ATAAT | ATTGCCACATTTTCATGC<br>TCA  | GAATTCCTTACAATCG<br>GCAA    | 60.1                             | 345                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33047107  | Ca5                                     | 33047107                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAA/<br>ATAATAATAATAATAATAATAAT<br>ATAATAATAATA                      | TAGAAAGGGCCAGAAA<br>AGCA   | CGATACAAGTCGTAGG<br>AAGGG   | 60.0                             | 236                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33223744  | Ca5                                     | 33223744                      | ACGAACATATTC/AC                                                                                                    | GGAGAGGAGCCAAGA<br>GAACC   | CCAATGACGAATATTG<br>CACG    | 60.3                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33354598  | Ca5                                     | 33354598                      | TAAAAAAAAA/TAAAAAAAAA                                                                                              | TGACAGTTACAAACCG<br>CTGC   | CAATTCTACCAATTC<br>CCCA     | 59.9                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33355834  | Ca5                                     | 33355834                      | TAAAAAAAAA/TAAAAAAAAA                                                                                              | ATTCCCGAGAATCCAC<br>ACAA   | AAGCCGGAGAATTGAA<br>TGTG    | 60.3                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33395960  | Ca5                                     | 33395960                      | AATTATTATTATTATTATT/AATTATT<br>ATTATTATT                                                                           | TTTATCGGCTAAGGGA<br>CACG   | GTGCTGCCTAGACAAT<br>CGGT    | 60.1                             | 768                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                      | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                    |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_33438225  | Ca5                                     | 33438225                      | CTTTTTTTTTTT/CTTTTTTTTTTT                                                                                          | ACTTAAGCGGCGTCAA<br>CTGT  | CACTTGTGCGTTGCAT<br>ATGAG | 59.9                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33439122  | Ca5                                     | 33439122                      | ATT/ATTT                                                                                                           | AAATCGATCAAACCTCG<br>CACC | CGAAATTCGATACTCG<br>ACCG  | 60.1                             | 347                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33441420  | Ca5                                     | 33441420                      | ATTT/ATTTT                                                                                                         | GTGTGTGAGAGGTTGT<br>TGCG  | TAACCTGAACCAACCG<br>ATCC  | 59.0                             | 204                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33541448  | Ca5                                     | 33541448                      | ATAATTTTTTTTTTAATTTTT/ATAA<br>TTTTTT                                                                               | GCTTTGATTTGGGCTT<br>TGAG  | CCAAAAACCGAATTTC<br>CCA   | 59.8                             | 877                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33542100  | Ca5                                     | 33542100                      | GTTTATTTATTTATTTAT/GTTTATTT<br>ATTTATTTATTTATTTAT                                                                  | AATTCGGTTTTTGGCG<br>TGTA  | GTTAAGGGACCACGAA<br>TGCT  | 60.4                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33549168  | Ca5                                     | 33549168                      | TAAAAAAAA/TAAAAAAAA                                                                                                | CAAAACGGGTTTCAC<br>CAAC   | GCTCTGCATCCAATTC<br>CATT  | 60.2                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33567356  | Ca5                                     | 33567356                      | GATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAA/GATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAA | AGCAAGTCACCTTGTC<br>CGTT  | TGGGTTTTGCATAGTC<br>GGTT  | 59.8                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33606817  | Ca5                                     | 33606817                      | ATTTTACTTGTTTT/ATTTT                                                                                               | GACCTTGCCGGCTACT<br>CTCT  | ATATTTCTCATAGGGG<br>CGGC  | 60.9                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33682329  | Ca5                                     | 33682329                      | GATATATATATATATATATATATA<br>T/GATATATATATATATATATAT                                                                | AACGGTGAGGTGTGG<br>GTAAA  | TGAGGATTTTGTGCA<br>CTCG   | 60.3                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33797968  | Ca5                                     | 33797968                      | AT/A                                                                                                               | GCGGAATGACCTACCG<br>AATA  | ATAGGCTAGGTCGTCC<br>GTCA  | 59.9                             | 263                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_33798523  | Ca5                                     | 33798523                      | ATTTTT/ATTTTT                                                 | TGACGGACGACCTAGC<br>CTAT    | TCATTTTCCCAATCTCT<br>CCG    | 59.7                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33883232  | Ca5                                     | 33883232                      | AATTTAACTATATTT/AATTT                                         | TGACATAAAGCACCCAC<br>TGTTCA | TCCTACGGTCTTGTTTT<br>GGG    | 59.2                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33908663  | Ca5                                     | 33908663                      | TTTTTATTTTATTTTATTTTATTTT<br>TTTATTTTATTTTATTTTATTTT<br>T     | ATCGAAATGTGCGTGA<br>ACAA    | GCAGCTTCTTTTCATTC<br>GCT    | 60.1                             | 373                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_33967986  | Ca5                                     | 33967986                      | AATATATATATATATATATA/AAATA<br>TATATATATATATA                  | ATTGGTTAGGCGAAGA<br>TGGA    | TTCCCTCCCCTTTCCTA<br>AAA    | 59.5                             | 506                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_34220162  | Ca5                                     | 34220162                      | GAAAAAAAAA/GAAAAAAAAA                                         | CCACTAACCTATTCGG<br>AATCCA  | GGCAATTGTCGGCACT<br>TAAT    | 60.2                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_34466553  | Ca5                                     | 34466553                      | TAAAAAAAAA/TAAAAAAAAA                                         | TGTTGTTCTCTTTTCA<br>CGTTG   | ACCAAAGTAATGCGGT<br>TGAA    | 60.2                             | 762                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_34523237  | Ca5                                     | 34523237                      | GTTTTTTTTT/GTTTTTTTTT                                         | ATTGAACTCGGAGACG<br>GAAA    | CCTTGACCCTGAACCA<br>AATC    | 59.7                             | 457                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_34546420  | Ca5                                     | 34546420                      | TAGAGAGAGAGAGA/TAGAGAGAGA<br>GA                               | TGTCGGCCACTCAAAC<br>ATAA    | TTGGGTTTTCATACAAT<br>CATGTG | 60.1                             | 330                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_34716959  | Ca5                                     | 34716959                      | GA/GAGGGAATTGTAGGGAAA                                         | AATTCGCAAGAAATCT<br>CAGCA   | AGGGGCTGCATGAACA<br>ATTA    | 60.0                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_34851417  | Ca5                                     | 34851417                      | TA/TAA                                                        | GACAGAGAGATGACGG<br>GGAA    | AAACCGAAAAGTTGAAA<br>AACTGA | 60.2                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                        | Forward primers (5'-3')        | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------------|--------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                      |                                |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_34981999  | Ca5                                     | 34981999                      | ATTTTTTTTT/ATTTTTTTT                                                                                                                 | ATGTACCCGCACCAGA<br>ACTC       | TTCAGGTTTCTCCACC<br>CAAC   | 60.0                             | 249                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35032056  | Ca5                                     | 35032056                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATA/AAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA | GTGGAGTTGGGGAGA<br>GTCTG       | TTTCATGAGCAAACCAA<br>GCA   | 59.7                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35048447  | Ca5                                     | 35048447                      | AATATATATATATA/AATATATATATA<br>TATA                                                                                                  | TGGAGTTAGGAGGATT<br>CATGG      | TCAACCGTTGTTACAT<br>GTTC   | 59.0                             | 952                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35058244  | Ca5                                     | 35058244                      | TGA/T                                                                                                                                | TACACCGGTGGGATT<br>GACT        | CCTTTACCTCCCATT<br>CCA     | 60.2                             | 798                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35070670  | Ca5                                     | 35070670                      | TATTAATTAATTAATTAATT/TATTA<br>TTAATTAATTAATTAATT                                                                                     | TGTGACCTGCAGTGAT<br>ATTTTG     | ATAATGTTGCGAATGG<br>AGGC   | 58.7                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35091533  | Ca5                                     | 35091533                      | TATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAA/TATAATAATAATAATA<br>ATAATAATAATAATAATAATAA                             | TGGTGTGTAATAATAA<br>AAAGCTAAAA | TGATAATGCATGGAAA<br>GCAAA  | 57.0                             | 237                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35115270  | Ca5                                     | 35115270                      | TA/T                                                                                                                                 | CCACCAATTCGCAAG<br>TATT        | AAAGAGGCAGGTAGGG<br>TCGT   | 59.8                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35149505  | Ca5                                     | 35149505                      | CTTTTTTTTT/CTTTTTTTTTT                                                                                                               | CAATCACATGGCTTGG<br>ATGA       | CAGCCACACCGATTAC<br>CTTT   | 60.5                             | 400                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35247530  | Ca5                                     | 35247530                      | TAAAAAAAA/TAAAAAAAAA                                                                                                                 | GCTCACACGAGTGTTA<br>ATGGAA     | GAAAAGTAGCAAGTAC<br>GGGTCG | 60.2                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_3526464   | Ca5                                     | 3526464                       | AATATATATATATATATATATA/AA<br>TATATATATATATATA                                                                                        | TTAAGGAAGCCCAAGT<br>TCCA       | AAAAAGCCTTTGGGAA<br>ATCG   | 59.7                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                     | Forward primers (5'-3')    | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------|----------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                   |                            |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_35328160  | Ca5                                     | 35328160                      | ATTTTTTTTT/ATTTTTTTTT                                                                                                             | ACCACGTGACCCCTTA<br>ACTT   | TGATGAAATTACGTTAT<br>ATTGAGGATG | 58.4                             | 204                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_3535001   | Ca5                                     | 3535001                       | ATTTTTTTTT/ATTTTTTTTT                                                                                                             | TACCTTCAAGTGGGCC<br>AAAC   | TGACCCCATCAAGGCT<br>TTAG        | 60.0                             | 300                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35397670  | Ca5                                     | 35397670                      | AATATATATATATAT/AATATATATAT<br>ATATATAT                                                                                           | GGGGTGAATATCCTTT<br>TCATTG | CATACACACGCATTAG<br>AGCATT      | 59.6                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35425903  | Ca5                                     | 35425903                      | GATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAA/GATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAA | CACCAAAGTTCGTTGG<br>ACCT   | CCTCATCATCTTCGTTG<br>GTTC       | 60.0                             | 837                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35462508  | Ca5                                     | 35462508                      | CATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>T/CTTTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATT   | AGTAAACAAGCACCA<br>CCGC    | CTTTTGCTCACACCCAA<br>CAA        | 60.2                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35463186  | Ca5                                     | 35463186                      | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATATA                                                                           | GTGAGCAAAAGCATCA<br>TTCG   | TCTTGCTTATTTCTCTC<br>AAAGCA     | 59.4                             | 987                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35485623  | Ca5                                     | 35485623                      | TAAAAAAAA/TAAAAAAAA                                                                                                               | CCCAACTTCTTCATTGC<br>CTC   | GGACCCAGCAGAGTTG<br>GTAA        | 59.7                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35495079  | Ca5                                     | 35495079                      | AATATATATATATATATATATATA/<br>ATATATATATATATATATATAT                                                                               | ATTCTAGCATGGTGG<br>GACG    | CGTGTTGATTGAAATG<br>AGCG        | 60.0                             | 854                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35595695  | Ca5                                     | 35595695                      | TTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAAT/TTAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAAT                                | ACCATTCAAACGGCGA<br>GTAG   | ATGCAATCGTATCTCGT<br>GGT        | 60.1                             | 306                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35599782  | Ca5                                     | 35599782                      | TTATATATATATATATATATA/TTA<br>TATATATATATATATATA                                                                                   | ATTCCAACTGTTTGG<br>GCAG    | TACTAGATCGCGTCCC<br>ACG         | 60.0                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')       | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|-------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                           |                               |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_35701781  | Ca5                                     | 35701781                      | T/TTAA                                                                    | TCCGACACATCTCGAA<br>TAGAA     | TTAAAAACATGGCGATT<br>CTGC    | 58.3                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35751387  | Ca5                                     | 35751387                      | AATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATATA<br>TATATATATATAT | TCATTTTTCTTTCAATT<br>TTGTCCTT | TTTTCACCTGGCATCCA<br>TCC     | 59.5                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_3575663   | Ca5                                     | 3575663                       | A/AC                                                                      | TTTGACGAAGAGCCAT<br>GTTG      | CGGGAATCAGTTTTGA<br>GGAA     | 59.8                             | 254                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35783091  | Ca5                                     | 35783091                      | ATATATTTATATTTATATTT/ATATAT<br>TTATATTTATATTTATATTT                       | TGACATCTCGTCGACA<br>TTTTATC   | TGAATTAGATGATTGTG<br>GTGAAGG | 59.1                             | 819                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35836224  | Ca5                                     | 35836224                      | ATTTTTTTTTTT/ATTTTTTTTTTTT                                                | TAGGGAAAAGGGTGGT<br>GTGA      | GAGACATTTTGTGCTG<br>GCCT     | 60.3                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35872148  | Ca5                                     | 35872148                      | TAAAAAAAAAAAA/TAAAAAAAAAA                                                 | ACCCTCACGTAAGCCT<br>GATG      | TCGCCTTCGTAATAAC<br>GATT     | 60.1                             | 357                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35899388  | Ca5                                     | 35899388                      | CTTTTTTTTTT/CTTTTTTTTTTT                                                  | TTTGAGCTAGCATGCA<br>CACC      | CGATCTCCATTTGCGTT<br>TTT     | 60.0                             | 688                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_35915901  | Ca5                                     | 35915901                      | ATTTTTTTTTT/ATTTTTTTTTT                                                   | AGCATGTGTTCTTGTG<br>GCAG      | TCGGAAGTTTCACATTC<br>ATCC    | 59.9                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_36023155  | Ca5                                     | 36023155                      | TCCCC/TCCC                                                                | CAATCCGAGAGATTTA<br>GGTGG     | ATTTTGTAAATGACGGC<br>CCA     | 58.7                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_36031906  | Ca5                                     | 36031906                      | A/ATCTATTATTATT                                                           | TTGAATGCAGGCAAAAC<br>CATA     | AAGGATGCACCATTGC<br>TACC     | 60.1                             | 914                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                 | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_36101390  | Ca5                                     | 36101390                      | TAAAAAAAAA/TAAAAAAAAA                                                                                         | AGAGCAAAATCCTTT<br>CGTGA    | TAGTGCAATGGGCC<br>TCTC     | 59.0                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_36317817  | Ca5                                     | 36317817                      | CTTTTTTTTT/CTTTTTTTTT                                                                                         | TCTCACCTCGGACACC<br>AAAT    | TGGAAGGTACAAGTGA<br>GGGG   | 60.5                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_36414102  | Ca5                                     | 36414102                      | AATATATATATATATATA/AATATATA<br>TATATATATATA                                                                   | TGTTGCAAAGCATAAC<br>TTGACC  | TGTGACCATGATTTGT<br>GGG    | 60.2                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_36583877  | Ca5                                     | 36583877                      | CATATATATATATATAT/CATATAT<br>ATATATATATATAT                                                                   | TCACTTTTAGGATCCG<br>TTTGA   | CACAATGGACCATGCA<br>CTTC   | 57.4                             | 809                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_36657829  | Ca5                                     | 36657829                      | CTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATT/CTTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATT | CGTGAGATTTTCTGCT<br>CGGT    | AGAGGTCTTCCGTGTA<br>TGCC   | 60.4                             | 877                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_36702458  | Ca5                                     | 36702458                      | AATATATATATATATATATATATAT<br>AT/AATATATATATATATATATATATA<br>TATATAT                                           | CACCCGACTAATCGGA<br>GAAA    | TTTGGCCCCAGCAAAT<br>ATAC   | 60.1                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_36814159  | Ca5                                     | 36814159                      | TTATATATATATATATATATATATA<br>/TTATATATATATATATATATATA                                                         | GGAGTAAATTTGCAAG<br>TCAAAGC | TTTCACGCACTCAACTC<br>GTC   | 59.3                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_36904833  | Ca5                                     | 36904833                      | GCTCTCTCTCTCTCTCTCTCTCTCT<br>CTCTCTC/GCTCTCTCTCTCTCTCTC<br>TCTCTCTCTCTCTCTCTC                                 | TTCTGGAGAAAGAGGC<br>GAAG    | TGCGTAATTTGGTGCT<br>GGTA   | 59.7                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_36963374  | Ca5                                     | 36963374                      | CTTTATTTATTTATTTATTTATT/CTT<br>TATTTATTTATT                                                                   | TGCCGCTGTGTCAGTT<br>AGTT    | GACAATTATTTGTCAA<br>TGACGC | 59.5                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_36963472  | Ca5                                     | 36963472                      | TATAATAATAATAATAATAATAAA<br>TAATAATAATAATAATAA/TATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAA                 | TGCCGCTGTGTCAGTT<br>AGTT    | GTACCGCTCGGTCTC<br>TAAA    | 59.5                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                 |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_37010323  | Ca5                                     | 37010323                      | TAT/TAGTATATTGAT                                                                | TGCGTGAAAGGTTGAA<br>AATG  | TTGGTTTCATTGTGG<br>GAAT    | 59.7                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_37188296  | Ca5                                     | 37188296                      | TT/TTAT                                                                         | TCAAACCCCATTTTTC<br>TTG   | CGAAGCTGGCCGTTTA<br>TTTA   | 59.8                             | 809                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_37200733  | Ca5                                     | 37200733                      | CATATATATATATATATATA/CATATA<br>TATATATATATATATA                                 | CATGCATGGTTTCTTCT<br>CCA  | TCCGTCTTTAATGGGAT<br>TGG   | 59.6                             | 161                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_37218586  | Ca5                                     | 37218586                      | TATACATACATACATACATATA/T<br>ATACATACATACATACATA                                 | CACTCGTATCATGCTT<br>GTCG  | CTTTTCGCCACCATTT<br>GTT    | 57.9                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_37222608  | Ca5                                     | 37222608                      | CTATATATATATATATATATAT/CT<br>ATATATATATATATATAT                                 | AAACTCGGTTGACCTT<br>GCAC  | ACGAGCGTTGAAGCTT<br>GATT   | 60.2                             | 348                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_37235701  | Ca5                                     | 37235701                      | AATATATATATATATATATATATA/<br>AATATATATATATATATATATA                             | GTTGGAGCCAAAAC<br>AGCG    | ACATTCATTGGCCCTTT<br>TGA   | 59.9                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_37278974  | Ca5                                     | 37278974                      | CTATTTATTTATTTATTTATTTATTTA<br>TTTATT/CTATTTATTTATTTATTTAT<br>TTATTTATTTATTTATT | AGTGAGTGGAATCGG<br>GTTG   | AACGTCCCATCAAGTT<br>CACA   | 60.0                             | 199                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_3742109   | Ca5                                     | 3742109                       | TT/TTACATAT                                                                     | ATTTACGAGCAGCGGA<br>AAGA  | TGGTCATGCAGAACT<br>CAGC    | 60.0                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_37633576  | Ca5                                     | 37633576                      | TAAAAAAAAA/TAAAAAAAAA                                                           | TGCAATGTTAAAGATG<br>GTTGG | GTGCGAATTTGTGATT<br>ACTGA  | 58.5                             | 264                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_37670957  | Ca5                                     | 37670957                      | GTTTTTTTTT/GTTTTTTTTT                                                           | GCCTGCTCTTCTTTTT<br>GGTG  | TGAAAATATACATCTGT<br>GGGGG | 60.0                             | 294                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                 |                               |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_37690036  | Ca5                                     | 37690036                      | TAAAAAAAAA/TAAAAAAAAA                                           | GGAGACGAGAAGGTC<br>GTGAG      | TTTTTATTCAAGTTGGC<br>CCG   | 60.0                             | 270                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_37851777  | Ca5                                     | 37851777                      | CATTTATTTATTTATTTATTTATTT/C<br>ATTTATTTATTTATTTATTTATTTATT<br>T | TGCTTGTAATCACAACA<br>AGACCT   | GCCAACTGCTTTGGGT<br>AGAA   | 58.8                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_37905515  | Ca5                                     | 37905515                      | ATTTTTTTTT/ATTTTTTTTT                                           | TGATCGAAGACAATTT<br>GTGTCA    | CCGATCTCACATGCTT<br>CCTT   | 59.2                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_37930695  | Ca5                                     | 37930695                      | TT/TTTTCATAGGT                                                  | TCCTTGCTCCACTTTTC<br>CAT      | TGGTTGATTGGCTGAT<br>TAATTG | 59.7                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_37953081  | Ca5                                     | 37953081                      | ATATTTTAATTATTTTAA/ATATTTTA<br>A                                | TCAAATTGCCACACTCT<br>AAAAA    | TGCAAAATATGTTTGG<br>ATTGTC | 57.5                             | 834                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_37955990  | Ca5                                     | 37955990                      | ATTTTT/ATTTTTTT                                                 | GGCAAGACAAAAGAC<br>AACGA      | CCGTGATTGCAACTAA<br>GTGAA  | 60.3                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38005397  | Ca5                                     | 38005397                      | CTCT/C                                                          | TGAGAGACCTTGATTG<br>ATACAAATG | TCAATTTGGTTCCAACG<br>TCAT  | 59.6                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38006809  | Ca5                                     | 38006809                      | G/GATCGTT                                                       | TGGAAGTGCATATGAT<br>GTTGG     | CGAGGTGTTGCACATG<br>ACTT   | 59.4                             | 585                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38023980  | Ca5                                     | 38023980                      | AACACAC/AACAC                                                   | CCGCAGTAAGAGTTTG<br>ACCA      | TTCGGAGGAATGGTTG<br>TTTC   | 58.9                             | 548                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38025852  | Ca5                                     | 38025852                      | AT/A                                                            | ATGCCAAAAATAAACG<br>CCAG      | TGAGGTTGAGAAGCCA<br>AACC   | 60.0                             | 647                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_38027475  | Ca5                                     | 38027475                      | T/TA                                                          | TGGAGTGATACACT<br>TTGTGG  | TGCTTACAAGGTATTCT<br>TGCCA | 59.9                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38033573  | Ca5                                     | 38033573                      | GTTTTTTTTT/GTTTTTTTTTTT                                       | AAAGCGGCATTATCTC<br>GTTG  | CGCGTCAAATAAAGCA<br>TTGA   | 60.2                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38034465  | Ca5                                     | 38034465                      | AATTATTAT/AATTAT                                              | TGCTATTGCGATCCCT<br>CTCT  | TTGTGCGTATAAATCG<br>GACG   | 59.9                             | 311                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38034605  | Ca5                                     | 38034605                      | CG/CGG                                                        | CTGCTATTGCGATCCC<br>TCTC  | TTTTGAACGCAAGAAAA<br>CAGAA | 59.9                             | 800                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38034644  | Ca5                                     | 38034644                      | GTAT/GTATATAT                                                 | CTGCTATTGCGATCCC<br>TCTC  | TTTTGAACGCAAGAAAA<br>CAGAA | 59.9                             | 800                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38034841  | Ca5                                     | 38034841                      | TTTA/TTTAATTA                                                 | TCGTCCGATTTATACC<br>GACA  | CGACGAGGTATATGCC<br>AACA   | 59.0                             | 856                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38036769  | Ca5                                     | 38036769                      | TAA/TA                                                        | TGATAACTCGTCGGCT<br>TGTG  | TTTTTCCTTCCAAATAA<br>GCCTC | 59.9                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38042717  | Ca5                                     | 38042717                      | CAAAAAAAAA/CAAAAAAAAA                                         | TTGGACCAAACTGAT<br>GAAAAA | CCAAAGTTGCCTTGTC<br>CTTC   | 59.5                             | 716                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38043767  | Ca5                                     | 38043767                      | GTTTTTTT/GTTTTTTTTTTTTT                                       | AGGAGGCTAATTGAGG<br>GAGC  | TGTGGGTGCATGGTAG<br>AAAA   | 59.8                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38043824  | Ca5                                     | 38043824                      | ATTTTT/ATTTTTT                                                | AGGAGGCTAATTGAGG<br>GAGC  | TGTGGGTGCATGGTAG<br>AAAA   | 59.8                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_38046137  | Ca5                                     | 38046137                      | GT/GTAT                                                       | GCCCCAAATATGAATA<br>ACCG       | TGAAATGCGAAAGAGG<br>TGAA   | 59.1                             | 190                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38049889  | Ca5                                     | 38049889                      | TAAAAAAA/TAAAAA                                               | TCAAATGCATAATCATG<br>AAAGGA    | TCTCATTACAAAACGAC<br>CCA   | 59.4                             | 190                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38051854  | Ca5                                     | 38051854                      | TTTTCTTT/TTTT                                                 | AAAAGTTGGCCTTTCC<br>TAACAA     | TCAATTGTGTGCATCA<br>GTTTCA | 59.2                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38091321  | Ca5                                     | 38091321                      | C/A/C                                                         | TCTGTTGCTTCGCTGA<br>CATC       | GCTGGAATGGCTTTTG<br>GTTA   | 60.1                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38093452  | Ca5                                     | 38093452                      | TCTAG/TCTAGCTAG                                               | GCCTGCAGTCTCACTC<br>TTCC       | TGCTAAATTCTGCGAC<br>CCAT   | 60.1                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38094477  | Ca5                                     | 38094477                      | ATTTTTTTTT/ATTTTTTTT                                          | TCAATTGCACAAACAAT<br>TAGTTAAAA | ATTGCGAGCATGAGAA<br>GTTG   | 59.1                             | 147                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38100297  | Ca5                                     | 38100297                      | AC/ACGC                                                       | GTTGCCAGTTTTGGTC<br>CACT       | ATCGGATTAGGAAGGT<br>TGGG   | 60.0                             | 855                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38100833  | Ca5                                     | 38100833                      | TA/T                                                          | CGAATTTGAACCCGAG<br>ACAT       | CATCATAACCGAGCAC<br>ATGG   | 59.9                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38122220  | Ca5                                     | 38122220                      | A/AGTT                                                        | AGCCTAACCCTAAAC<br>CCAA        | TGTGCAAAAGTTTCAC<br>GACAT  | 59.8                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38126712  | Ca5                                     | 38126712                      | TAA/TAAAGGCTCAA                                               | GCATTACGACTTTGTT<br>GCGA       | TACGGAGGCCTAAGAC<br>CAAA   | 59.9                             | 234                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_38133701  | Ca5                                     | 38133701                      | TAAA/TAAAA                                                    | AAAGTTTCGAATGTGG<br>GGTG  | CGAATTGACCGAATTT<br>GTCC  | 59.8                             | 821                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38140361  | Ca5                                     | 38140361                      | GTATTATTATTATTATTAT/GTAT<br>TATTATTATTATTAT                   | TCACTCCACATCGGCA<br>TAAC  | TGCATATGACGTGAGA<br>TTTGG | 59.5                             | 782                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38140913  | Ca5                                     | 38140913                      | AT/ATT                                                        | CGTCATATGCAGATTTT<br>GCG  | AAGCCCAAAAAGAAAT<br>GAGG  | 60.2                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38141802  | Ca5                                     | 38141802                      | AC/ACC                                                        | TGGTCAGTTGAGGACA<br>AACG  | GAAGACAAGGTGGTGC<br>CAAT  | 59.7                             | 162                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38152938  | Ca5                                     | 38152938                      | TTTAGATTAAATTAGATTAAAT/TTTA<br>GATTAAAT                       | TTGTGAAGGAGGAGGA<br>CCAG  | GCGGAAAACGAGAAAT<br>TTTG  | 60.2                             | 950                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38154241  | Ca5                                     | 38154241                      | AAGA/AA                                                       | GCTTTTGGGTTGTTTCG<br>TGTT | TTTCCCCCTATTTTACG<br>GCT  | 60.0                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38154626  | Ca5                                     | 38154626                      | AG/A                                                          | TTGTGGGCAAGGTTGA<br>CATA  | AGGCACCACTTTTGAT<br>CGAC  | 60.0                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38155355  | Ca5                                     | 38155355                      | TTT/TTTATTTTATT                                               | TGTTGTTGTTGGATTG<br>GCAT  | AAACGGTATCGCGTTT<br>AACTT | 59.8                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38155410  | Ca5                                     | 38155410                      | TAAAAAAAA/TAAAAAAAA                                           | TGTTGTTGTTGGATTG<br>GCAT  | AAACGGTATCGCGTTT<br>AACTT | 59.8                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38155679  | Ca5                                     | 38155679                      | CTTA/CTTAATTA                                                 | TGTTGTTGTTGGATTG<br>GCAT  | AAAATGGAGCATTGGA<br>AAAA  | 59.8                             | 769                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                  |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_38165078  | Ca5                                     | 38165078                      | GTATA/GTATATA                                                    | AGCAGGAGCAAGGAA<br>CAAA    | CTGAAGGGGTGTGGT<br>GAGT    | 60.0                             | 678                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38229056  | Ca5                                     | 38229056                      | GCAT/GCATACAT                                                    | CAATCTGATCGTGGT<br>GGTG    | GGCTCTTGAGGCACTT<br>GTTC   | 60.0                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38255302  | Ca5                                     | 38255302                      | AAATAATAATAAAT/AAATAATAAT<br>AAT                                 | TGCCTCAACTCAACAC<br>TTGC   | CAATTTACCAATCGCAC<br>GAA   | 60.0                             | 762                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38407056  | Ca5                                     | 38407056                      | CT/C                                                             | TCTCAAAGTCTCAATG<br>GTCCAA | TTGAAGTCAAATTCGC<br>CAG    | 59.7                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38407176  | Ca5                                     | 38407176                      | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATAT<br>TATAT | TCTCAAAGTCTCAATG<br>GTCCAA | TTGAAGTCAAATTCGC<br>CAG    | 59.7                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_3862372   | Ca5                                     | 3862372                       | TAAA/TAA                                                         | TTCACATCCCCTCTAAA<br>CCAA  | TCCCAATGACTCATCG<br>TCAA   | 59.4                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_3865777   | Ca5                                     | 3865777                       | CTTTTTTT/CTTTTTTTT                                               | ATGTGACACCCTAAAC<br>CCCA   | TTGGTTTAGAGGGGAT<br>GTGAA  | 60.1                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_3869500   | Ca5                                     | 3869500                       | ATACAAAATTACAA/ATACAA                                            | CATTAATGTGTGCAA<br>GGATCAA | GAGAGGTTGAAGCCTC<br>AAAAGA | 59.9                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38704218  | Ca5                                     | 38704218                      | CATATATATATATATATATATATATA<br>TA/CATATATATATATATATATATATA<br>TA  | TTAACCTCACCCACTC<br>CACC   | ACCTTCGCAGCCAAT<br>ATCA    | 59.8                             | 395                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38718876  | Ca5                                     | 38718876                      | AATCAATTTATCAATTTAT/AATCAAT<br>TTATCAATTTATCAATTTAT              | CTTCGAAAAACCAAC<br>CGAA    | TGATTGCATAACCAGC<br>CAAA   | 60.1                             | 429                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                 | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_3874588   | Ca5                                     | 3874588                       | AC/A                                                                                                                                                          | GACCTTGCTTTGGGGT<br>TGTA   | CACATCCCCTCTAAAC<br>CAACC | 60.0                             | 409                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38755876  | Ca5                                     | 38755876                      | TA/TATGA                                                                                                                                                      | GAAGTTGAGCGCAATG<br>TTGA   | TTAAGACGGGTGATGG<br>AAGC  | 60.0                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38755924  | Ca5                                     | 38755924                      | TAAAA/TAAA                                                                                                                                                    | GTCTGCCACATCACCC<br>TTTT   | CGGATCAACTTTTCTTT<br>GTGG | 60.0                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38829826  | Ca5                                     | 38829826                      | CTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTAT/CTTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTAT | TGCAAAACAAAGTAACG<br>CCTG  | TGCTACAACCAAACGA<br>TGGA  | 59.9                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38866965  | Ca5                                     | 38866965                      | AATTATTATTATTATTATTATTATT<br>TATTATTAT/AATTATTATTATTATTA<br>TTATTATTATTAT                                                                                     | CGCCTTCGATCAACAT<br>CTTT   | GGTGCAGGAAGAAGA<br>AGAA   | 60.2                             | 730                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38880462  | Ca5                                     | 38880462                      | ATATT/AT                                                                                                                                                      | ACACGTGAGAGGCACA<br>AATG   | CAATTGCACGTGGAGT<br>GTTC  | 59.8                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38902709  | Ca5                                     | 38902709                      | TAAAAAA/TAAAAAA                                                                                                                                               | GAAGGGGTGAATGCTG<br>ACAT   | ATGACCCCTTCACTTT<br>GTG   | 59.9                             | 729                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38912622  | Ca5                                     | 38912622                      | AATATATATATATATATA/AATATATA<br>TATATATATATA                                                                                                                   | GTGGACCCCAATTTTC<br>AATG   | TCTCTCAAACCTCCAC<br>CAC   | 60.0                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_38998221  | Ca5                                     | 38998221                      | GAAAAAAAA/GAAAAAAAA                                                                                                                                           | ATGCGTGCGATAGGGA<br>ATAC   | TGCCAATACACATTTG<br>GGAC  | 60.0                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_39159883  | Ca5                                     | 39159883                      | CAAAAAAAAA/CAAAAAAAAA                                                                                                                                         | TTGTCAAATAAAAGAAA<br>GGGGG | TCTACCATTGCACAAA<br>CCA   | 59.4                             | 837                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')    | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                           |                            |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_39219117  | Ca5                                     | 39219117                      | TAAAAA/TAAAAA                                                             | TCACATTGACCAGGAA<br>TGGA   | TGTTGGAAAGGCTCTG<br>CTTT       | 59.9                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_39404451  | Ca5                                     | 39404451                      | AAAATATA/AA                                                               | TGATTGACACTTAGGC<br>CTGC   | TGCGTGCTGAATACCG<br>TTTA       | 58.9                             | 263                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_39448578  | Ca5                                     | 39448578                      | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATATA<br>TATAT           | TGGTTAAGAACGAACG<br>GGAC   | GCAACAAAGCACGGTG<br>AATA       | 60.0                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_39484033  | Ca5                                     | 39484033                      | GATATATATATATATATATATATA<br>T/GATATATATATATATATATATAT                     | TTGATATCTTAACAAT<br>GCGTCG | ACCAATGGTGGAGCTT<br>GAAC       | 59.2                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_39533615  | Ca5                                     | 39533615                      | TTATATATATATATATATATATATA<br>TATATATAT/TTATATATATATATA<br>TATATATATATATAT | TTTCATGTCATGGCAAGA<br>GTTT | GTTTTTCGTCCCGTCT<br>CAAA       | 59.3                             | 686                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_39537232  | Ca5                                     | 39537232                      | AATATATATATATATATATATATAT<br>ATATA/AATATATATATATATATAT<br>ATATATATA       | TTGGCAACCAGTCAAC<br>AAAA   | CACGTGAGAAAACCTC<br>GACA       | 60.1                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_39744759  | Ca5                                     | 39744759                      | AATATATATATATATATATATATAT<br>AT/AATATATATATATATATATATA<br>TATATATATAT     | AACTTCTTCCGTTGGC<br>AAAA   | AAAATCTCAAATGCG<br>GATCA       | 59.7                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_39762076  | Ca5                                     | 39762076                      | ATTTTTTTTTT/ATTTTTTTTTT                                                   | CCTCAGTTTTGGTCCC<br>TCAA   | TTGTTTCTCCCACTTC<br>TGG        | 60.1                             | 222                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_39804095  | Ca5                                     | 39804095                      | TAAAAAAAA/TAAAAAAAAA                                                      | TGTGTTCAGTGCACAT<br>CTCATC | TCCAACACATAAGATG<br>GAATTATTTA | 59.8                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_3988569   | Ca5                                     | 3988569                       | A/AT                                                                      | CCAATTTTGCCGACC<br>ATT     | TCGTGGTGGTAGTTTG<br>TGGA       | 59.7                             | 689                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                               | Forward primers (5'-3')    | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------|----------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                             |                            |                                 |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_3993030   | Ca5                                     | 3993030                       | CA/C                                                                                        | CAATTTTTCATGCTCGC<br>AAC   | CAGGATAATTGTTTGAC<br>TCCTTG     | 59.3                             | 250                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_39937669  | Ca5                                     | 39937669                      | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATATA<br>TATAT                           | ATGGTGCAGCAATTGT<br>CAAA   | AATCCACTTCAAAAGTC<br>TCTCG      | 60.1                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_39990866  | Ca5                                     | 39990866                      | TC/T                                                                                        | AGCCTTTTCCGGGTTA<br>AGAA   | CAGCGTGACAACGATC<br>AAGT        | 60.1                             | 506                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_40190697  | Ca5                                     | 40190697                      | CAAAA/CAAA                                                                                  | ACTCAGTCGCCAATTC<br>AAGG   | CCACCCACTCATGAAT<br>AAATGTT     | 60.3                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_40259990  | Ca5                                     | 40259990                      | AATATATATATATATATATATATAT<br>ATATATATAT/AATATATATATATATA<br>TATATATATATATATATATATATAT<br>AT | TGTGTGGAGATGCTCC<br>ATATTC | TCCGATGTCACAAAGC<br>CATA        | 60.0                             | 236                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_40274404  | Ca5                                     | 40274404                      | TA/TAAAA                                                                                    | CGGTTGACTAACTGTG<br>CCAA   | TGCTTTAGTACAATGCC<br>CCC        | 59.8                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_40319759  | Ca5                                     | 40319759                      | ACATTTTATAGTGCTCATTTTATAG/<br>ACATTTTATAG                                                   | GGCTTCTTCAACAAAA<br>GCGT   | TTTCCCAATCGATTTGC<br>TTC        | 59.5                             | 722                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_40361243  | Ca5                                     | 40361243                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                                               | CAATTCAACAGAAGGT<br>CGCA   | TGCCAAAAACAAATGAC<br>GTGT       | 59.8                             | 341                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_40392907  | Ca5                                     | 40392907                      | GTATATATATATATATATATATATAT<br>ATATATAT/GTATATATATATATATAT<br>ATATATATATAT                   | GCATTATCACGAGCAA<br>CACG   | TCAATGTGGTTCGCAA<br>AAGA        | 60.3                             | 192                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_40417439  | Ca5                                     | 40417439                      | AATATATATATATATATATATATATAT<br>ATATATATATA/AATATATATATATAT<br>ATATATATATATATATATATA         | TGAAATATGCACGGGA<br>CAAA   | TGATTGCTCTAATTTTT<br>ATGTAGTCCA | 59.9                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                               |                               |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_40434180  | Ca5                                     | 40434180                      | A/ACATCTG                                                                     | TTTACCCAGTAGGAG<br>GTCG       | TGAACCGGAAGAACCT<br>CAAC   | 60.1                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_40512133  | Ca5                                     | 40512133                      | GAAAAAAAAA/GAAAAAAAAA                                                         | TGTTGTAGCCCCGTCA<br>ATTT      | CCACATGGCATTGACG<br>ATAC   | 60.4                             | 448                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_40512625  | Ca5                                     | 40512625                      | GTATATATATATATATA/GTATATATA<br>TATATA                                         | ATTTCCGTATCGTCAAT<br>GCC      | TGCGGACAAAATTCAA<br>AACA   | 59.8                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_40572884  | Ca5                                     | 40572884                      | ATTTTTTTT/ATTTTTTT                                                            | TTAGAGGAGCCACGTA<br>AGCC      | CCCTAGCCACTTTCTCT<br>CCC   | 59.5                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_40615956  | Ca5                                     | 40615956                      | AATATATATATATATATATAT/AAT<br>ATATATATATATATATAT                               | ATTAAACCAACGCAC<br>GGAA       | TGTGAACACCCTACGT<br>GACAA  | 60.4                             | 925                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_40616297  | Ca5                                     | 40616297                      | AATATATATATATATATATATATAT<br>ATATA/AATATATATATATATATAT<br>ATATATATATATATATATA | TTCTCAACAAATAAGC<br>TCGAA     | AACATTTTACGGCGGA<br>CAAC   | 59.0                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_4064742   | Ca5                                     | 4064742                       | G/GC                                                                          | TATGTTTGTTTTGCCGT<br>CCA      | AGGATGTACCATCTT<br>GCGG    | 60.0                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_40692265  | Ca5                                     | 40692265                      | AATATTAAATATAT/AATATTAAATAT<br>ATTAAATATAT                                    | TACGTCCTCACTCCCA<br>ATCC      | CGTAAAAGTGTCATTG<br>CCTCC  | 59.9                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_40747443  | Ca5                                     | 40747443                      | C/CT                                                                          | TTGCAGAGAAAGAAAA<br>CTTGATATG | TGTGGAAGTTCCTAAA<br>ATACGC | 59.0                             | 237                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_40792737  | Ca5                                     | 40792737                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                                 | CGACCTTCTTTGAACCT<br>TGAGG    | GACAACAGTCCAGCCC<br>ATTT   | 60.3                             | 184                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                         | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                       |                             |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_40819075  | Ca5                                     | 40819075                      | TATATA/TATACATATA                                                                                     | TGAGCTCGTAAAAACC<br>CCAG    | TGCCACAATTATCGGA<br>CAAA      | 60.2                             | 874                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_41108441  | Ca5                                     | 41108441                      | GTTTTTTTTTTT/GTTTTTTTTTTT                                                                             | GGAGCGGAAAAGACTG<br>AAAA    | TTTTGTCTATGCGCACA<br>AGG      | 59.4                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_41219552  | Ca5                                     | 41219552                      | AATATATATATATATATAT/AAAT<br>ATATATATATATATATATAT                                                      | AGGAGAAGTGCGGAGA<br>AAAA    | CCATCAAATGCCTAATG<br>GTTC     | 59.1                             | 160                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_41226745  | Ca5                                     | 41226745                      | CAAAAAAAAA/CAAAAAAAAAAA                                                                               | GCCCAAAATCAAAAC<br>TCCA     | TGTGTCGTAAAAAGAT<br>GTCTAAGCA | 59.9                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_41423998  | Ca5                                     | 41423998                      | CTTTTT/CTTT                                                                                           | TCCCAAATGATTTTGCA<br>TATTTT | GGACGAAGCAGTATGC<br>CATT      | 60.0                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_41428729  | Ca5                                     | 41428729                      | T/TA                                                                                                  | TGAATTGAGTTTGGTT<br>GATTTGA | AAAGGATGCAGTATGG<br>GTTTTT    | 59.5                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_41428807  | Ca5                                     | 41428807                      | TTATATATATATATATATATATATA<br>TATATATATATATATAT/TTATATATA<br>TATATATATATATATATATATATAT<br>ATATATATATAT | TGAATTGAGTTTGGTT<br>GATTTGA | AAAGGATGCAGTATGG<br>GTTTTT    | 59.5                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_41428920  | Ca5                                     | 41428920                      | TAAGGAAG/TAAG                                                                                         | TGAATTGAGTTTGGTT<br>GATTTGA | AAAGGATGCAGTATGG<br>GTTTTT    | 59.5                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_41429223  | Ca5                                     | 41429223                      | TAGAGAGAGAG/TAGAGAGAG                                                                                 | AAAAACCCATACTGCAT<br>CCTTT  | GATGAAAGCTCCAAA<br>GTTCAAA    | 58.9                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_414590    | Ca5                                     | 414590                        | GAAAAA/GAAAAAA                                                                                        | TTGCACATGATTTTCCA<br>AACA   | CGTAAAAAGGTGCAGC<br>AACA      | 60.0                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                     | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                   |                           |                             |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_41460731  | Ca5                                     | 41460731                      | ATTTTGTTTTTTGT/ATTTTGT<br>TT                                                                                      | GGTGGATCAGGAAGTT<br>GCAT  | GCAGCCAAAATCCCA<br>AATA     | 59.9                             | 414                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_41467725  | Ca5                                     | 41467725                      | CTT/CTTT                                                                                                          | CTCATTTTCCACCCAA<br>GTGA  | AGCGACAAGATGAAAG<br>CTCC    | 60.0                             | 529                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_41467977  | Ca5                                     | 41467977                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATT/TT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>T | CTCATTTTCCACCCAA<br>GTGA  | AGCGACAAGATGAAAG<br>CTCC    | 60.0                             | 529                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_41495328  | Ca5                                     | 41495328                      | GTATAAAGTTA/GTA                                                                                                   | CTCAGCAGTCAATCAG<br>CTCG  | CCATAAAGAACACGTA<br>CAGACGA | 59.9                             | 352                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_41509481  | Ca5                                     | 41509481                      | GTTTTTTTTT/GTTTTTTTTT                                                                                             | CCTGAAATTGCCAAAC<br>CTTC  | GCCACGTGGTGTTTCAT<br>ACTG   | 59.5                             | 710                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_41603707  | Ca5                                     | 41603707                      | GTATATATATATATATATATATAT<br>GTATATATATATATATATATATAT<br>ATATATAT                                                  | ACGTCCATTTCCATGT<br>GGT   | TTGCCATTTCCATCTTC<br>CTC    | 60.1                             | 444                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_41614182  | Ca5                                     | 41614182                      | AATATATATATATATATAT/AAAT<br>ATATATATATATATATATAT                                                                  | TGTGGATTCATGATCC<br>TTGTG | TTTAACGTCAATGCCAA<br>CTTT   | 59.4                             | 916                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_41753735  | Ca5                                     | 41753735                      | CTTTTTTTTT/CTTTTTTTTT                                                                                             | CCGGGTGAGACTCATG<br>AATAA | AACGCAAAAGCTAAGA<br>GGCA    | 59.9                             | 650                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_41795988  | Ca5                                     | 41795988                      | ATT/AT                                                                                                            | TGGAATGCTACACAAG<br>CTGC  | TTGAGGTGCATCGATC<br>AAAA    | 60.0                             | 317                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_4179599   | Ca5                                     | 4179599                       | GATATATATATAT/GATATATATAT                                                                                         | CGGTTTAGGGATTGGG<br>TTTT  | TCGATTGAGTCTTTTGC<br>ACTT   | 60.0                             | 166                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                               | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                             |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_4180242   | Ca5                                     | 4180242                       | AGGTTTAGGGTTTAGGGTTT/AGGT<br>TTAGGGTTTAGGGTTTAGGGTTT                                                        | GGGTTTGGGGTTTAAG<br>GTTT  | TCCATTTCGTCTTTTGC<br>ACTT    | 59.1                             | 321                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_41990694  | Ca5                                     | 41990694                      | TTATATATATATATATATATATATATA<br>TATA/TTATATATATATATATATATAT<br>ATATA                                         | AATTTTGTGGCGGATT<br>GACT  | TCAACTGATTTGACGA<br>GAATGTG  | 59.4                             | 725                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_42071548  | Ca5                                     | 42071548                      | CATATATATATATATATATATATATA<br>TATATATAT/CATATATATATATATAT<br>ATATATATATATATAT                               | TGAATTTTCTGCTGCT<br>GACTC | GGGTCGTGTGATGTTT<br>TTTT     | 59.6                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_42133013  | Ca5                                     | 42133013                      | TTATATATATATATATATATATATATA<br>TATATATATATATAT/TTATATATATA<br>TATATATATATATAT                               | GCATACGAAGGAAGCG<br>AGTC  | AAACGCCAAAAAGATAA<br>TGGA    | 60.0                             | 328                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_42219742  | Ca5                                     | 42219742                      | GTATATATATATATATATATATATAT<br>ATATATATATATATATA/GTATATA<br>TATATATATATATATATATATATAT<br>ATATATATATATATATATA | AGAAAAACAAGCGTGTG<br>TGTG | GCAACACACAAGGAAG<br>CAAG     | 57.4                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_42231500  | Ca5                                     | 42231500                      | CC/CCGAGAACGTAC                                                                                             | TCAAAATCCACACCCC<br>ACTT  | GCCATCTCCAATAGCA<br>CCAT     | 60.2                             | 888                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_42363731  | Ca5                                     | 42363731                      | CTATATATATATATATATATAT/CTAT<br>ATATATATATATATATATATAT                                                       | AATTGTGATGGGAGAG<br>GGTT  | TGATGAAAAATATCTGA<br>GGAACCA | 58.3                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_42425779  | Ca5                                     | 42425779                      | CATGTTTTATGTTTTA/CATGTTTTA                                                                                  | TCAATGGAATGGAGTC<br>GTCA  | CGACAATTTTATTATCC<br>GTCC    | 60.0                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_42488342  | Ca5                                     | 42488342                      | AATATATATATATATATATATATATAT<br>ATATATAT/AATATATATATATATATA<br>TATATATATATATAT                               | TTACCAAATGGCATCC<br>AACA  | CCCCCAACAAAAGTTG<br>AAGA     | 59.8                             | 687                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_42535531  | Ca5                                     | 42535531                      | AT/A                                                                                                        | GAAATTCACCTCCAA<br>TCCA   | TTGGCCGTAGGTAGAT<br>TTGC     | 59.7                             | 269                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_42557966  | Ca5                                     | 42557966                      | TAAAAAA/TAAAAAA                                               | TGAAAGTGCATGTGAC<br>CGAT  | CACAAACCAACGTGGA<br>AGTG    | 60.1                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_42578018  | Ca5                                     | 42578018                      | ATTTTTTTTT/ATTTTTTTTT                                         | GTTGAAACCGGTTGCG<br>TAAT  | AACACTTTTCGCTGCC<br>AACT    | 59.9                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_42600585  | Ca5                                     | 42600585                      | TAAAAAAA/TAAAAAAA                                             | CACCCCATATCCCT<br>AGTT    | TTGATTGGTCCAACC<br>CACT     | 59.9                             | 681                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_42627539  | Ca5                                     | 42627539                      | GAAAAA/GAAAAAAGATAAAAAA                                       | CTTCCGAATCCGTACA<br>TCGT  | CACCTCCGTTACGCGT<br>ATTT    | 60.0                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_4273567   | Ca5                                     | 4273567                       | CTATATATATATATAT/CTATATAT<br>ATATATATATAT                     | TTGGAAGGAGCCCTTA<br>CCTT  | CGATTGAGGACCAAGG<br>ATGT    | 60.1                             | 908                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_4275629   | Ca5                                     | 4275629                       | GC/G                                                          | TTAGGGTTTAGGGTTT<br>CGGG  | TGACTTTTGCCTAATT<br>GGACG   | 60.2                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_42902485  | Ca5                                     | 42902485                      | TTATATATATATATATAT/TTATAT<br>ATATATATATAT                     | GTGGTTTTGCTTCGAC<br>CAGT  | CATTGCAACTATTTGT<br>CATTGAT | 60.2                             | 326                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_42989134  | Ca5                                     | 42989134                      | TCC/TC                                                        | GGCTTTGTTGAGTGGG<br>GTAA  | TCCCTGAGCAACTCGC<br>TTAT    | 60.0                             | 434                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_43481826  | Ca5                                     | 43481826                      | TA/TACCTAAATATCA                                              | TGCAATGCTGTTATCG<br>ACTCA | CACTCCCTCCCTCTAAT<br>CTTGA  | 60.4                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_43495179  | Ca5                                     | 43495179                      | GAAAAAAA/GAAAAAAA                                             | TGCGGCAAATCAGTTT<br>ACAA  | TCCGTTTATCTTAATGT<br>GTGCAA | 60.3                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                 | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_43517939  | Ca5                                     | 43517939                      | AATATATATATATATATATATA/AA<br>TATATATATATATATATATATAT<br>ATATATA                                                                                               | TGAGATGTTCACTACT<br>GCGTTG | AATTTTTCGCGCCAAG<br>TATG  | 58.8                             | 876                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_43575232  | Ca5                                     | 43575232                      | GTAATAAATTAATAATAAATTA<br>TAATAATAAATTTATAGTAATAAAT<br>AATAATAAATTT/GTAATAAATTA<br>TAATAATAAATTAATAATAAAT<br>AATAATAAATTTATAGTAATAA<br>AATAATAAATTTATAGTAATAA | TCGGAAGTTTGGTCTT<br>CAATG  | CGAAATGTAATGCTCG<br>AAACA | 60.1                             | 338                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_43615551  | Ca5                                     | 43615551                      | TTATATATATATATATATATATA<br>TAT/TTATATATATATATATATATA<br>TATATATATATAT                                                                                         | AAGAAAGGATCACCTC<br>AAATCC | GCCTATTTCAATGTAGC<br>CCC  | 58.6                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_43733246  | Ca5                                     | 43733246                      | CTTTTTTT/CTTTTTTTT                                                                                                                                            | TGATTTGTCGGTCTAG<br>CTCATC | TGGAAGAAAGGGAACA<br>TGAA  | 59.3                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_43796946  | Ca5                                     | 43796946                      | TTTATTATTATTATTATTATTATC<br>ATTATTATTATTCATTATTATTATT<br>ATTATTATTATT/TTTATTATTAT<br>TATTATTATTATTATCATTATTAT<br>TATTATCATTATTATTATTATTAT<br>TATTATT          | AGCCTGTACGCAAAAA<br>GCAT   | GGATAACGCGGAGGTA<br>TTGA  | 59.9                             | 668                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_43798003  | Ca5                                     | 43798003                      | AATATATATATATATATATATGTA<br>TATATATAT/AATATATATATATAT<br>ATATATATATATATGTATATATAT                                                                             | ATCGACTCCCGAACTC<br>AAAA   | CTCCTATATGTGATGC<br>GCGA  | 59.7                             | 751                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_43825873  | Ca5                                     | 43825873                      | TAATAAAATAAATAAATAAATAA<br>ATA/TAATAAAATAAATAAATAA<br>TA                                                                                                      | ACGCCGTACTTGATTG<br>ATGA   | TCGGTACACATCGCTA<br>CAACA | 59.2                             | 227                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_43839431  | Ca5                                     | 43839431                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                                                                                                                     | TTCCGCCCTTTTAACAA<br>CAC   | ATTTTCAGCCGTCGCAT<br>ATTT | 60.0                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_43847991  | Ca5                                     | 43847991                      | GT/GTGTGTGTGTCT                                                                                                                                               | GGAAACTCGTTTTTGA<br>GTGGA  | TGTCATGTGCCAAAG<br>TATCG  | 59.2                             | 679                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_4389073   | Ca5                                     | 4389073                       | CTTTTTATTTTTTTTTTTTTTTTTT/C<br>TTTTTATTTTTTTTTTTTTTTTTTAT<br>TTTTTTTT                                                                                         | TTTACCACTTGGAGTT<br>GGGC   | TCCTTTGCTAGCCCTTT<br>TGA  | 60.0                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                    | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                  |                           |                              |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_43897317  | Ca5                                     | 43897317                      | TTATATATATATATATAT/TTATATAT<br>ATATATATATAT                                                                                      | GTGTCAAGGTGTCATC<br>ACGG  | TGTTCAAGTCCGGAATC<br>ACAAT   | 60.0                             | 615                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_43900579  | Ca5                                     | 43900579                      | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATAT                                                                            | AGGCTCCCTATCAACC<br>ACAA  | CACCTAATTGGGACAA<br>CAACTG   | 59.6                             | 517                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_43918951  | Ca5                                     | 43918951                      | CTTTT/CTTT                                                                                                                       | TTGCAAGGTAAAAGC<br>ACGA   | ACGATGCCCCATACAA<br>TGAT     | 59.5                             | 783                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_43967867  | Ca5                                     | 43967867                      | AATT/AATCTAATTATT                                                                                                                | TATGCTCCGAGTTAGA<br>CGCA  | CCATGCGTCGCACATA<br>AATA     | 59.6                             | 471                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_44086162  | Ca5                                     | 44086162                      | CTTTTTTTTT/CTTTTTTTTTT                                                                                                           | CGGGTCAACTTTGATA<br>GACGA | GATGTGCCGTGAAAA<br>AATG      | 60.1                             | 594                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_44171535  | Ca5                                     | 44171535                      | TATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAA<br>ATAATA/TATAATAATAATAATA<br>ATAATAATAATAATAATAATAA<br>AATAATAATAATAATAATAATAA | ATGAACTTGCCGTTTT<br>GGAC  | TCCCCATTAATAATTC<br>AGTGATAA | 60.0                             | 776                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_44177714  | Ca5                                     | 44177714                      | GTATATATATATATAT/GTATATAT<br>ATATATATATAT                                                                                        | GGTCACGAACATCCCA<br>AAAT  | CCATGGTGAGAGGGTC<br>AAAT     | 59.7                             | 377                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_44215833  | Ca5                                     | 44215833                      | TAAAAAAAAA/TAAAAAAAAA                                                                                                            | TTGCTTTGGTTTGATGT<br>GGA  | GGGGGAAAAACAAGGAA<br>GAAG    | 60.1                             | 788                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_445610    | Ca5                                     | 445610                        | GCCC/GCCCC                                                                                                                       | ACAGTGGCTTCAATTC<br>CCAC  | CCAGCCAAATAGCTGG<br>AATG     | 60.0                             | 336                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_44596809  | Ca5                                     | 44596809                      | ATT/ATTT                                                                                                                         | TTGGCACATGCATTTT<br>GTT   | GACCAAATCTGTTGTT<br>GCAGA    | 60.0                             | 582                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                   |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_44597112  | Ca5                                     | 44597112                      | CTATA/CTATATATA                                                                   | GGGGTTAGTGCAAGCC<br>AAAT   | GTTCGCACGTGATGAA<br>CAAT   | 61.2                             | 862                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_44729729  | Ca5                                     | 44729729                      | CATATATATATATATATATATATA<br>TATATATATATAT/CATATATATATAT<br>ATATATATATATAT         | GGGGATTTGGAGGGTA<br>ACAT   | GTGTTGGAACGGGTTT<br>TGAT   | 59.9                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_44783564  | Ca5                                     | 44783564                      | ATTTTTTTTT/ATTTTTTTTTTT                                                           | ATTCACGGTAGCGGAT<br>CAAC   | AATCCGTGGAACCAAT<br>TTTT   | 60.0                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_44784631  | Ca5                                     | 44784631                      | TTTTCTGTCTA/T                                                                     | TCTGCCACGTTATTCA<br>TCG    | GAGGCGTCGGTGTGT<br>TATT    | 59.7                             | 293                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_44844449  | Ca5                                     | 44844449                      | A/AGCCTGG                                                                         | GGCTACCGAATATGGA<br>ACGA   | ACCGACTGTTGCTGGT<br>TTTC   | 59.9                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_44911043  | Ca5                                     | 44911043                      | CAAAAAAAAA/CAAAAAAAAAA                                                            | ACATCACCTTTTGCTGA<br>CCC   | CGCAATCTTGTCCTG<br>GTTT    | 60.0                             | 409                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_44914869  | Ca5                                     | 44914869                      | TTATATATATATATATATATATATA<br>/TTATATATATATATATATATATAT<br>ATA                     | TTTCGAGCAATCTCATC<br>CCT   | CGGCAGCTTTTACTA<br>CCCA    | 59.8                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_45086826  | Ca5                                     | 45086826                      | TA/TAA                                                                            | CAAACGCAAAATTAAC<br>ACACAA | AATACAGCTGGGTTTG<br>TGGC   | 60.0                             | 367                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_45093671  | Ca5                                     | 45093671                      | AATATATATATATATATATATATAT<br>ATATATATATA/AATATATATATAT<br>ATATATATATATATATATATATA | AAAGGAGAAGAAAGGT<br>CCAAGG | AAACACATGCGCTTTCA<br>TTG   | 60.1                             | 727                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_45094437  | Ca5                                     | 45094437                      | TG/T                                                                              | AATCCATCCGAACCTT<br>TTTC   | TTGTCAATGTTGCATGT<br>CTGAA | 60.1                             | 259                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                  | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_45097547  | Ca5                                     | 45097547                      | ACTTTGAAACCTTTGAAAC/ACTTTG<br>AAAC                                                                                                             | CCGCTCTTTTCGAAACA<br>TACA   | AAAACCCCGGATTGG<br>ATAG  | 58.9                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_45098220  | Ca5                                     | 45098220                      | ATTTTT/ATTTTTTT                                                                                                                                | ATGTTCGAAACGCTGA<br>TTCC    | TTGCCAAGCCTTTTGAA<br>ACT | 60.1                             | 121                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_45277984  | Ca5                                     | 45277984                      | ATTAGT/ATTAGTTAGT                                                                                                                              | TGTTGCGTTAAATGAG<br>TTGGA   | ATATTAGCGCGACCCA<br>AAAA | 59.2                             | 285                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_45309218  | Ca5                                     | 45309218                      | AATATATATATATATAT/AATATAT<br>ATATATATAT                                                                                                        | GTCGTTGCCTTTTG<br>GTTT      | GCAAATTGACTACGGT<br>CGGT | 60.0                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_45321319  | Ca5                                     | 45321319                      | TTATATATATATATATATAT/TT<br>ATATATATATATATATATATATAT<br>TAT                                                                                     | TGGTATCCCTATTTAA<br>CCGATTT | TACGGAAGAACCGACA<br>AGTG | 59.1                             | 902                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_45371143  | Ca5                                     | 45371143                      | CTTTTTTTTTTT/CTTTTTTTTTTT<br>TT                                                                                                                | TTGAACGTGGACACCC<br>ATAA    | GTTGTGCATGTACCTT<br>CGCT | 59.8                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_45372527  | Ca5                                     | 45372527                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTA/TTTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA | CCCAGTGTACCGTCT<br>TTTT     | TTACACAAATGTCCAC<br>CAA  | 60.0                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_45557067  | Ca5                                     | 45557067                      | CATATATATATATATATATATATA<br>TAT/CATATATATATATATATATAT                                                                                          | CAATGAAAAAGTGTGG<br>CCCT    | ACGTTGATGGAACAAT<br>GCCT | 60.0                             | 873                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_456196    | Ca5                                     | 456196                        | CTTTTTTT/CTTTTTTTTTTT                                                                                                                          | TGCTACAACCACACA<br>TGCT     | CGTTTTCCGATTCATGC<br>TTT | 60.2                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_456689    | Ca5                                     | 456689                        | GGAAAACGAAAACG/GGAAAACG                                                                                                                        | TGTTGAGTTTTGCACA<br>GGC     | TGAAAGGAGTCGGTTT<br>TGTG | 59.9                             | 257                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                              |                            |                             |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_45724530  | Ca5                                     | 45724530                      | AATTATTATTATTATTATTATTAT<br>TATTATTAT/AATTATTATTATTAT<br>TTATTATTATTATTATTAT | GCGGTTGAATAAATGT<br>GACAAA | TAGTTGGAGGTGCTG<br>ACCC     | 59.9                             | 616                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_45792229  | Ca5                                     | 45792229                      | TAAAA/TAAAA                                                                  | TCTCCATTACGTTTGT<br>GTTTTT | TTTGTACCAAGTCCTC<br>CGC     | 57.8                             | 386                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_45795356  | Ca5                                     | 45795356                      | GTTTTTTTTT/GTTTTTTTTT                                                        | ACGGCTTGGAAATGA<br>TGAA    | CCATCGATTTCACTGT<br>GTCA    | 60.4                             | 404                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_45967395  | Ca5                                     | 45967395                      | GTATATATATATATATATAT/GTAT<br>ATATATATATATATATAT                              | TTTGATGCTTGTCTTT<br>GCG    | TTCTTCGGTGTCAT<br>GTCA      | 60.0                             | 479                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_46005130  | Ca5                                     | 46005130                      | AATATATATATATATA/AATATATA<br>TATATATA                                        | AGTCGCCATTGGAAT<br>TACG    | AACAATCCTGAAATGC<br>GGAG    | 60.0                             | 335                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_46086372  | Ca5                                     | 46086372                      | ATTTTTTTTT/ATTTTTTTTT                                                        | GGCATTATGTGAAA<br>CGGG     | TCCTTGCTTCTTGCCC<br>AAT     | 60.2                             | 726                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_46091748  | Ca5                                     | 46091748                      | CTTTTTTTTT/CTTTTTTTTT                                                        | ATTCGTCACCACACAC<br>CAGA   | CTAGCTGTGCAACATC<br>GCAT    | 60.0                             | 550                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_46180569  | Ca5                                     | 46180569                      | A/ATAATAATAATAAT                                                             | AGCGGCTGCTGTGTTT<br>AGTT   | CCAAATCGAAGAAGAA<br>CAAGG   | 60.1                             | 614                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_46208612  | Ca5                                     | 46208612                      | AAT/AATAT                                                                    | ATGCAGCACAAAATGC<br>AAGT   | TTCGAATCTTATTTGA<br>CAATTTT | 59.4                             | 502                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca5_P4_46390107  | Ca5                                     | 46390107                      | GAAAAAAAAA/GAAAAAAAAA                                                        | GCAAGAATAGCACAAA<br>CAAGCA | ACGTCGCGCAACTGTG<br>ATA     | 60.4                             | 239                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                    | Forward primers (5'-3')  | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------|--------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                  |                          |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_46393868  | Ca5                                     | 46393868                      | AG/AGTGATG                                                                       | ACAGTTCAAAGTCCCT<br>GGCA | TCAATCATTAAAATTA<br>CTCTGAATCG | 60.7                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_464166    | Ca5                                     | 464166                        | ATGT/AT                                                                          | TCTTCAACGCTGAAAT<br>GAAA | AACTTGTGTATTAATGT<br>TTGCTGC   | 58.5                             | 716                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_46429100  | Ca5                                     | 46429100                      | GAAAAAAAAA/GAAAAAAAAA                                                            | TGCTCACGTTCTTTGT<br>TGG  | TTGGTCTTGCTTCTTTC<br>AAATG     | 59.9                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_464299    | Ca5                                     | 464299                        | TAAAAAAAA/TAAAAAA                                                                | TCAAAGTGTGTAATT<br>GGTCA | AACTTGTGTATTAATGT<br>TTGCTGC   | 58.2                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_46552360  | Ca5                                     | 46552360                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTA/TTTATTATTATTA<br>TTATTATTATTATTATTATTA | CGAATAGCATGTCACG<br>TTTG | TGGGTGGCATCAAAG<br>TTGC        | 57.8                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_46561532  | Ca5                                     | 46561532                      | TTATATATATATATATATATATAT<br>TATATATATATATATATATATATAT<br>ATATATA                 | TAGACTGAGGTCCACC<br>ATGC | TGCAATCAATTTTACT<br>CTTCATCC   | 58.7                             | 506                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_46661039  | Ca5                                     | 46661039                      | AATATATATATATATATATAT/AA<br>TATATATATATATATATATAT                                | TGGAATTCAAGGGACC<br>AAAA | ACTTGCGAGATAATTTA<br>GTAGGGA   | 60.3                             | 863                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_46676212  | Ca5                                     | 46676212                      | ATTTTTTTTT/ATTTTTTTTTT                                                           | GCCACCACACCTCCAA<br>CTAT | TTGAGATGGGACTTTG<br>GAGC       | 59.9                             | 880                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_46879029  | Ca5                                     | 46879029                      | ATTTTTTTTT/ATTTTTTTTTT                                                           | GGGGTCAATCGACAAG<br>AGAA | CGGTTGTCACGTCAGA<br>AAAA       | 60.1                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_46886435  | Ca5                                     | 46886435                      | TA/TTAACTATACTCAAACA                                                             | CAGCCATGCTCGTATG<br>CTAA | AGAACCCCATCCAAAC<br>AATG       | 60.0                             | 444                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                     | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                   |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_46910930  | Ca5                                     | 46910930                      | CATATATATATATATA/CATATATATA<br>TATA                                                               | TTCATTGCGAGCCCTA<br>CTCT   | TGCGCTGTAATAGGTG<br>CATT    | 60.0                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_46985054  | Ca5                                     | 46985054                      | AATTATTATTATTATTATTATTATT<br>TATTATTATTATTATT/AATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATT | TCGCATTTTAAGGGAG<br>GAAA   | AGCAAGGAAGCATCAT<br>CCAA    | 59.7                             | 212                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_47133305  | Ca5                                     | 47133305                      | ATTTTTTTTT/ATTTTTTTTTTT                                                                           | TAATGATATCCACCCC<br>GCAT   | AGGACCACCTGCTGAA<br>ACAT    | 60.0                             | 935                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_47138535  | Ca5                                     | 47138535                      | CTATTATTATTATTATTATTATTA<br>/CTATTATTATTATTATTATTATT<br>ATTATTA                                   | TGAATCTTTCCGCATT<br>GTG    | CCTGAAAGACTTAGAC<br>GGCG    | 59.7                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_47213382  | Ca5                                     | 47213382                      | CAAAAAAAAA/CAAAAAAAAA                                                                             | GGATGTTGCACAATCA<br>AGGA   | GCTCATGCACCTTGCT<br>CCAA    | 59.5                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_47226447  | Ca5                                     | 47226447                      | TTTATATTATATTATATTATAT/TTTA<br>TATTATATTATATTATATTATAT                                            | ACCGTTACCTTTTGTG<br>GCTG   | GAAGCTTTCACGTACG<br>GAGC    | 60.0                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_47478750  | Ca5                                     | 47478750                      | AATATATATATATATATATATATAT<br>ATATATAT/AATATATATATATATATA<br>TATATATATATATATATATATAT               | TGGGATGTGTCTAACG<br>TTTGTT | GTAAGAGTTGGTGCCG<br>ATCC    | 59.4                             | 983                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_47512183  | Ca5                                     | 47512183                      | GTTTTTTTTT/GTTTTTTTTTTT                                                                           | TGGCATATTCCTATCC<br>CATA   | TGTGGGTATAAATGAG<br>GGGC    | 60.9                             | 404                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_47676757  | Ca5                                     | 47676757                      | GAAAAAAA/GAAAAAA                                                                                  | GACCAAACTGCACTT<br>AAGCC   | CTCCCCATCTCTCTCA<br>CCA     | 58.9                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_47677095  | Ca5                                     | 47677095                      | TTATATATATATATATATA/TTATATA<br>TATATATATA                                                         | TGGTGAGAGAGATGGG<br>GAAG   | TTGAATTATTGGAGGTT<br>GACACA | 60.2                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                              | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                            |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_48164734  | Ca5                                     | 48164734                      | AGG/AG                                                                                                                     | GTTTGCAATTATGGGA<br>AATGTT | AACTCTAAATCCCCGC<br>AAGG   | 60.0                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_4829908   | Ca5                                     | 4829908                       | AATATATATATATATATATATATAT<br>AT/AATATATATATATATATATATA<br>TATATAT                                                          | GTTGGTCCCTAGCAC<br>CGTA    | TGGATATTGAACTCGG<br>AGGC   | 60.0                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_4857245   | Ca5                                     | 4857245                       | GAAAA/GAAAAA                                                                                                               | CCCACATTTCTTTGGC<br>AGTT   | TGTGCCTAAACTTGCT<br>GGTG   | 60.0                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_4870580   | Ca5                                     | 4870580                       | GG/GGGTCAGTAATG                                                                                                            | CCAATCCTCCTTTAC<br>CTTC    | ACGGTCACCACTTTCTT<br>TGG   | 58.6                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_492638    | Ca5                                     | 492638                        | AT/ATAGCAAGTTT                                                                                                             | ATTCTTGACCCGAAAT<br>GTGG   | TCATTTTGGCATCTAG<br>GGC    | 59.8                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_4970490   | Ca5                                     | 4970490                       | T/TG                                                                                                                       | ATTCTACGCGATTAC<br>CACG    | CCCGTGATAGGCAGTA<br>CGTT   | 60.0                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_497099    | Ca5                                     | 497099                        | GAAAA/GAAA                                                                                                                 | TTGAGTGCAGCTGGAG<br>AAGA   | TCACTCAAAAACCAAGC<br>ACG   | 59.9                             | 110                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_5013490   | Ca5                                     | 5013490                       | TATAAATAAATAAATAAATAAATAA<br>TAAA/TATAAATAAATAAATAAATAA<br>TAAATAAATAA                                                     | GAGGGATGTCATTAT<br>TTTCG   | TGTGATCATTGGGGAA<br>CTCA   | 59.4                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_5038314   | Ca5                                     | 5038314                       | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAA/A<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAA | ATTTGTGGTGTGTGC<br>TGGA    | CATCAAACTCAAGTGC<br>AAACAA | 60.0                             | 869                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_5038531   | Ca5                                     | 5038531                       | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATT                 | TGTGGTTGAGTAGTTG<br>TGCCA  | TGCGGTTGATTAGTTG<br>TGCA   | 60.2                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                       | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                                     |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_5190851   | Ca5                                     | 5190851                       | CTATATATATATATATATATAT/CT<br>ATATATATATATATATATATAT                                                                                                                 | AGCGCTATGTGACCCT<br>TTTG | AATGTGAATCCCACCA<br>GGAA  | 60.3                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_5318962   | Ca5                                     | 5318962                       | TC/T                                                                                                                                                                | ACGTTGACCAATTCAG<br>CTCC | CACTAGGGACCCTTTG<br>GTGA  | 60.1                             | 720                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_5408571   | Ca5                                     | 5408571                       | TTATATATATATATATATATA/TTATA<br>TATATATATATATATATA                                                                                                                   | CCATTTTCCCTCGCTC<br>ATAA | CGTTGGTCATGATCCT<br>TCCT  | 60.0                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_5410568   | Ca5                                     | 5410568                       | A/ACC                                                                                                                                                               | TGCTTTGACTCGCACC<br>ATAG | TCTTCATCAATGAGCGT<br>TGC  | 60.0                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_5492827   | Ca5                                     | 5492827                       | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTAT/TTT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTAT | TATCCCCTCGATTGCT<br>TTCA | TTTGCCTCAAAAAGTT<br>TCACA | 60.5                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_5618412   | Ca5                                     | 5618412                       | ACCCC/ACC                                                                                                                                                           | TTTGTCGTGGGATGAA<br>CTGA | TGGGTCCATGTTCCAT<br>TTTT  | 60.1                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_5705191   | Ca5                                     | 5705191                       | GA/G                                                                                                                                                                | AATCGATTGGCTTTGA<br>TTCG | CTCTCATCTGAGGGCA<br>AAGC  | 60.0                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_5798731   | Ca5                                     | 5798731                       | TTATATATATATATATATATA/TTA<br>TATATATATATATATATATATAT<br>A                                                                                                           | CTTCGACACTGTAGCA<br>CCCA | ATATTTCTGCGCATTCT<br>CGC  | 59.9                             | 217                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_5836817   | Ca5                                     | 5836817                       | TACCCTAAACC/TACCCTAAACCCTA<br>AACCCTAAACC                                                                                                                           | GTATGAGGAGGATCTT<br>GCGG | TCAAAATGCACCATAAA<br>CCG  | 59.7                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_5837067   | Ca5                                     | 5837067                       | ACCTAAACCCTAAACCCTAAACCCT<br>AA/ACCTAAACCCTAAACCCTAA                                                                                                                | AAAGAAAAACACTCGC<br>GCTG | AGCGTTTTGGGTTTAG<br>GGTT  | 60.6                             | 825                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                         | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                       |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_5888717   | Ca5                                     | 5888717                       | AATATATATATATATATATATATATATATATATA/AATATATATATATATATATATATATATATATATATATATATATATATATA | TCTTGAGCTACTGGGG<br>CTTG  | CAAGTTTGAAATGGAG<br>GGGA    | 60.5                             | 882                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_5906369   | Ca5                                     | 5906369                       | TA/TACTCA                                                                             | AACATCATGCTTGGGA<br>CAAA  | TCTTGTGGATGACAATT<br>ATTTCG | 59.0                             | 271                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_5912049   | Ca5                                     | 5912049                       | TAAATATACATCAAATATA/TAAATATACATCAAATATACATCAAATATA                                    | TTTTTGTGTCTCACTC<br>GATCA | CAGTGTTAATTGGCAC<br>GAAA    | 58.4                             | 276                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_5969929   | Ca5                                     | 5969929                       | CG/C                                                                                  | GAGGACGAAAATGACC<br>CAAA  | TGCATCCGATACGTGT<br>GTTT    | 59.9                             | 853                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6074415   | Ca5                                     | 6074415                       | ATATTATT/ATATT                                                                        | AGTCAGACGCTACTCG<br>GCAT  | AGCATGCATCTGCACA<br>CAAT    | 60.0                             | 625                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6199138   | Ca5                                     | 6199138                       | TTTATTATTATTATTATTAT/TTTATTATTATTATTATTATTATTATTATTAT                                 | GCATTCCCGTATGCGA<br>CTAT  | GGCACATGTTATTGT<br>TTGG     | 60.0                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6200121   | Ca5                                     | 6200121                       | CT/CTT                                                                                | TTCGCAACTCCACTCTT<br>CCT  | GATCCATTTTCCCCAA<br>ATC     | 60.0                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6200571   | Ca5                                     | 6200571                       | AT/ACT                                                                                | GGTAAGGGCTCCTTCC<br>AAAC  | CCCCTCCTTAACGTCC<br>AGTT    | 59.9                             | 990                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6227147   | Ca5                                     | 6227147                       | ATT/ATTT                                                                              | GGTTTAAACTCCACCG<br>GGAT  | CGGTAACCGGAAAAAG<br>TCAA    | 60.1                             | 408                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6369660   | Ca5                                     | 6369660                       | TC/TCAC                                                                               | GAGGAAACACGGTGAA<br>TGGT  | CGCTCACTAGTCGAAC<br>GAGA    | 59.8                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_64660     | Ca5                                     | 64660                         | CAAAAA/CAAAA                                                  | TGGATCATCAAAGATC<br>AACGG | ATTGAAAGTTGCGGGG<br>ACTA | 60.8                             | 438                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6510151   | Ca5                                     | 6510151                       | CTTTTTTTTT/CTTTTTTTTTT                                        | TCGCGTTCATGATTTT<br>GTGT  | CGGAGTGATAATTGGT<br>GCAA | 60.1                             | 816                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6532288   | Ca5                                     | 6532288                       | AAAAGAACAAAA/AAAAA                                            | TGTCTTCAACTTCTGC<br>GGTG  | TTGCAACGTGTCATTGT<br>CCT | 60.0                             | 831                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_655741    | Ca5                                     | 655741                        | C/A/C                                                         | AGGTCATTTTCGTCCT<br>CCCT  | TTGGATGCACACGATT<br>TGTT | 59.9                             | 767                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6663718   | Ca5                                     | 6663718                       | CAA/CAAA                                                      | AGGGAGGACGAAAAATG<br>ACCT | TAACCAATCTTGTGCAC<br>CCA | 59.9                             | 171                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6754121   | Ca5                                     | 6754121                       | TA/T                                                          | AAAGAGGCAAAGCTGA<br>TGGA  | CACGTGTCGTCTTCTG<br>CTTC | 60.0                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6763101   | Ca5                                     | 6763101                       | AGGG/AGGGG                                                    | CAAATGTCGGGAGCTA<br>CCAT  | GGATCCCCAATCGATA<br>ACCT | 60.0                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6763849   | Ca5                                     | 6763849                       | AATATATATATATATATATA/AATATA<br>TATATATATATA                   | TGGGTGGGAGTAATTC<br>TTCG  | GAGTTGCGGCGAGAGT<br>AGAT | 59.9                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6765484   | Ca5                                     | 6765484                       | CATATATATATATATATATATAT/C<br>ATATATATATATATATATATATATA<br>T   | CGAAGCTGCCAGGTAA<br>AAAG  | TGAGTCCATTCTCCAAA<br>CCA | 60.0                             | 652                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6772280   | Ca5                                     | 6772280                       | CTTTTTTTTTTT/CTTTTTTTTTT                                      | CCAATGGCTTCGACAT<br>TTCT  | AAGTCACCCCTCGTTG<br>TTTG | 60.1                             | 726                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_6772456   | Ca5                                     | 6772456                       | GCACACA/GCACACA                                               | TGCACAACAAAAGCAC<br>AACA      | TGTACCATCATAGTGG<br>CGGA        | 59.9                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6832771   | Ca5                                     | 6832771                       | ATTAAATTATATGATTA                                             | TGCTAGGAACCGAGCC<br>TTTA      | CGTGTGCGTTTGTAAAT<br>TGATG      | 60.0                             | 217                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6833175   | Ca5                                     | 6833175                       | TT/TTATTATTAT                                                 | GAGAGCTCACAGCCTT<br>GTCC      | TTGGCATCGTGATTTTA<br>TGC        | 60.1                             | 873                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6833700   | Ca5                                     | 6833700                       | ATATT/AT                                                      | GCATAAAATCACGATG<br>CCAA      | CGATTTTTCGTCTACAT<br>GTGC       | 59.5                             | 211                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6833833   | Ca5                                     | 6833833                       | AATA/AATATA                                                   | AAATCACGATGCCAAA<br>GAAAA     | AAGAAAGTTGTAAATGT<br>GTTTTATGGA | 59.6                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6833924   | Ca5                                     | 6833924                       | ATTT/ATT                                                      | AAATCACGATGCCAAA<br>GAAAA     | AAGAAAGTTGTAAATGT<br>GTTTTATGGA | 59.6                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6834263   | Ca5                                     | 6834263                       | CT/C                                                          | GCTTAATCCATAAAACA<br>CATTACAA | TTCTCATGCGCTTGACT<br>AATG       | 57.9                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6834706   | Ca5                                     | 6834706                       | TAAAAAA/TAAAAAAA                                              | TGCATAAAATCACCAT<br>GCCA      | TTGTACGTTTCTTTTCT<br>ATGATTTC   | 60.9                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6834978   | Ca5                                     | 6834978                       | ATATTATTATTATTATTATT/ATA<br>TTATTATTATTATTATTATT              | TAGTCAAGCGCATGAG<br>AAAA      | GGCATGATGATTTTATG<br>CATATT     | 57.3                             | 748                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6837967   | Ca5                                     | 6837967                       | TAAAAAAAAAAAAA/TAAAAAAAAA                                     | TCGAGAACAACCTCGTC<br>TCGTG    | AATTTGCAGTGTCGCA<br>AAAA        | 61.6                             | 254                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_6872599   | Ca5                                     | 6872599                       | ATTATTTATTATT/ATTATTTATTTA<br>TTTATT                          | CGGCCATCACACAATG<br>ATAA | TCAGGATGTCACCACG<br>AAGA | 60.3                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6906256   | Ca5                                     | 6906256                       | AT/A                                                          | CATCGGAATGAACGAG<br>TGTG | TTTAGCGTGTCAAACC<br>AACG | 60.1                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6907615   | Ca5                                     | 6907615                       | A/AGTG                                                        | GGTTGTGTTATCCCTC<br>GACA | AGGGTGCCACATTTAC<br>TCCA | 58.4                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6907876   | Ca5                                     | 6907876                       | GA/GAATA                                                      | GGTTGTGTTATCCCTC<br>GACA | AGGGTGCCACATTTAC<br>TCCA | 58.4                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6909501   | Ca5                                     | 6909501                       | TATATATAATTTAAATATATAATTTAA<br>AT/TATATATAATTTAAAT            | AATGATGGAGGGAGTG<br>AAGC | AACTGTCCATTTGTGA<br>GGGC | 59.1                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6909628   | Ca5                                     | 6909628                       | ATTTTTTT/ATTTTTT                                              | AATGATGGAGGGAGTG<br>AAGC | AACTGTCCATTTGTGA<br>GGGC | 59.1                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6909656   | Ca5                                     | 6909656                       | TAAA/TAA                                                      | AATGATGGAGGGAGTG<br>AAGC | AACTGTCCATTTGTGA<br>GGGC | 59.1                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6909949   | Ca5                                     | 6909949                       | CAAAGA/CA                                                     | CCTAAGCCCTCACAAA<br>TGGA | TAAAGGGAGAAAAGCA<br>GCCA | 60.1                             | 304                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_6910554   | Ca5                                     | 6910554                       | A/AC                                                          | CTTTCAGGAACCAACA<br>ACCA | CCAAATTACCAACGC<br>CAAC  | 58.6                             | 328                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_7019330   | Ca5                                     | 7019330                       | T/TGCAC                                                       | GCTCACTTATCCCGCC<br>AATA | TGGCTATGAGTGGTTC<br>CCTT | 60.1                             | 996                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                    | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                  |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_7092837   | Ca5                                     | 7092837                       | AT/A                                                                             | TCCCAGTAACTAGCCG<br>TTGG   | GGGCCATATCAACAAT<br>TTGG    | 60.1                             | 221                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_7100474   | Ca5                                     | 7100474                       | ACACCACCACCACCACCACCA<br>CCACCACCAC/ACACCACCACCAC<br>ACCACCAC                    | TGGACATTCTAGATT<br>CAGCC   | TCATCAATCCGACACCT<br>TCA    | 59.1                             | 299                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_7107813   | Ca5                                     | 7107813                       | G/GA                                                                             | TGTCTCGAGTTCTATC<br>CCGAA  | TCACACACTTTCTTCCA<br>ACCTTT | 59.8                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_7116888   | Ca5                                     | 7116888                       | CAAAAAA/CAAAAAA                                                                  | TTAACAACCTCTGGTTC<br>GGG   | GTGGACTGTCGGTTCG<br>ATTT    | 60.0                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_7261145   | Ca5                                     | 7261145                       | ATTT/ATT                                                                         | CGCTGTAAAAGACATG<br>CGCT   | ACATCCATTTCGGTC<br>CATA     | 61.5                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_7293090   | Ca5                                     | 7293090                       | AATATATATATATAT/AATATATATAT<br>ATATAT                                            | GCGAACATGAGAAATT<br>GTCG   | AACCAAGCAAGTCATAA<br>CATTCA | 59.3                             | 684                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_7541226   | Ca5                                     | 7541226                       | AATATATATATATATATATATATAT<br>ATATAT/AATATATATATATATATA<br>TATATATATAT            | GCCTCATACTCAAGAC<br>ATTGGA | GCTTGGAGAGAATGAG<br>TCCG    | 59.2                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_7780304   | Ca5                                     | 7780304                       | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTA/TTTATTATTATTA<br>TTATTATTATTATTATTATTA | TCGTAAATATCCATCG<br>GGGA   | TGACCTTCATGCTTTTG<br>TCG    | 60.1                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_7874012   | Ca5                                     | 7874012                       | AAGAGAGAG/AAGAG                                                                  | TCCTCCCTGCCAGACA<br>TAAC   | TGTCCTTGCTCAAGC<br>TTTT     | 60.1                             | 966                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_7898685   | Ca5                                     | 7898685                       | TAAAAAAA/TAAAAAAA                                                                | TCACTGTTCAAGATGTT<br>TGTGC | GATGAGGAAAAAGTGG<br>ATTTCA  | 58.8                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_7937565   | Ca5                                     | 7937565                       | GT/GTT                                                        | ATCGTTTTGTTTCGGG<br>ACTG | ATGCCCATGCATGTTT<br>GTAA | 60.0                             | 404                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_7941049   | Ca5                                     | 7941049                       | GA/GAA                                                        | TCTCATTTCCTTAA<br>CTTTCG | TAAGCAAGCCATTGCA<br>AAAA | 57.6                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_8035650   | Ca5                                     | 8035650                       | T/TTA                                                         | GCGTTTCATGGTGTG<br>TTTG  | CACGAGTCCGATAAGG<br>GTGT | 60.0                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_8098662   | Ca5                                     | 8098662                       | ATT/AT                                                        | TCGTCAATGTTGTGC<br>CATT  | TTGTATGTCCCACAAA<br>GCTC | 60.0                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_812188    | Ca5                                     | 812188                        | AATATATATATATATATATATAT<br>/AATATATATATATATATAT               | TGCAATTTCTGTTTT<br>GCTG  | CGGGACCCATTGAAC<br>ATTA  | 58.8                             | 806                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_8128213   | Ca5                                     | 8128213                       | A/ATAT                                                        | CCAATTTGAATTGTCC<br>GTCC | CCAATTGGTTGCACCT<br>TTCT | 60.2                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_8241804   | Ca5                                     | 8241804                       | ATTTT/ATTT                                                    | TGACAGGAGCTTCCCT<br>GAGT | GTACGAACCTCCTCCC<br>ACGA | 60.0                             | 678                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_8259506   | Ca5                                     | 8259506                       | AATATATATATATATATA/AATATA<br>TATATATATATATATATA               | TCGTTCTGATCAATGG<br>TGGA | AATTTTAAACCTGCCG<br>CCT  | 60.0                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_8314073   | Ca5                                     | 8314073                       | GTATATATATATATAT/GTATATAT<br>ATATATATATAT                     | CCCAAACCCACATATA<br>GCCA | TTCCATCATCAATTCTG<br>CCA | 60.6                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_8314333   | Ca5                                     | 8314333                       | ATT/ATTT                                                      | TGGGGTTTAGGGTGTC<br>ACAT | TTCCATCATCAATTCTG<br>CCA | 60.1                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                               | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                             |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_8345571   | Ca5                                     | 8345571                       | CTTTTTTTTT/CTTTTTTTT                                                                                        | GCAGCCGTTCTCTTTC<br>ATTCT | TGTGGTCTAACGGCTC<br>CTTC    | 60.0                             | 474                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_8596558   | Ca5                                     | 8596558                       | GATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAA/GATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAA | CGAAGCCGAGAAAATG<br>ACTC  | AGAGGCAAACAAGAAC<br>CGAA    | 60.0                             | 343                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_8735941   | Ca5                                     | 8735941                       | AATATATATATATATATATATAT<br>TTA/AATATATATATATATATAT<br>ATTTA                                                 | TCAAACCTCTGCTGGCA<br>CATC | AAGCGACCTCCTACTG<br>GGTT    | 60.0                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_8759374   | Ca5                                     | 8759374                       | ATTTTTATTTTTATTTTTA/ATTTT<br>ATTTTTATTTTTATTTTTTA                                                           | TTGTCCCTACCTCAA<br>CAAG   | AAAAATTAAGAACAACA<br>GGGGAA | 59.1                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_8780838   | Ca5                                     | 8780838                       | AATATATATATATATATATATAT<br>ATATATATATATA/AATATATATAT<br>ATATATATATATATATATATATA<br>TATATATATATATA           | CAACACATCACAACCA<br>TCCA  | TTGACCTTTATGGATT<br>TGAGA   | 58.8                             | 374                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_885224    | Ca5                                     | 885224                        | ATATATATATATATATATATATGT<br>ATATATATAT                                                                      | AGAGGGGTTTGTGTTT<br>GACG  | TGAATTTTGACTCGGA<br>GGCT    | 60.0                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_8975436   | Ca5                                     | 8975436                       | AT/ATCT                                                                                                     | GCTGTTGGAGATGCTT<br>CAAGT | TTGACTTTCTCCCGTT<br>GAC     | 59.5                             | 423                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_8998961   | Ca5                                     | 8998961                       | A/AAT                                                                                                       | TGCAATAATGGCATTTC<br>CAA  | TGAGCTTGAATGGCAA<br>GATG    | 59.9                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_8999793   | Ca5                                     | 8999793                       | CA/CAAA                                                                                                     | CTCGATCAATGACCAG<br>AGCA  | TCACCTCTCCCCATT<br>TTG      | 59.9                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_9250070   | Ca5                                     | 9250070                       | AAAGAAGAAGAAGAA/AAAGAA<br>GAAGAAGAAGAAGAA                                                                   | CCAGGATAAACAGCC<br>CAGA   | TTCTGAGGCACTCTCC<br>TGGT    | 60.1                             | 317                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                               | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                             |                               |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_9264601   | Ca5                                     | 9264601                       | ATTTTTTTTTT/ATTTTTTTTTT                                                                     | TTCCAGAAAATTGCATT<br>TTGAA    | ACCTTCACAAAGATCG<br>TCAA  | 59.6                             | 756                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_9264762   | Ca5                                     | 9264762                       | CATATATATATATATATATATAT/C<br>ATATATATATATATATATATATATA<br>TAT                               | TTCCAGAAAATTGCATT<br>TTGAA    | GTGCCAATGCCAAAGA<br>AAAT  | 59.6                             | 802                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_927603    | Ca5                                     | 927603                        | TTAATAATAATAATAATAATAAT<br>AATAATAA/TTAATAATAATAATAA<br>ATAATAATAATAATAATAA                 | GGTCTTTTGAAAATAAT<br>CTTAACGC | AAGGGGGAAGTTAAGC<br>CAGA  | 58.8                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_927667    | Ca5                                     | 927667                        | TTAATAATAATAATAA/TTAATAA<br>TAATAATAATAATAA                                                 | AAAAGGAACGGTTAA<br>AATGTCTT   | AAGGGGGAAGTTAAGC<br>CAGA  | 58.7                             | 224                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_9384842   | Ca5                                     | 9384842                       | GT/GTT                                                                                      | TCAACAGTTTTGGTTCA<br>TCCC     | TGCTTGATTCCGTTTT<br>GAG   | 59.8                             | 372                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_9384889   | Ca5                                     | 9384889                       | GAAAAAAAAA/GAAAAAAAAA                                                                       | TCAACAGTTTTGGTTCA<br>TCCC     | TGCTTGATTCCGTTTT<br>GAG   | 59.8                             | 372                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_9403420   | Ca5                                     | 9403420                       | CT/CAACCTT                                                                                  | GGCACTTTTCACGTCC<br>ATTT      | ACAGCAGAAATGGGGTA<br>GTGG | 60.0                             | 836                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_9441399   | Ca5                                     | 9441399                       | AATTTATTTT/AATTTATTTTATTTT                                                                  | TGCGATGGAGAAATCA<br>AAGC      | CTAGTTTGGCTTGACG<br>GGAA  | 61.3                             | 865                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_9441477   | Ca5                                     | 9441477                       | CAAAAAAAAA/CAAAAAA                                                                          | TCGTGTCTCAAAATCA<br>AGGAG     | CTAGTTTGGCTTGACG<br>GGAA  | 59.4                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_9586243   | Ca5                                     | 9586243                       | ATATTATTATTATTATTATTATTA<br>TTATTATTATTA/ATATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTA | GAAACGCGTTCGCTGT<br>ATTT      | TTAGGCCTCCATGCAA<br>GAGT  | 60.0                             | 131                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_966920    | Ca5                                     | 966920                        | TTTATTATTATTATTATTATTATT<br>/TTTATTATTATTATTATTATTATT<br>TATT | CAAGTTAAGCACCCCA<br>ACAT     | TGGGTGAGAACTTCG<br>ATCC        | 59.9                             | 773                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_9708216   | Ca5                                     | 9708216                       | AATATATATATATATATATATATA/<br>AATATATATATATATATATATATAT<br>A   | GGCAACGTATGTGTGT<br>TTGG     | AGAGTTGTCAATGGAT<br>CGGA       | 59.9                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_9741710   | Ca5                                     | 9741710                       | GTTTTTTTTTTT/GTTTTTTTTTTT                                     | TTCAACTCAACTTCATT<br>AGACCG  | CATTGGTGCGTTTGT<br>GTC         | 58.4                             | 434                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_9890157   | Ca5                                     | 9890157                       | GAAAAAAAAA/GAAAAAAAAA                                         | TTTCCTTCAATTGAGC<br>GGT      | ACAGGGGGAGGAAATG<br>AGAT       | 59.7                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10003572  | Ca6                                     | 10003572                      | CTTTTTTTTT/CTTTTTTTTT                                         | GCTGATTATCGCATTG<br>AGGC     | TGCTAGAGGCTGGAG<br>CAAAA       | 60.7                             | 739                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10127292  | Ca6                                     | 10127292                      | CAA/CA                                                        | TGGTTGCGACTTGTGT<br>TGTT     | CCGACTCAAATCAAAG<br>GGAG       | 60.2                             | 100                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10141273  | Ca6                                     | 10141273                      | TAAAAAAAAA/TAAAAAAAAA                                         | GGAAATATCAAATGTT<br>GTTACCGA | TCCAAAAACGACTTAGA<br>CCTCA     | 59.2                             | 736                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10174889  | Ca6                                     | 10174889                      | GTTTTTTTT/GTTTTTTTT                                           | CCGAACCTCAACAAC<br>CATTC     | AAAACAAAGTGTAACTG<br>TAAATGCAC | 59.6                             | 709                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10244839  | Ca6                                     | 10244839                      | TATAATA/TATAATAATA                                            | GGAAGAAGCCCTGTTG<br>TTTTT    | CATGGCTTCAAACACC<br>CTTT       | 59.6                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10326205  | Ca6                                     | 10326205                      | CTATATATATA/CTATATATATATA                                     | CAACATGTACCGTGA<br>ACTCAAA   | CATGGGTACATCACCA<br>CCAA       | 59.9                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_10335306  | Ca6                                     | 10335306                      | TG/TGG                                                        | CAATTCCCACAGGTAC<br>GCTT    | CAAACCCTAATTTTCA<br>AACACG   | 60.0                             | 305                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10351153  | Ca6                                     | 10351153                      | GTTATTATTATTATTATTAT/GTTATT<br>ATTATTATTAT                    | CAATTCCCACAGGTAC<br>GCTT    | ACAACCATAGACAGCC<br>GGAG     | 60.0                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10503058  | Ca6                                     | 10503058                      | AATATATA/AATATA                                               | AAACATGCTTTTGCATT<br>TTTGTT | GACTTCAACCGGTAGC<br>TGGA     | 59.9                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10503227  | Ca6                                     | 10503227                      | TG/T                                                          | AAACATGCTTTTGCATT<br>TTTGTT | GACTTCAACCGGTAGC<br>TGGA     | 59.9                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10513785  | Ca6                                     | 10513785                      | AT/A                                                          | CCTCCAGTGGCTGAAC<br>AAAT    | CGACTCAATGACGGGT<br>TTTT     | 60.1                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10514411  | Ca6                                     | 10514411                      | CAAAAAAAAA/CAAAAAAAAAAA                                       | TTCGCAATCTGTGTTTT<br>TCG    | CAAGAATTCGTATCGT<br>CTAAATGC | 59.8                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10514563  | Ca6                                     | 10514563                      | TAAAAAAAAA/TAAAAAAAAAAAAA                                     | TCACCAATCCTATGCT<br>GTTGTC  | ACGAAGTGACACATGA<br>CCCA     | 60.0                             | 924                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10516096  | Ca6                                     | 10516096                      | TA/T                                                          | ATTTGCGTGTGTGCCT<br>ACAA    | CACACACATTGCCTTAA<br>CGA     | 60.2                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10517494  | Ca6                                     | 10517494                      | GTT/GT                                                        | ACTCACGTGTTGGGG<br>TAA      | ACCATGCCCAAATTGA<br>AGT      | 60.3                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10552453  | Ca6                                     | 10552453                      | GTT/GTTT                                                      | ATAAGCAACGACAACC<br>ACCA    | CTCAACAAGTCATTGG<br>CCCT     | 59.1                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_10552509  | Ca6                                     | 10552509                      | CTTTTT/CTTTTT                                                 | GCCCGCATTAAATTG<br>TCAC    | TGAACATGAGGCTGCA<br>AAAG | 60.3                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10554117  | Ca6                                     | 10554117                      | TTATA/TTA                                                     | TAACTATCCCATCGGC<br>CAAA   | GGTGTATATTTAGCAT<br>GGGG | 60.3                             | 708                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10554507  | Ca6                                     | 10554507                      | AT/ATTT                                                       | TGGGTTAACGGAGAGT<br>AGCC   | ACTAGGACGACGAAAA<br>CGCA | 59.2                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10555535  | Ca6                                     | 10555535                      | GT/GTATTATT                                                   | AGCATGTGGAGCAGTT<br>GTTG   | CCCCGTTAATCCACTT<br>GCTA | 59.9                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10556820  | Ca6                                     | 10556820                      | ATTT/ATTTT                                                    | TATGACGGGCACACTT<br>GAGA   | CGTCATTTGCAAAAC<br>GACTT | 60.3                             | 474                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10560990  | Ca6                                     | 10560990                      | TAA/TAAA                                                      | CTTCACAATTCAAAT<br>CTCCA   | TGAAGAAAAATGCGGG<br>TCTT | 59.2                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10563725  | Ca6                                     | 10563725                      | TA/T                                                          | TCGAAAAAGCGGGATG<br>TTAC   | GGGTGTCACATGTTGA<br>TGGT | 60.1                             | 916                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10564033  | Ca6                                     | 10564033                      | AATATAT/AAT                                                   | GAAAATCCCAATCCAA<br>ATTTCA | GCAGCACACAGCATAG<br>GAAA | 60.0                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10564611  | Ca6                                     | 10564611                      | TAGAGA/TAGA                                                   | TTTCCTATGCTGTGTG<br>CTGC   | CTTTTCACCTTGATCG<br>GAA  | 60.0                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10572244  | Ca6                                     | 10572244                      | TAAA/TAA                                                      | CCGATGTAAGACTCTC<br>CCCA   | TGTTTCAACCTTGATT<br>GGA  | 60.1                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_10575764  | Ca6                                     | 10575764                      | ATTTTTTT/ATTTTTTTT                                            | TTTGTTGTGTGTGTG<br>CGC   | CCCCATGATACCCTT<br>CCTT     | 59.2                             | 294                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10576490  | Ca6                                     | 10576490                      | CTTTTT/CTTTTTT                                                | TTGCCAAAGGTTAATG<br>CACA | ATGGTGGTTGCTAGGT<br>TTGC    | 60.1                             | 888                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10586822  | Ca6                                     | 10586822                      | CAAAAAA/CAAAAAAA                                              | TTCCAGTTCTTTACCC<br>CAG  | AACTGTAACACACGTG<br>GCGA    | 60.1                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10592926  | Ca6                                     | 10592926                      | AAACTCATA/AAACTCATAACTCATA                                    | GGCTAGTGCTAAACCG<br>TTGG | AAAATCTGGCTGGATT<br>GCTT    | 59.8                             | 955                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10596898  | Ca6                                     | 10596898                      | TTATTATATATT/TTATT                                            | CCGACATAACAAGCAC<br>ATGG | GCCCTCCTCCATGACA<br>TAAA    | 60.0                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10608315  | Ca6                                     | 10608315                      | TG/TGG                                                        | ACCCGCTTAATTGTGG<br>CTAA | ACATTACCCGCATCCA<br>CCTA    | 59.6                             | 383                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10608634  | Ca6                                     | 10608634                      | TA/TACA                                                       | ACGAAGCTGGTACAAA<br>TGGG | CGAACCACCTACCA<br>TGAGA     | 60.0                             | 773                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10609160  | Ca6                                     | 10609160                      | AATTA/AA                                                      | TGGTTAAACGGCTCAA<br>TCAA | TTCTGGGAGATGCTCC<br>AAAT    | 59.2                             | 162                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10616106  | Ca6                                     | 10616106                      | TC/T                                                          | TATCCCCCTTCGTCT<br>CAG   | CGAATTGCAGGAATGT<br>GTTG    | 59.1                             | 801                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10616549  | Ca6                                     | 10616549                      | ATTTTTTT/ATTTTTT                                              | CAACACATTCTGCAATTCG      | AACTGTGAGGAGAGAG<br>AAGCAAA | 60.1                             | 219                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_10617092  | Ca6                                     | 10617092                      | C/CA                                                          | TTGTTTAATTGTTGGG<br>GGAGA  | AACGTAAGTTGGCACC<br>ATGC  | 59.3                             | 222                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10618337  | Ca6                                     | 10618337                      | TAAAA/TAAAAA                                                  | TGGAGAAGAAACATTC<br>ACGG   | AAAGATCGGCTCAAAT<br>GAACA | 58.7                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10618951  | Ca6                                     | 10618951                      | ATTTTT/ATTTTT                                                 | TGTTCAATTTGAGCCGA<br>TCTTT | GAGATAGGCTACCGCA<br>CAGG  | 59.7                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1061969   | Ca6                                     | 1061969                       | TAAAAAA/TAAAAAA                                               | AAATGAATGTGGAGTG<br>ACCAAA | TCAAAAGGGCTTTTCAT<br>TGG  | 59.3                             | 877                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10620292  | Ca6                                     | 10620292                      | TAAAAACA/TAAAAACAAAAAAC<br>A                                  | CAGTTGTGGCGATTGA<br>TTTG   | GGATCTGAAATCCCT<br>CTCC   | 60.1                             | 836                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10622254  | Ca6                                     | 10622254                      | AATATATATATAT/AATATATATAT                                     | TCTTCTCGAAAACAATT<br>TGTC  | AATTGTGCACATCGCT<br>GATT  | 57.5                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10622699  | Ca6                                     | 10622699                      | TCACGCTAGCAAATAGC/TC                                          | ATCAGCGATGTGCACA<br>ATT    | CAACCGTTGTTGAGG<br>CTAT   | 59.2                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10623512  | Ca6                                     | 10623512                      | TTTTCTT/TTT                                                   | TGGATGCCAAATAAT<br>CTCCA   | CCAACTCCCTCACTA<br>CCCA   | 60.3                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10623994  | Ca6                                     | 10623994                      | AAAGAAGAA/AAAGAA                                              | TGGGTAGTGAGGGAGT<br>TTGG   | TTAAAGGGCCTTGAT<br>GTTG   | 60.0                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10625658  | Ca6                                     | 10625658                      | AAA/AATAA                                                     | GCTCTCCAAGACTTCA<br>ACGG   | TCCAACCTTCCCTCATC<br>TTG  | 60.0                             | 782                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_10625726  | Ca6                                     | 10625726                      | GTTTTTTTTTTTT/GTTTTTTTTT                                      | TTTCCCCTAACTACCAC<br>CCC | TCCAACCTTCCCTCATC<br>TTG    | 60.0                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10640465  | Ca6                                     | 10640465                      | C/CGTAAGTATGA                                                 | CCTTCAGCATTAGACT<br>CCGC | AATCGCGAATATGGTC<br>CAAG    | 60.0                             | 787                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10642500  | Ca6                                     | 10642500                      | C/CCTATAGA                                                    | CGATTTGACAGCAAAA<br>GCAA | GACAACCTTCGTTGCC<br>CTAA    | 60.0                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10661984  | Ca6                                     | 10661984                      | A/AGT                                                         | TCCCTTCGCTACAAGA<br>AGGA | TTTGCAGACAACTTGA<br>GCTG    | 59.9                             | 752                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10664293  | Ca6                                     | 10664293                      | AATATATAT/AATATAT                                             | TACACCTGCAAAAGGT<br>GCAA | TTTGTTGTACCAAGCA<br>CACAC   | 60.3                             | 293                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10664476  | Ca6                                     | 10664476                      | GAAAAAAAAAAAAA/GAAAAAAAAA                                     | TACACCTGCAAAAGGT<br>GCAA | TCAATGTATTGGAAGG<br>TGAGACA | 60.3                             | 700                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10664595  | Ca6                                     | 10664595                      | TAAAA/TAAA                                                    | ACCACAATCACGGTGA<br>ACAG | TCAATGTATTGGAAGG<br>TGAGACA | 59.4                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10689201  | Ca6                                     | 10689201                      | AAT/A                                                         | TGTTGCATCAATGCCG<br>TTAT | TTCCCAATAACCAAAC<br>CAA     | 60.0                             | 758                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10700691  | Ca6                                     | 10700691                      | AG/A                                                          | ATAAAGAGAAGCGGAG<br>GGGA | CAACGAAGAGCGTCGA<br>GAAT    | 60.2                             | 909                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10701503  | Ca6                                     | 10701503                      | GTTATAA/GTTATAACTTATAA                                        | TCGACGCTCTTCGTTG<br>ACTA | GTGCACGGTACATTTC<br>TCCC    | 59.7                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_10702347  | Ca6                                     | 10702347                      | CTTTCGAAAGTT/CTTTCGAAAGTTG<br>AATTTTCGAAAGTT                  | TTGATGAATTGAAAGT<br>TCCGA      | TCCAGATTTTGAAGCTT<br>TTGC | 59.6                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10795007  | Ca6                                     | 10795007                      | AT/A                                                          | TTGGTTTTGAAACATTG<br>ATTGAT    | CATTACCTCGTGCAC<br>CACT   | 58.4                             | 374                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_10968845  | Ca6                                     | 10968845                      | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATAT         | TGAAACCTTCATTTCT<br>TTATTGAGTC | GCACATGGTTGCATGA<br>AAAA  | 58.5                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11031611  | Ca6                                     | 11031611                      | AGTCAGCAATAGCACTT/A                                           | GTGAAGCTGTTGGGGT<br>TGAT       | GACCGGCAACCAGAGA<br>ATTA  | 60.0                             | 238                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11035330  | Ca6                                     | 11035330                      | ATTTTTTTTT/ATTTTTTTTTT                                        | TGGCTAAATTACATTG<br>TGGTCC     | AGACGCATTCTTCTGT<br>CCGT  | 60.1                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11084875  | Ca6                                     | 11084875                      | ATTTTTTTTT/ATTTTTTTTTT                                        | GCGAATGTGTTAAAT<br>GGGG        | ACGTCCTTTGAAATGTC<br>GGC  | 60.2                             | 257                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_112870    | Ca6                                     | 112870                        | TG/T                                                          | AACTCCTTGGGACCGT<br>GATT       | ACCTTGCAACTGGAGC<br>AAAT  | 60.7                             | 242                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11310241  | Ca6                                     | 11310241                      | GTTTTGCATA/G                                                  | CATGTGGAAGAAGCTC<br>CACA       | TCCTCCGGAACATAAC<br>TTGG  | 60.0                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11310976  | Ca6                                     | 11310976                      | AT/ATT                                                        | TTTTGCCAGAAGAATT<br>TGG        | TTTTTCCTTTGGTGGA<br>TGG   | 60.0                             | 175                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11316099  | Ca6                                     | 11316099                      | AC/A                                                          | GTTTGTTGTGGTTGCA<br>GTGG       | GCTGATTGTTGCCTC<br>TCTC   | 60.0                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_11362880  | Ca6                                     | 11362880                      | ATTTTTTTT/ATTTTTTTT                                                     | CCCCACCATCCATGAT<br>AAAC   | TTGTTCTCTACGCTGAA<br>TTGGA | 59.9                             | 873                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11391053  | Ca6                                     | 11391053                      | ATTTTTTTT/ATTTTTTTT                                                     | CGACGAAAATAGAGGG<br>ACCA   | TGTGGGAGCCACATGT<br>ATTT   | 60.1                             | 370                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11490708  | Ca6                                     | 11490708                      | AATATATATATATATATATATA/AA<br>TATATATATATATATATATA                       | CGTGAATGTTTGTGTT<br>TGCC   | TGTTATCCAGTCATGGT<br>GTCAA | 60.0                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11497940  | Ca6                                     | 11497940                      | ATTTTTTTT/ATTTTTTTT                                                     | TTATTGCCTATTGCCAC<br>ACA   | GTGTGAGTGTGAGACC<br>CGTG   | 57.7                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11546028  | Ca6                                     | 11546028                      | CAAA/CAAAA                                                              | GATCGATTTGGGCTAC<br>GAAA   | ATCAGATTGCTGCAGG<br>CTTT   | 60.0                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11546493  | Ca6                                     | 11546493                      | TAAAAAAAAAAAAAAAAA/TAAAAAAAAA<br>A                                      | TCGGAAAGGTCATTCA<br>AAGC   | TTTGTGTCCAAGCATT<br>CTCC   | 60.2                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11565007  | Ca6                                     | 11565007                      | CTTTTT/CTTTTTTT                                                         | TGATCATTTGATGAAC<br>GTTTGA | CAACCACTCCTTGAAAA<br>CCAA  | 59.0                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11565258  | Ca6                                     | 11565258                      | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATA<br>TATATATATATAT | TTGGTTTTCAAGGAGT<br>GGTTG  | TTGCTGCCTCAACCAT<br>ACAG   | 60.0                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11568345  | Ca6                                     | 11568345                      | AA/AACA                                                                 | ATTGCCCAACCAATTAT<br>GGA   | GAGGGTGCATCAGCT<br>AAAG    | 60.0                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11569101  | Ca6                                     | 11569101                      | T/TAAGTAA                                                               | CAAAAGGGGGTATTTT<br>GGTTC  | CGTTCAATTCCTGCCA<br>AAT    | 59.6                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_11569249  | Ca6                                     | 11569249                      | ATATTT/AT                                                     | ATTGGCAGGAAATTG<br>AACG    | TCGGTGGTTGCACATT<br>CTTA | 59.9                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11590997  | Ca6                                     | 11590997                      | CTTTT/CTTTT                                                   | ATGTGCTCCCCACAAA<br>AGTC   | CCCTCCAGTAGCATCA<br>CCAT | 60.0                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11592242  | Ca6                                     | 11592242                      | GTTA/GTTATTGAATTCCTTTA                                        | TGTTGAACTCAAGGAT<br>TGCG   | ACCCAATTTGTTTGGG<br>ATGA | 59.8                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11599026  | Ca6                                     | 11599026                      | TATTA/T                                                       | AAAATGGATTTTCCCA<br>AGG    | GCAAGGATTGACATGG<br>GAGT | 60.0                             | 607                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11610694  | Ca6                                     | 11610694                      | T/TA                                                          | CTCGACATGGGGTAGG<br>TTGT   | GCGCCCAATTAATGGA<br>TACT | 59.8                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11654526  | Ca6                                     | 11654526                      | ATTTTTTTTTTT/ATTTTTTTTTTTT                                    | GCGGCTAATAGTTGGT<br>CGTG   | TGTCGGCTCACGTTTT<br>TGTA | 60.7                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11661530  | Ca6                                     | 11661530                      | GAAAAA/GAAAAAA                                                | GTTGAGTTGCGGGTGT<br>TTTT   | ATATTCCCCTCCCAACA<br>TCC | 60.0                             | 421                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11663719  | Ca6                                     | 11663719                      | CAAAA/CAAA                                                    | GCATTACCGATCATGG<br>GTGT   | CAGTCACGTCAAAGTG<br>CTCG | 60.6                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11671266  | Ca6                                     | 11671266                      | TAAAAA/TAAAA                                                  | TTGAATGGATATGCTTT<br>TGGTG | TGCCCTAGCAAAGGTA<br>GTCA | 59.8                             | 936                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11679999  | Ca6                                     | 11679999                      | T/TA                                                          | CTCACCCAAACACACA<br>CTCA   | CATGGAAAGCAGAAGC<br>ACAA | 58.1                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_11685034  | Ca6                                     | 11685034                      | TGGG/TGG                                                      | ATCGCCAGCAACTTTA<br>GCAT | GGGAACCAAAGTGTTG<br>ACCA  | 59.9                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11687884  | Ca6                                     | 11687884                      | GTTTTTTTTT/GTTTTTTTTT                                         | CCTTTGAGTTTGGTCC<br>TCCA | GGAGGAGGAGGAGAA<br>GGATG  | 60.1                             | 716                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11693016  | Ca6                                     | 11693016                      | TTAATAATAATAATAAT/TTAATA<br>ATAATAATAAT                       | TGACCTGCTGAATGAT<br>TTGG | TCGACGAAATCCTAAAT<br>GTGG | 59.6                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11706831  | Ca6                                     | 11706831                      | AT/ATT                                                        | TCATCCACATTGGTGC<br>TGTT | TGGAATTGGGCCTAAA<br>GATG  | 60.0                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11722419  | Ca6                                     | 11722419                      | TATATT/TATATTAATATT                                           | CCTTCGCCGTATATGA<br>TTCC | AAGCAAAGGTCCTGAG<br>CAAA  | 59.4                             | 185                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11728216  | Ca6                                     | 11728216                      | T/TG                                                          | TGAGTTGTTAGTCGTC<br>GGGA | TCATGAGAATGCCTTT<br>GTGA  | 59.3                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11738985  | Ca6                                     | 11738985                      | TAAAAAAA/TAAAAAAA                                             | TTCAGCAGCTTCTTCG<br>ACAA | ATTACCGACATTGCAG<br>AGGG  | 59.9                             | 254                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11741312  | Ca6                                     | 11741312                      | GCAGTACA/GCA                                                  | TGGAACCAAGGTCCA<br>AGTC  | GCACTGCAAAATCATTC<br>CCT  | 59.9                             | 308                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11742023  | Ca6                                     | 11742023                      | ATTTTTTT/ATTTTTTTT                                            | GCGCTTCAATTTACAA<br>CGCT | TTTTCGCACGAAATCAA<br>TCA  | 60.4                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_11744525  | Ca6                                     | 11744525                      | AAAAAAA/AAAAAATAAAAAA                                         | TTTGCGGAATGGTGAT<br>TCTT | TTGTGAACGAAATGCG<br>AGTC  | 60.4                             | 370                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                 |                           |                            |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_11746077  | Ca6                                     | 11746077                      | AATATATATATATATATATA/AATATA<br>TATATATATATATATATATA                                             | TGCAAGTCGAAATTCA<br>CACG  | TGGGTCAAGCCCAATA<br>AAAC   | 60.8                             | 538                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_11746285  | Ca6                                     | 11746285                      | TTA/TTAGTATTAGTA                                                                                | TGCAAGTCGAAATTCA<br>CACG  | TTTGTGGGAAAACCC<br>AAAG    | 60.8                             | 930                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_11755125  | Ca6                                     | 11755125                      | GTCAAAGATTTTCTTCAA/GTCAA                                                                        | CGATCATGTTGATTT<br>TGTTCA | TGAAATCCCTGAGCT<br>GGTC    | 59.9                             | 527                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_11762104  | Ca6                                     | 11762104                      | A/AG                                                                                            | TAAGCATTGGGGTTG<br>AAAG   | ACGTTGAGGAGACACC<br>TGCT   | 59.9                             | 259                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_11788716  | Ca6                                     | 11788716                      | TTTGGATAATTGGATAATTGGAT/TT<br>TGGATAATTGGAT                                                     | GGTTCAGCAACCGAGA<br>GTTC  | TGATAATGCGACGAAA<br>ACCA   | 59.9                             | 363                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_11996420  | Ca6                                     | 11996420                      | CATATATATATATATATATATATA<br>TATATA/CATATATATATATATATATA<br>TATATATATATATA                       | GGGCGACTTTTCCTTA<br>TTCC  | TATTTTCTTGGTTTGC<br>GGG    | 59.9                             | 233                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_12253200  | Ca6                                     | 12253200                      | AATATATATATATATATATATATAT<br>ATATATATATATATAT/AATATATATA<br>TATATATATATATATATATATATAT           | CTCCGTTTATCTCCGTT<br>GGA  | CGTGATGATTGATGCA<br>TTTCA  | 60.1                             | 746                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_12325715  | Ca6                                     | 12325715                      | T/TAC                                                                                           | TTGTGAATGGCATGTT<br>TTGG  | TGAGAACTTTTCCGCT<br>GCT    | 60.4                             | 868                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_12565656  | Ca6                                     | 12565656                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATT/TTTATTATTAT<br>TATTATTATTATTATTATTATTATT<br>TATTATT | ACATCCAATGAAATAG<br>CCGC  | AAAATAGCCTTTTCGCC<br>ACC   | 59.9                             | 825                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_12680067  | Ca6                                     | 12680067                      | CATTATTATTATTATTATTATTATT<br>TATTATTAT/CATTATTATTATTATTA<br>TTATTATTATTATTAT                    | CCGGTCTCTGTGGTGA<br>CTG   | AAGGACATGTTGGTTG<br>AAACAC | 60.3                             | 643                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                                 |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_12680394  | Ca6                                     | 12680394                      | CATATATATAT/CATATATATATATAT                                   | TGTGTTTCAACCAACAT<br>GTCC | GGAAACATGCAATTG<br>GACT         | 59.3                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12705859  | Ca6                                     | 12705859                      | ATTTTTT/ATTTTT                                                | AATAACACACCAAACC<br>CCCA  | CAACTTAGGGTTAACTT<br>ATGCATTTTT | 59.9                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12787897  | Ca6                                     | 12787897                      | AATATATATATATATATATAT/AA<br>TATATATATATATATATATATAT           | ATCAAACAAATGTTGC<br>GAGC  | CAAACCCCTATTTTTGT<br>GATTGA     | 58.8                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12861842  | Ca6                                     | 12861842                      | ATTTTTTT/ATTTTTTT                                             | TCAATCCCTTCATTG<br>GAAG   | TCGATAGTGGGTTTCG<br>TGTTTC      | 60.0                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12868319  | Ca6                                     | 12868319                      | TTGCG/T                                                       | GCATGTCAAGATAATG<br>GGCA  | CCGCATAACCAAAAC<br>TCAC         | 59.5                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12870795  | Ca6                                     | 12870795                      | TAAAAAAAA/TAAAAAAAAA                                          | CATCCCAAGCAAAAC<br>GAAT   | CATTGAGAGGATCCAA<br>AATCAA      | 59.9                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12872062  | Ca6                                     | 12872062                      | AGG/AG                                                        | TTTTCTTTCATCTGTGG<br>GGC  | CCCAAACACAAAATCAT<br>GGA        | 60.1                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12877302  | Ca6                                     | 12877302                      | CG/CGCTTTTTTTG                                                | GTTTCGTAAAGGACGGG<br>ATGA | CTTTTACAGCGCTTTCT<br>GGG        | 59.9                             | 235                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12888429  | Ca6                                     | 12888429                      | T/TC                                                          | CCGTCAATTTATATCCT<br>CCCA | AATCAGGGTGCCATTG<br>TAGC        | 58.8                             | 733                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12898258  | Ca6                                     | 12898258                      | TAAAAAAAA/TAAAAAAAAA                                          | ACTACCATGTTTGGTG<br>GGGA  | CACATTGAAAATCAACT<br>TTACACCA   | 60.1                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_12899367  | Ca6                                     | 12899367                      | ATTTTTTTT/ATTTTTTT                                            | TTGGATGTATACGGCG<br>AACA  | TCCTACGAAAGTTTTAG<br>TCATTGC | 60.0                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12910939  | Ca6                                     | 12910939                      | CG/CGG                                                        | ATCAATGAAAGCCCCA<br>AGTG  | TCTTCCTCTTTCTTCCT<br>CTTTCA  | 59.9                             | 852                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12919764  | Ca6                                     | 12919764                      | TTAATAAT/TTAAT                                                | TTGTTCCGACATTGTT<br>TGG   | CCACACACTCCACGAG<br>AGAA     | 59.4                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12920238  | Ca6                                     | 12920238                      | CAAAAA/CAAAAA                                                 | TTCTCTCGTGGAGTGT<br>GTGG  | TTGAAGAACCTCCTTC<br>CTTCC    | 59.9                             | 377                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12922857  | Ca6                                     | 12922857                      | A/AC                                                          | TTTTACGCGGAAACA<br>AATC   | CAGAAACAGCAGAGAC<br>AGCG     | 59.9                             | 686                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12923575  | Ca6                                     | 12923575                      | TTTACATATCATTACA/TTTACA                                       | TGTTGGCAGAGATGAA<br>GTGG  | ATGGGGATGCAGAAGA<br>GAGA     | 59.8                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12923712  | Ca6                                     | 12923712                      | AT/ATT                                                        | TGTTGGCAGAGATGAA<br>GTGG  | ATGGGGATGCAGAAGA<br>GAGA     | 59.8                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12931395  | Ca6                                     | 12931395                      | CAAAAAAAAA/CAAAAAAAAAA                                        | CACGGTTTACATGGGC<br>AATA  | ATCTGGTATCAAATGC<br>CCCA     | 59.3                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12931779  | Ca6                                     | 12931779                      | TAAAA/TAAA                                                    | CTTGGGGCATTGATA<br>CCAG   | TTGTTTGTGGCGATAG<br>TTGC     | 60.3                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12933054  | Ca6                                     | 12933054                      | CTTTTTTTTT/CTTTTTTTTTTTT                                      | TTTCACAAATTAATGA<br>CCCAA | TGATTCAGAGCCATTAA<br>ACCA    | 58.5                             | 442                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')         | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                 |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_12933312  | Ca6                                     | 12933312                      | AT/ATT                                                        | TTTCACAAATTAATGA<br>CCCAAA      | TCAACCCACTTAAATTA<br>AATCTTTTT | 58.5                             | 481                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12933675  | Ca6                                     | 12933675                      | TG/T                                                          | AGTGGTTTAATGGCTC<br>TGAATC      | TGCAAGTTTGGAGTCT<br>ATAATTCATC | 57.4                             | 717                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12933836  | Ca6                                     | 12933836                      | TAAAAAAAAA/TAAAAAAAAA                                         | GTTAATCGAAAAAGAAA<br>AGAGTAAAAA | CCCCTCCAAATAAATT<br>TCACAA     | 57.3                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12934479  | Ca6                                     | 12934479                      | ATTTTTGTTTT/ATTTTTGTTTT<br>TGTTTT                             | CGGTTTGAAGATGAGG<br>TTCAC       | TTCTCCCTCTAGATTG<br>TTTGC      | 59.6                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12944504  | Ca6                                     | 12944504                      | TCCC/TCC                                                      | CATTGGTGCTTCAAAC<br>CGAT        | TCCCTCGTACTTCCAAA<br>ACG       | 60.9                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12945433  | Ca6                                     | 12945433                      | G/GATTCAGAT                                                   | TGGTGGTGAGGTCCA<br>CAGA         | TTACGGTGTTCAAATT<br>CGT        | 60.0                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12948486  | Ca6                                     | 12948486                      | ATTTT/ATTT                                                    | CCGATGATTTCAAAAAT<br>TTAACC     | CAAGTTTGTGTACCAG<br>GCCA       | 58.8                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12949470  | Ca6                                     | 12949470                      | GTATATAT/GTATATATAT                                           | TTGGATGGACCAACT<br>CAAT         | GTCACCCATCAACGCC<br>TATT       | 60.2                             | 305                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12952484  | Ca6                                     | 12952484                      | TTATATATATATATATATATATATA<br>/TTATATATATATATATA               | TCGGAAAACAATGCAA<br>ATCA        | GATTTGAGTTCCAAATT<br>TGATGA    | 60.1                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12955482  | Ca6                                     | 12955482                      | A/AATT                                                        | TGTGCAATTGGATGTT<br>GTTG        | AACCCCATCAAATGAT<br>GAA        | 59.0                             | 215                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_12955724  | Ca6                                     | 12955724                      | TG/T                                                          | TGTGCAATTGGATGTT<br>GTTG    | ACTCGTTTGGTCATTC<br>GTGA | 59.0                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12957166  | Ca6                                     | 12957166                      | T/TC                                                          | TGAATCCCGAAATTGA<br>CCAT    | AAAAGCAAACAGGTGA<br>ACCG | 60.1                             | 404                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12957525  | Ca6                                     | 12957525                      | CAAA/CAAAA                                                    | CGGTTACCTGTTTGC<br>TTTT     | TGAAAAGCTTGAGGAA<br>GGGA | 60.1                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12957709  | Ca6                                     | 12957709                      | T/TC                                                          | CGGTTACCTGTTTGC<br>TTTT     | TGAAAAGCTTGAGGAA<br>GGGA | 60.1                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12958210  | Ca6                                     | 12958210                      | ATTTTTTTT/ATTTTTTTTTT                                         | CTATTCCGCTTGGTCG<br>AAAA    | GAAGCGATAGAGAGAG<br>GCGA | 60.2                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12958383  | Ca6                                     | 12958383                      | TAAAAA/TAAAAA                                                 | TCCCTTCCTCAAGCTTT<br>TCA    | TTTCTGGAAGAGGCAG<br>AAGC | 59.9                             | 880                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12958420  | Ca6                                     | 12958420                      | TTATATATATATATAT/TTATATATAT<br>ATATATAT                       | TCCCTTCCTCAAGCTTT<br>TCA    | TTTCTGGAAGAGGCAG<br>AAGC | 59.9                             | 880                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12964004  | Ca6                                     | 12964004                      | ATAT/A                                                        | CTCGTGGCATGGTTCT<br>CTTT    | CAGCCCGTCCTAAATC<br>TTCA | 60.3                             | 506                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12964933  | Ca6                                     | 12964933                      | TCATTA/T                                                      | CTTGTTGCCAAGTAGG<br>GTCG    | CCAAGGGAGAGGTGCT<br>TAAA | 60.7                             | 976                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12965919  | Ca6                                     | 12965919                      | ATTTTTTTT/ATTTTTTTTTT                                         | GCACACAATCAAAATG<br>TATCACC | ACATTTTTGCCCTCATT<br>TCG | 59.3                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                  |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_12967108  | Ca6                                     | 12967108                      | TA/TAA                                                           | ATAAGCCCCAAGACTG<br>TCCA   | CCCCTTAATTTTGCAT<br>GGTT | 59.6                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_12982915  | Ca6                                     | 12982915                      | GTAATAA/GTAA                                                     | TCATGAAATGTTGCCT<br>GGAA   | TGACATACGGCTGGAA<br>TGAA | 60.0                             | 850                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13001289  | Ca6                                     | 13001289                      | GACACA/GACACACA                                                  | CGTTTTGTTGGGCATA<br>ATCA   | CCTAGGCCAAAATTCA<br>AGCA | 59.4                             | 773                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13003025  | Ca6                                     | 13003025                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATATAT                    | CTCCCACTTGCATCCA<br>TCTT   | TCTTCTTCTGGTGCAAT<br>CCC | 60.1                             | 770                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13016905  | Ca6                                     | 13016905                      | TCC/TCCC                                                         | TGGATCACCACAAACC<br>ACAC   | GAACGGCACAGAGAGG<br>AAAC | 60.3                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13033375  | Ca6                                     | 13033375                      | CTATATATATATATATAT/CTATAT<br>ATATATATATATATATAT                  | TCCTAGAGTCAATGGA<br>TCCCC  | GGGAGGTGGTTCAGAG<br>TCAT | 60.3                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13061150  | Ca6                                     | 13061150                      | CTAT/CTATAT                                                      | TCCTTATGGTCCAAGC<br>GAAC   | CAAGTTATGCCCTTTT<br>GACA | 60.1                             | 758                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13128943  | Ca6                                     | 13128943                      | CTTTTTTTTTTT/CTTTTTTTTTTT                                        | CACCACGAGATCAAAA<br>CCCT   | CCATTGGCAGTGAAC<br>TCTT  | 60.0                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13170216  | Ca6                                     | 13170216                      | AATATATA/AATATATATA                                              | TCAACCAAGAATTGCT<br>GCTAAA | AGGGAGTATTCACGGC<br>ACAC | 59.9                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13180103  | Ca6                                     | 13180103                      | TTTATTATTATTATTATTATTATT<br>AT/TTTATTATTATTATTATTATT<br>ATTATTAT | TTTGAGTCAGTCAACG<br>CAGG   | TAAACCATTCAAACCCC<br>CAA | 60.0                             | 830                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_13381796  | Ca6                                     | 13381796                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                 | GGGTTTCGTAGTTGTAT<br>GCGAA    | CATGGATCAGAGTTGC<br>CTTG   | 60.0                             | 883                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1343859   | Ca6                                     | 1343859                       | GAAAAA/GAAAAA                                                 | CAACGAGTTTGATTCT<br>ATTCTAACG | TTGGGTAGCCAAGGTT<br>TCAC   | 59.7                             | 721                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13447479  | Ca6                                     | 13447479                      | TTATATATATATATAT/TTATATATAT<br>ATATATAT                       | TCATGATGAGTCGGCA<br>ACAT      | TCTCCGACCTTTAAAT<br>CAACAA | 60.1                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13450334  | Ca6                                     | 13450334                      | CAAAAA/CAAAAA                                                 | TGATGCGCTTGCATAT<br>GTTT      | TGTCAGTACCCACCCA<br>CTCA   | 60.2                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13469022  | Ca6                                     | 13469022                      | CAATTAA/CAA                                                   | CTCAAATTCTGTTTGG<br>GGGA      | TTGTGGTCCCTCAGAG<br>AAGG   | 59.9                             | 170                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13475824  | Ca6                                     | 13475824                      | AAAGAAGAAGAAGAAGAA/AAA<br>GAAGAAGAAGAAGAA                     | TGTGGTCCCAACAAT<br>CTCA       | TTTTGGGTCAAGGAAA<br>ATGG   | 59.9                             | 330                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1350878   | Ca6                                     | 1350878                       | A/AGTCTGT                                                     | ACACATCAGCTTTTTG<br>GCTG      | AGCCCACTCACCTTCT<br>TCCT   | 58.9                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13536206  | Ca6                                     | 13536206                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                 | TTAACAAATAAGCCGG<br>CGAC      | AGGGGTTGTGAAGTCG<br>ACAC   | 60.1                             | 302                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1354322   | Ca6                                     | 1354322                       | GAA/GAACCAA                                                   | AATTTCATAGGCGGT<br>GAAG       | GGTGTACAGCTTTCAT<br>GAACAA | 60.1                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13578932  | Ca6                                     | 13578932                      | AATATATATATATATATATAT/AAT<br>ATATATATATATATATAT               | TCAGCAATGGCAAATA<br>TGGA      | AAAAATCCATCTATGC<br>TTCACA | 60.0                             | 848                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                             | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                           |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_13654782  | Ca6                                     | 13654782                      | GTTT/GT                                                                                                                   | CATCAAACTCAAACG<br>CATCA   | CACGTCAATTTTCGACA<br>TGA    | 59.7                             | 721                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13838996  | Ca6                                     | 13838996                      | CCT/CCTTCT                                                                                                                | TGTGTGATTGGTGTG<br>AGCA    | GCAACAACGGGTGAAA<br>ATCT    | 59.7                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_13959907  | Ca6                                     | 13959907                      | CTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAA/CTAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAA | ATCTCCTTCTTTCGCAC<br>CAA   | TTTTTCTGGCACGTATT<br>GGA    | 59.8                             | 722                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_14163783  | Ca6                                     | 14163783                      | CATATATATATATATATATATATA<br>TATA/CATATATATATATATATATA<br>TATATATATATATA                                                   | TAATCGGGAAAAACCT<br>GCAC   | AATTTAATATCCCGTCC<br>GGC    | 59.9                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_14171375  | Ca6                                     | 14171375                      | TGAAAAATTCGAAA/TGAAA                                                                                                      | CATGCAACTCCACAGG<br>AAAA   | GGTCTTTGGTTTGAGA<br>TGCC    | 59.7                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_14206895  | Ca6                                     | 14206895                      | CCATCATCAATC/CCATCATCAATCA<br>TCATCAATC                                                                                   | TGCAACCAGAACCAAT<br>GTGT   | TGACCATACCTCACCA<br>ACCC    | 60.0                             | 930                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_14222488  | Ca6                                     | 14222488                      | GATATATATATATATATATATA/GA<br>TATATATATATATATATA                                                                           | TTTCAATGGGGGAAAG<br>AATG   | CTGAACAACCTTGTGC<br>AACC    | 59.7                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_14260813  | Ca6                                     | 14260813                      | AATATATATATATATATATATATAT<br>ATATATAT/AATATATATATATATATA<br>TATATATATATATATAT                                             | GGAGAAAATTAAGAGG<br>GAGGGA | TTGATTTTGAAATGCAC<br>CCA    | 59.9                             | 411                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_14410304  | Ca6                                     | 14410304                      | TTTTATTTATTTATTTATTTATTT<br>TATTTATTTATTTAT/TTTTATTTATTT<br>ATTTATTTATTTATTTATTTAT                                        | TTGTGCATGGTTGTGG<br>ATCT   | TCTCAAGTTTGTAAGC<br>GAGTCAA | 60.0                             | 193                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_14519498  | Ca6                                     | 14519498                      | TG/T                                                                                                                      | TTGGTGTCACAATCAA<br>CGAAA  | TTTAAACCACATCGCA<br>CCA     | 60.0                             | 442                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_14553627  | Ca6                                     | 14553627                      | TTATATATATAT/TTATATATAT                                                 | TGTTTCATCAAGACCTG<br>CACTG   | CAAAAATTTGTGAGAGA<br>CCAAA  | 59.9                             | 232                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_14661772  | Ca6                                     | 14661772                      | ATTTTAATTT/ATTTTAATTTCACTTT<br>TAATTT                                   | TGGCTTTTCAAACATAA<br>GCAAA   | TCTGATGTTGTCAATTG<br>TGAAGG | 59.1                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_14676799  | Ca6                                     | 14676799                      | TTCTCTCTCTCTCTCTCT/TTCTC<br>TCTCTCTCTCTCTCTCT                           | AGTGGGTGGTGCCAA<br>AGAG      | ACCCAGGCTATGGAAT<br>GTCA    | 60.0                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_14755534  | Ca6                                     | 14755534                      | AATATATATATATATATATATAT/A<br>ATATATATATATATATATATATATA<br>TATATAT       | TTTTAACCGTGGTTGA<br>AACTT    | AGTCAGACGCTACTCG<br>GCAT    | 57.8                             | 212                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_14884145  | Ca6                                     | 14884145                      | ATTTTTTTTTTTT/ATTTTTTTTTTT                                              | AGCACCGATTAGATGA<br>GTTGAA   | CAAGCTCGACTAGCAG<br>CTCA    | 58.9                             | 719                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_14938058  | Ca6                                     | 14938058                      | TAAAAAAAAA/TAAAAAAAAA                                                   | CCTCCTACATTGTGGG<br>TGCT     | ACATTTGGCCCATTTG<br>GTGA    | 60.0                             | 754                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_14959810  | Ca6                                     | 14959810                      | CTTTTTTTTTTT/CTTTTTTTTTTT                                               | GCGAAATGCTTCTCAA<br>AACC     | CGTTACAACGTTGCTG<br>AATGA   | 59.8                             | 745                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1506907   | Ca6                                     | 1506907                       | CTTTTT/CTTTT                                                            | CTGGAAAAAGCACTTC<br>AGGC     | GCAAGAGGAAAAGACG<br>AACG    | 60.0                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15073082  | Ca6                                     | 15073082                      | CATATATATATATATATATATATA<br>TATATATATA/CATATATATATATATA<br>TATATATATATA | CACTCACTCTCCGCCA<br>CTTA     | CATTCTCGGGTGGAG<br>AAAA     | 59.0                             | 780                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15097608  | Ca6                                     | 15097608                      | AATATATATATATATATATATATATA<br>A/AATATATATATATATATATATATA<br>ATATA       | TGTTTGAAAATTTGAT<br>GACTTTTT | AACAAGTTTTGATTGCA<br>GGAA   | 58.3                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                        | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                                      |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_15277411  | Ca6                                     | 15277411                      | AATTATTATTATTATTATTATTAT<br>TATTATTATTATTATT/AATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATT                                                                           | CGTCTTTCTAATATTTT<br>GCCGA   | CATGAAAGTGGTCAGA<br>TGCG   | 58.5                             | 700                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1540640   | Ca6                                     | 1540640                       | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTAT/ATAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT | GGAAATGGTGGTTTGA<br>TTGC     | TGATAAGGAGTTGGTT<br>GGTGTG | 60.2                             | 780                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15412187  | Ca6                                     | 15412187                      | CAAAAAAAAA/CAAAAAAAAA                                                                                                                                                | TATAACCACGCGCAAA<br>ATCC     | GCACCGAATACCGACA<br>TCTT   | 59.8                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1542114   | Ca6                                     | 1542114                       | ATT/ATTT                                                                                                                                                             | TGCACTTTGTCACTC<br>CTTA      | GTAAATGCTGCGTGCA<br>AACA   | 58.1                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15429919  | Ca6                                     | 15429919                      | TAAA/TAAAA                                                                                                                                                           | TCGACCACATCAGCA<br>CTTC      | CCGATGGCTCTATGTC<br>TTCC   | 59.8                             | 737                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15528104  | Ca6                                     | 15528104                      | ATTTTT/ATTTTTT                                                                                                                                                       | TGCACCAAATGAGTCA<br>CATTATTA | TGTTGTGGATTGAGC<br>ACTTCT  | 59.4                             | 374                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15555599  | Ca6                                     | 15555599                      | AATATATA/AATATA                                                                                                                                                      | TGTGGGCACATTAGTA<br>GGCA     | TCATCGTCGTTGCTTG<br>AGTC   | 60.1                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15559125  | Ca6                                     | 15559125                      | CTTT/CTT                                                                                                                                                             | TCACCAAACAAAACT<br>GGGG      | CTACATTCCGGTTAGG<br>GCAA   | 60.8                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15559149  | Ca6                                     | 15559149                      | AG/A                                                                                                                                                                 | TCACCAAACAAAACT<br>GGGG      | CTACATTCCGGTTAGG<br>GCAA   | 60.8                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1556325   | Ca6                                     | 1556325                       | TAAA/TAAAAAAAAAAAAA                                                                                                                                                  | ATTGTTCTCCGTTGTCA<br>GGG     | GTGATCGACATACTTC<br>GGCA   | 60.0                             | 864                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_1556869   | Ca6                                     | 1556869                       | TAAAAA/TAAAAA                                                 | CAATTTGGTTGGCGT<br>AAAC    | TTGCTTTATACTCATAT<br>TTTGGCCT | 60.2                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1557117   | Ca6                                     | 1557117                       | TAAAAAAAA/TAAAAAAAAA                                          | GCTTTTCTTTCATATTG<br>CCGT  | TTTGAGCGGAAAGAG<br>TCGT       | 59.6                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1559094   | Ca6                                     | 1559094                       | TATGA/TTTTAATTTTAAAGTAATGA                                    | CAGAGCAGTGTGACAG<br>CAAGA  | TCAAAAATTTCAAACAA<br>AATCCA   | 60.4                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1559285   | Ca6                                     | 1559285                       | GTTA/GTTATTA                                                  | CAGAGCAGTGTGACAG<br>CAAGA  | TCAAAAATTTCAAACAA<br>AATCCA   | 60.4                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1559581   | Ca6                                     | 1559581                       | ATTTTTTTTTTT/ATTTTTTTTTT                                      | TGAAGTTAAATTAAGG<br>ATCGCA | TATTTTATCCACC GC<br>TGC       | 58.0                             | 283                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1559995   | Ca6                                     | 1559995                       | AT/A                                                          | AATATTACTGCAGCGG<br>TGGG   | ATGCCAATTTTACCCTG<br>CAC      | 60.0                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1560016   | Ca6                                     | 1560016                       | TTT/TTTAATT                                                   | AATATTACTGCAGCGG<br>TGGG   | GGACCACAAGAAATCC<br>TCCA      | 60.0                             | 719                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15727094  | Ca6                                     | 15727094                      | ATTTATTTTATTTT/ATTTATTTTATTT<br>TATTTT                        | TCCCCCGTCTAACTAG<br>GGTT   | CCACTTGTGTCCTAAC<br>AATTCAA   | 59.8                             | 268                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15727514  | Ca6                                     | 15727514                      | ATTTATTTTATTTTATTTTATTT/ATTT<br>ATTTTATTTTATTTTATTTTATTT      | TTAGTTTGGGCTTGGG<br>TTTT   | TTGCTCCTACGTATCTC<br>CCG      | 58.6                             | 911                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15728024  | Ca6                                     | 15728024                      | AA/AAATA                                                      | CGGGAGATACGTAGGA<br>GCAA   | TCGATTATGCGTAGGG<br>AAGG      | 60.2                             | 248                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                              |                          |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_15730699  | Ca6                                     | 15730699                      | TAAA/TAA                                                                                                     | ATTTGAACCTGGCAGC<br>AAAA | GTTTGTAAAAAGGGT<br>GATG      | 60.6                             | 175                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15730843  | Ca6                                     | 15730843                      | T/TGA                                                                                                        | ATTTGAACCTGGCAGC<br>AAAA | GCTTGATGAATAATCA<br>ATGGCT   | 60.6                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15731057  | Ca6                                     | 15731057                      | TAAAA/TAA                                                                                                    | ATTTGAACCTGGCAGC<br>AAAA | GGGACAAAAGGCTAGT<br>TTGG     | 60.6                             | 909                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15897034  | Ca6                                     | 15897034                      | AATATTATATTATA/AATATTATA                                                                                     | TGCACCCACCTCTTTT<br>AGA  | CGGAAAACCTTGAGGT<br>TTCAA    | 58.4                             | 245                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15966204  | Ca6                                     | 15966204                      | GTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTA/GTTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTA | CTGCCTGAAATTTGGT<br>TGCT | AGATGCGACCTCCTAC<br>TTGC     | 60.2                             | 229                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_15999975  | Ca6                                     | 15999975                      | A/AG                                                                                                         | AAGTGTGGGCATTTC<br>TTTG  | ATGGACCTCTGTATTC<br>GCCA     | 60.0                             | 137                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_16012701  | Ca6                                     | 16012701                      | TA/TAA                                                                                                       | TAAGAGTTTGGTTCCG<br>GTGG | TGTGCAGATAAATGGC<br>CAAA     | 60.0                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_16063357  | Ca6                                     | 16063357                      | AT/ATT                                                                                                       | CGTGGAACCTCCCT<br>CAAA   | TGAGTGGTTAGTCCCA<br>CATTGA   | 60.1                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_16093896  | Ca6                                     | 16093896                      | AAAAAATATATAAAAAATATA/AAAAA<br>TATA                                                                          | TGCAAAAAGATGGCAA<br>TGAA | TTTCCTTAAATATCCAT<br>CCAGTCA | 60.2                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_16121564  | Ca6                                     | 16121564                      | ACATCAATCTCATCAAT/ACATCAAT                                                                                   | TCGGTTGCCTATGGTA<br>CTCC | ACGGCAGTAGCCATT<br>GAGT      | 60.0                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                     |                               |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_16191754  | Ca6                                     | 16191754                      | GAAAAAAAAA/GAAAAAAAAA                                               | GGAAAGAGAGGAAACC<br>AGGG      | GCAGCTGAGTCATCCC<br>CTAT    | 60.0                             | 717                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_16259714  | Ca6                                     | 16259714                      | GTTATTATTATTATTATTATTATT<br>ATTATT/GTTATTATTATTATTATT<br>TATTATTATT | GGGGGCAAGTTATATC<br>CACC      | TGGAAATGTAACACC<br>CCAAA    | 60.4                             | 782                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_16286125  | Ca6                                     | 16286125                      | CTTACTTTTT/CTTACTTTTTACTTTT<br>T                                    | TGTTGGGATATTTCCTT<br>TGGA     | CTTGAAAGAGCCGCAA<br>GAAG    | 59.3                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1629307   | Ca6                                     | 1629307                       | TTACTACTACTACTACTACTA/TTAC<br>TACTACTACTACTA                        | GGAGTGAGTACCGTGG<br>GAGA      | TGTGACACATCCCGTG<br>TCTT    | 60.1                             | 229                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_16370279  | Ca6                                     | 16370279                      | AATATATATATATATATATATA/AA<br>TATATATATATATATATATATAT<br>ATATA       | CAGATTCATGCATATG<br>GTCAAAA   | GGAAAGCTTGCTTGAT<br>AAATACG | 59.8                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_16400010  | Ca6                                     | 16400010                      | TTATATATATATATATATATA/TTATA<br>TATATATATATATA                       | GGATGATCAAACTCGC<br>AGGT      | TTGACGCTTTTAGAGG<br>CAGAA   | 60.1                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_16522140  | Ca6                                     | 16522140                      | GAAAAAAAAA/GAAAAAAAAA                                               | CAAAAGCAAAAGAGGT<br>TGAACA    | TGGATTGACGATGAAG<br>GAAA    | 59.4                             | 907                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_16557006  | Ca6                                     | 16557006                      | GTTTTTTTTT/GTTTTTTTTTTT                                             | TTGCTTCAGGCGCTTA<br>CATT      | CAGTTTCACGCACTCA<br>ATCG    | 59.7                             | 700                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_16579245  | Ca6                                     | 16579245                      | ATTTTATGT/ATTTTATGTTTATGT                                           | AAGGAATACGTTATCA<br>CCGATAAAA | CCTTTGAAATAAACATG<br>CTGC   | 59.3                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_16693405  | Ca6                                     | 16693405                      | GAAAAAAAAA/GAAAAAAAAA                                               | TCGGACGACTAGTCCC<br>AATC      | CAACCAAAGCAGGGGT<br>TTTA    | 60.1                             | 767                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)          | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                        |                            |                              |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_16710889  | Ca6                                     | 16710889                      | AATATATATATATATATATA/AATA<br>TATATATATATATATATATATA                    | TGTAACCAACACAAGG<br>GGGT   | TCTCGCGTCTAAAAG<br>TACAC     | 60.1                             | 615                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_1682722   | Ca6                                     | 1682722                       | GTGCATCTGTTT/G                                                         | GAGGCATTGTCTTTGG<br>TGGT   | GCAATGTTTGAATG<br>GCTT       | 60.0                             | 656                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_16911701  | Ca6                                     | 16911701                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                              | GTTTGGTGGGGATGAG<br>AAGA   | CACATGTTGAATGCATT<br>GACTAAA | 59.9                             | 794                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_16942985  | Ca6                                     | 16942985                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                              | TGGCAGGTGAACTCGT<br>GATA   | TGAATCATTTTGTCTG<br>TCCTCA   | 60.3                             | 544                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_16949745  | Ca6                                     | 16949745                      | GATATATATATATATATATAT/GAT<br>ATATATATATATATATAT                        | GGACGACATTGATGTG<br>GAAA   | TTGTTGGAAGTTTGTG<br>AGGC     | 59.3                             | 448                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_16995027  | Ca6                                     | 16995027                      | A/AT                                                                   | TTAAAGGCAGATGGGC<br>AAAC   | TCAACAACTGGTAGC<br>GTCG      | 60.1                             | 293                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_16999043  | Ca6                                     | 16999043                      | CTTATTATTATTATTATTATTATT<br>AT/CTTATTATTATTATTATTATT<br>ATTATTATTATTAT | TTTTCCACCACTTTTTC<br>TTCTC | TTCAATCTTTGTGCCAC<br>CAG     | 57.5                             | 196                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_17025329  | Ca6                                     | 17025329                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                              | TTTGTCTCCACGTTTTC<br>CTT   | GGCTTATAGGCCACG<br>TTTT      | 59.7                             | 562                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_17025431  | Ca6                                     | 17025431                      | ATTTTTTTTTTTTT/ATTTTTTTTTTT                                            | TTTGTCTCCACGTTTTC<br>CTT   | GGCTTATAGGCCACG<br>TTTT      | 59.7                             | 562                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_17025729  | Ca6                                     | 17025729                      | TAAAAAAAAAAAAA/TAAAAAAAAAAA                                            | TTTGTCTCCACGTTTTC<br>CTT   | GGCTTATAGGCCACG<br>TTTT      | 59.7                             | 562                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_17056993  | Ca6                                     | 17056993                      | ATTTTTTTT/ATTTTTTT                                            | AAAAGCTAGTTTTATTA<br>TGGAGCAGT | TGTGGCACGCACCTTC<br>TAAC  | 57.6                             | 817                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17057027  | Ca6                                     | 17057027                      | TAAAAAAA/TAAAAAAA                                             | TGGATACAACCTAAAAT<br>GCCG      | TGTGGCACGCACCTTC<br>TAAC  | 59.8                             | 337                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17058914  | Ca6                                     | 17058914                      | AT/A                                                          | TTGGTAAGGAAAGGGG<br>AAAAA      | TGAGATCAACGCTTTTT<br>GGTT | 59.8                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17059083  | Ca6                                     | 17059083                      | CGA/C                                                         | TGAGTAGATTCAGTC<br>ACCCA       | ATAAAATGGACACAGG<br>CGCT  | 59.2                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17063685  | Ca6                                     | 17063685                      | CA/CAA                                                        | CAGAAGATCAAGATGC<br>CCGT       | AAATTTTCGGGAGTTC<br>CACC  | 60.2                             | 344                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17076415  | Ca6                                     | 17076415                      | TT/TTAT                                                       | ACATCCCCTCACTCTC<br>AACG       | ATCGTTGCACTCAAAC<br>GACA  | 60.1                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17083127  | Ca6                                     | 17083127                      | AGA/AGAATTTTGA                                                | TTAGCTGAATCACGAA<br>CCCC       | TGATTGCGGAAAATAG<br>TCCC  | 60.1                             | 271                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17085039  | Ca6                                     | 17085039                      | GAAAAAAA/GAAAAAAA                                             | GGTTTATTGCAAGAGT<br>GGGC       | CAGTCATTTGCATTTTT<br>GCG  | 59.6                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17085352  | Ca6                                     | 17085352                      | TTTTATTTATTT/TTTTATTTATTTAT<br>T                              | CGCAAAAATGCAAATG<br>ACTG       | TTCCCCATGCATCACTA<br>TCA  | 60.3                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17088463  | Ca6                                     | 17088463                      | TAAAAA/TAAAAA                                                 | ACAAAGAGGGTGGTAA<br>GGGG       | AAATGTTGCCAAATTCC<br>ATTG | 60.2                             | 839                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_17089209  | Ca6                                     | 17089209                      | AT/ATCT                                                       | TTCAATGGAATTTGGC<br>AACA    | TTCCGAAGACGATGAA<br>AATTG  | 59.9                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17097536  | Ca6                                     | 17097536                      | TGAG/TG                                                       | TAACCATCGCAAACCA<br>TGTG    | AGGTTGCAACTTTTGG<br>TCAT   | 60.4                             | 915                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17101167  | Ca6                                     | 17101167                      | AT/A                                                          | AAAAGTTGTGCCTTTCT<br>TTTTCA | AGCAAGAAATGTGTGA<br>CGCTT  | 59.4                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17101873  | Ca6                                     | 17101873                      | AG/A                                                          | AAGCGTCACACATTC<br>TTGCT    | TCGCATTATTTAAAGCA<br>TCTCA | 59.9                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17102055  | Ca6                                     | 17102055                      | AG/A                                                          | AAAACATAAAGTGGGG<br>AAATCAA | AAGCGTTGGATGGAGA<br>GAGA   | 58.8                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17102897  | Ca6                                     | 17102897                      | TGG/TG                                                        | CTCTCTCCATCCAACG<br>CTTC    | ATCTCGATCCAGCGAT<br>CATT   | 60.0                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17103746  | Ca6                                     | 17103746                      | TAAAAA/TAAAAA                                                 | CCCTCTTTTACGAGTA<br>CCGTGT  | GGTTCATGCAGGTGGA<br>AAAT   | 59.6                             | 928                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17103901  | Ca6                                     | 17103901                      | CATGTATATGTATAT/CATGTATAT                                     | CAAAACAAAAACCATC<br>AAGAA   | GGTTCATGCAGGTGGA<br>AAAT   | 59.0                             | 311                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17109515  | Ca6                                     | 17109515                      | GTATATATATAT/GTATATATATAT<br>ATAT                             | TGCAGAGTGCAGATT<br>TGTC     | TCGATGTCTCGTGCA<br>T       | 60.1                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17136094  | Ca6                                     | 17136094                      | GAAA/GAA                                                      | AGACAAGCACGTCATT<br>GGTG    | TTTGCTTGTTGGTCCA<br>TGA    | 59.8                             | 219                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                       | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                     |                              |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_17136205  | Ca6                                     | 17136205                      | CAAAAA/CAAAAAA                                                                                      | TCATGGACCAACAAG<br>CAAA      | ATTTCTCGCGACATGC<br>ATTA     | 60.1                             | 238                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17138585  | Ca6                                     | 17138585                      | TC/T                                                                                                | GGGGTGGGAACTATG<br>TTCA      | AATTAGGGGGATCAGT<br>TCCG     | 59.6                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17139579  | Ca6                                     | 17139579                      | TA/T                                                                                                | TTACGAAAGGTTTTGG<br>CACA     | AACGAGGTTGAATAAT<br>GCGG     | 59.2                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17170239  | Ca6                                     | 17170239                      | GTATTATTATTATTAT/GTATTAT<br>TATTATTAT                                                               | TTGTGTTGGGGATGG<br>TAAA      | GGGTTTTAGTGTGGG<br>GGTT      | 60.0                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17170994  | Ca6                                     | 17170994                      | TTCTCTCTCTCTCTCT/TTCTCTC<br>TCTCTCTCTCTCT                                                           | AACCCCACTACTAAA<br>ACCC      | AGGGAATTCGGACTTA<br>CGGT     | 60.0                             | 747                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17191873  | Ca6                                     | 17191873                      | GTTTTTTTT/GTTTTTTTTT                                                                                | TTGATATTGTGTTTGAT<br>TTCGTTT | TTCGAGAGAAATTGGG<br>GTTG     | 57.7                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17199265  | Ca6                                     | 17199265                      | TTATATATATATAT/TTATATATATAT<br>ATAT                                                                 | TTCCACCCCTACTGC<br>TATG      | TTTCATATTCAAATTC<br>TCACATTG | 59.9                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1729337   | Ca6                                     | 1729337                       | GTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTAT/G<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTAT | TGGCTTAATTGTCCTTT<br>TTGATG  | TGCCGCTTCAATGCT<br>ACAG      | 60.3                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17333891  | Ca6                                     | 17333891                      | TTATATATATATATAT/TTATATAT<br>ATATATATATAT                                                           | TGCATAAGTTTCTCGTT<br>GCG     | CTTGCTGCAAAAATCG<br>TTGA     | 60.0                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17380756  | Ca6                                     | 17380756                      | GTTTTTTTT/GTTTTTTTTT                                                                                | CAAGTCATTTGCCGTT<br>GAGA     | TGGCAAGCAACATAAA<br>TGGA     | 59.8                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                           | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                         |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_17398675  | Ca6                                     | 17398675                      | ATTTTTTTTTTTT/ATTTTTTTTTTT                                                                              | TCCATTGATCGATGC<br>TTCA    | AACTTGGCGACACCAA<br>AATC   | 60.2                             | 305                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17414159  | Ca6                                     | 17414159                      | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATAT                                                   | CATGCAATTGGAAGCT<br>CTGA   | ATTGGCAACTCTTGG<br>GATG    | 59.9                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17503155  | Ca6                                     | 17503155                      | GATATATATATATAT/GATATATATAT<br>ATATAT                                                                   | ATTCCCATTAAGTGCC<br>CACA   | TCCAAATGGCGACTTC<br>CTAC   | 60.2                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1768942   | Ca6                                     | 1768942                       | CTTTT/CTTT                                                                                              | GCATGCAGCTAAATGA<br>ATCAA  | GTTCTTGGCCTGTTGT<br>GGTT   | 58.9                             | 212                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17710771  | Ca6                                     | 17710771                      | CAATAATAATAATAATAATAATA<br>ATAATAATAAT/CAATAATAATAATAA<br>TAATAATAATAATAATAATAAT                        | CAGCTAAGAGCGACTC<br>ATTGAC | GTGTTGTCTGGGCCCT<br>CATT   | 59.3                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17744108  | Ca6                                     | 17744108                      | CTTTTTTTTTTT/CTTTTTTTTTTT                                                                               | TTATTGCACGATTACAT<br>GTCG  | ATGCGTTAACGGAACA<br>TCAA   | 57.2                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17844765  | Ca6                                     | 17844765                      | GTATATATATATAT/GTATATATATAT<br>ATAT                                                                     | GCAAATATGCAACAAC<br>CTTCC  | TTAATTTGGGTTAGACG<br>CGG   | 59.5                             | 467                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17847880  | Ca6                                     | 17847880                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AA/AAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAA | TAGCCGGCTTTTAGTT<br>GACC   | TTCATGTTGAAAAGT<br>GATTGTG | 59.4                             | 357                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1788325   | Ca6                                     | 1788325                       | CTTTTTTTTTTT/CTTTTTTTTTTT                                                                               | AGGGTGTAAGGCATGG<br>ATGA   | CCATCAATCAAAGCAAA<br>CCA   | 60.3                             | 330                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_17930276  | Ca6                                     | 17930276                      | ATTTTTTT/ATTTTTTTT                                                                                      | TCCTCCCTTAATTCATT<br>CGTG  | TCAGTTGGTGACCCAT<br>GAAC   | 59.0                             | 391                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                      | Forward primers (5'-3')    | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------|----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                    |                            |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_1801492   | Ca6                                     | 1801492                       | GTTTTTTTT/GTTTTTTTT                                                                | ACGGTGAAGTGGTGA<br>CTTC    | TCACACATTCGCTCAA<br>TCC        | 60.0                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_181004    | Ca6                                     | 181004                        | TAAAAA/TAAAAA                                                                      | AAACCTATCCGCGTCA<br>ACAC   | TCGATGAATTATAAAG<br>GTCTTCAGTG | 60.0                             | 856                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1814002   | Ca6                                     | 1814002                       | TTCTCTCTCTCT/TTCTCTCTCT<br>T                                                       | TCGAAGTGACTCTGAA<br>GGATGA | TTGAACCAAGAACATC<br>GCA        | 60.0                             | 324                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_18175044  | Ca6                                     | 18175044                      | ATATATATAT/ATATATATATCTAT<br>ATAT                                                  | TTTCTTTCTTGCGTGAC<br>CATT  | GCCATGCACTGTCAAG<br>AGAA       | 59.7                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_18180870  | Ca6                                     | 18180870                      | TTATATATATATATATATATATAT<br>TATATATATATA/TTATATATATAT<br>ATATATATATATATATATATATATA | GAGGTCGATTGGTCAT<br>TATGG  | TCATCATTCCACCACAG<br>CAT       | 59.3                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_18216681  | Ca6                                     | 18216681                      | AATTATTATTATTATTATTATTAT<br>TA/AATTATTATTATTATTATTAT<br>TATTATTATTATTA             | TGTTCAACCGCATTAA<br>TTGA   | ATAGCAACTTCCGAGA<br>TGCG       | 59.1                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1824314   | Ca6                                     | 1824314                       | C/CTCACAAA                                                                         | TTGCAGAATGCATGGG<br>AATA   | TCCAACTCTCCGACC<br>AAAC        | 60.0                             | 779                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1824646   | Ca6                                     | 1824646                       | AG/A                                                                               | GTTTGGTCGGAGAGTT<br>TGGA   | CCCTCCTTATCCTTACG<br>GTTG      | 60.1                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1824728   | Ca6                                     | 1824728                       | ATTTTT/ATTTT                                                                       | GTTTGGTCGGAGAGTT<br>TGGA   | CCCTCCTTATCCTTACG<br>GTTG      | 60.1                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_1833817   | Ca6                                     | 1833817                       | AAGG/A                                                                             | AAGGTGGGTTGAGACC<br>TTCT   | ATTCTCGGTTGACGA<br>GATG        | 57.7                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)                                 | Forward primers (5'-3')   | Reverse primers (5'-3') | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------|---------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                |                           |                         |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | Tfs |
| Ca6_P4_1834196   | Ca6                                     | 1834196                       | TT/TTTTATTTTAT                                                                                 | CATCTCGTCAACCGAGGAAT      | ATTTGAGACTTGC GGG AGAA  | 60.1                             | 302                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_18414573  | Ca6                                     | 18414573                      | TTATATATATATATATATATATATATATATATAT/TTATATATATATATATATATATATAT                                  | TCAACAAACTTCGTCA CATTCA   | TCCTCACGGACGACTTAACC    | 59.2                             | 382                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_18423210  | Ca6                                     | 18423210                      | GTATATATATATATATATATATATA/G TATATATATATATATATATA                                               | CGCGGGGATGTATTTTCCAA      | TACCCGACGAACTCGA AAAC   | 60.7                             | 286                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_1843596   | Ca6                                     | 1843596                       | C/CCTAACG                                                                                      | AGCTGAGAGATGTGCC GTTT     | TCTGCGAATCCGTCTT AACC   | 60.0                             | 594                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_18471682  | Ca6                                     | 18471682                      | AATATATATATATATATATA/AATATA TATATATATATATATA                                                   | TCCTTTGTTGGATTCTT TGCT    | ACACCCGAACTGAACT CACC   | 58.8                             | 844                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_18508690  | Ca6                                     | 18508690                      | CTA/C                                                                                          | AACATGTGGTGGTGGG TTTT     | GCCGAGCCCATCTAAA CATA   | 60.0                             | 852                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_18567135  | Ca6                                     | 18567135                      | AAATAATAATAATAATAATAATAATA ATAATAATAATAA/AAATAATAATAAT AATAATAATAATAATAATAATAATAA TAATAATAATAA | TCAACGAGGTTGCATA CCAG     | TGATCCGATAAAAAATA GGAGG | 59.7                             | 426                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_18570186  | Ca6                                     | 18570186                      | ATTTTTTTTT/ATTTTTTTTT                                                                          | GGCTCAGGGGATTAT AGGC      | CCCACCAAACCGATCT AAAA   | 59.9                             | 517                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_18625376  | Ca6                                     | 18625376                      | TTAATAATAATAATAATAATAATAAT AATAATAATAA/TTAATAATAATAATA ATAATAATAATAA                           | CGAGTACATCGCTAAT TTGGA    | AGCGGTTTGTTTCAGT TTTG   | 59.3                             | 449                                           | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_18626197  | Ca6                                     | 18626197                      | TAGTCCA/TA                                                                                     | CCGACTATCTTTTTGTCTCAT AAC | CATCACC CATCAGGAG ACCT  | 59.5                             | 407                                           | INTERGENIC                                  | --                               | --                    | --  |





| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                   |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_2032078   | Ca6                                     | 2032078                       | CATTATTATTATTATTATTATT/C<br>ATTATTATTATTATTATTATT                                 | CCTCTCAACCCCTCTC<br>CTCT    | GTTGGTGAACAATGCA<br>CAGG  | 59.8                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_20659055  | Ca6                                     | 20659055                      | AC/A                                                                              | TGGAAATGAAAACAAC<br>ACCG    | TGAAATCGATACTGC<br>CCCT   | 59.4                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_20679328  | Ca6                                     | 20679328                      | CATATATATATATATAT/CATATATAT<br>ATATATATAT                                         | CAAAATTTGTCACGGAA<br>AGCA   | CAATACTTGTGTTGTG<br>GCGG  | 59.7                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_20697646  | Ca6                                     | 20697646                      | CATATATATATATATATATATATA<br>TATAT/CATATATATATATATATATAT<br>ATATATATATATATAT       | CAAACAAGAAACATGG<br>ACCTCA  | TGACGTTAACTTGCA<br>CCAC   | 60.0                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_2086027   | Ca6                                     | 2086027                       | CAATAATAATAATAATAATAATA<br>ATAATAATAA/CAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA | CGACCATCACAAACAA<br>ACAA    | TTGAAATGAAATCGG<br>TACACA | 58.0                             | 216                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_20883267  | Ca6                                     | 20883267                      | ACCTAATCCTA/ACCTA                                                                 | TGAAGGGGACACTTGCA<br>CAAA   | AATGTGTCGATGTGCG<br>CTAA  | 60.3                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_20995016  | Ca6                                     | 20995016                      | TAA/TA                                                                            | GCTTGGGGACAAGCAA<br>TAGA    | CCCAAGTTCCCAAGAG<br>TCAA  | 60.2                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21013539  | Ca6                                     | 21013539                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                                         | GATGCATAAATTACTTT<br>GCCACC | TCCTACACTCAGCCCA<br>GTCC  | 59.8                             | 256                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21021586  | Ca6                                     | 21021586                      | CTATTTATTTATTTATTTATTTT/<br>CTATTTATTTATTTATTTATTT                                | CACCGTCGTGTTTCATC<br>TGTC   | TTATTTACCGTCGTGT<br>CCA   | 60.2                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_2108083   | Ca6                                     | 2108083                       | A/ATTATGT                                                                         | CTGGAATTCCTCTGCTT<br>GGC    | CCATGATTTGGATTTTG<br>GTG  | 60.0                             | 807                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                              | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                            |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_21100809  | Ca6                                     | 21100809                      | ATTTTTTTTTT/ATTTTTTTTTT                                                                                    | TGAGGGATTCTCGAA<br>GTTG     | TGTGATTGTGTGGG<br>AAGAA    | 60.2                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21139884  | Ca6                                     | 21139884                      | ATTTTTTTT/ATTTTTTTTTT                                                                                      | CAGAAGGATTGCTCGT<br>GTGA    | TGCATAGGCCAAAATG<br>ATTGA  | 60.0                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21141563  | Ca6                                     | 21141563                      | GTTTTTT/GTTTTT                                                                                             | TCCGATAGGAAGAGCC<br>AATG    | ACGTTTATTTTCGGAC<br>CCC    | 60.2                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21154360  | Ca6                                     | 21154360                      | GATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAA/GA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAATA | TTTCGTCTGATGGATG<br>ACCA    | GCGTTGGTCTCTTTT<br>GCTC    | 60.0                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21245145  | Ca6                                     | 21245145                      | T/TAATAATAA                                                                                                | TCAAGACGAGCAGCCA<br>ACTA    | ATGTGTGGGACCCGAT<br>AAAA   | 59.7                             | 686                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21266964  | Ca6                                     | 21266964                      | AATTATTATTATTATTATTATTAT<br>T/AATTATTATTATTATTATTATT<br>ATTATTATT                                          | GAAGGAGAGGAGGAG<br>GAGGA    | TCCATTAGGGGTGGAA<br>ATGA   | 59.9                             | 826                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_2128046   | Ca6                                     | 2128046                       | CTTTTTTTTT/CTTTTTTTTT                                                                                      | AATTGCTTTGATTTTG<br>CCG     | GTGCTCGTGC GACTTG<br>TAAA  | 60.1                             | 562                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21340779  | Ca6                                     | 21340779                      | AT/ATT                                                                                                     | GTTGAGGTGATGGGTA<br>TGGG    | GACAATGAATCAATCAC<br>CATGA | 60.1                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21388665  | Ca6                                     | 21388665                      | GTATATATATATATATATAT/GTAT<br>ATATATATATATATAT                                                              | CGCTAGTCTTTTATCTC<br>AATTCG | TTCTTTGCACCATGCA<br>GTC    | 58.7                             | 366                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21399662  | Ca6                                     | 21399662                      | AAATAATAATAATAATAATAA/AAATA<br>ATAATAATAATAA                                                               | TCCCTAGTTGGAGGTC<br>GATG    | GTCCACCTAAATGCC<br>TTGA    | 60.1                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                         | Forward primers (5'-3')        | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------|--------------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                       |                                |                            |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_21400148  | Ca6                                     | 21400148                      | ATATTATTATTATTATTATT/ATA<br>TTATTATTATTATTATT                                         | GATGTGGAACCTCAAGG<br>GCAT      | AGCCAGCTGAAGACCA<br>AAAA   | 59.9                             | 349                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_21401312  | Ca6                                     | 21401312                      | C/CT                                                                                  | AGCTCAGTCCTCACAA<br>CCGT       | TTAGATCGGACAAGAA<br>ACCGA  | 59.9                             | 344                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_21470474  | Ca6                                     | 21470474                      | CAAAAAAAAA/CAAAAAAAAAA                                                                | TTTCACATATCTATCA<br>AACACATTTT | TTCGTTGCTCAAAGA<br>CTCC    | 59.2                             | 367                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_21485595  | Ca6                                     | 21485595                      | GTTTTTTT/GTTTTTTT                                                                     | TGCGGGCTAGCTCACT<br>TAAT       | TCAAAACAAATAGGCA<br>GGGG   | 60.0                             | 115                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_21485767  | Ca6                                     | 21485767                      | ACCCC/ACCCCC                                                                          | TGCGGGCTAGCTCACT<br>TAAT       | TTTGATTCTCTGGCCG<br>AGTT   | 60.0                             | 263                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_21605985  | Ca6                                     | 21605985                      | CTATATATATATATATATA/CTATATA<br>TATATATATATATA                                         | GATTTTCGCACTGAAC<br>GGAT       | TCCCTTCTATTTCCCT<br>TGAA   | 60.1                             | 437                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_216120    | Ca6                                     | 216120                        | ATTTTTTTTTTT/ATTTTTTTTTTT                                                             | TGCTGACGATGTGATG<br>GAAT       | GTGGTCGTCGTAGGGA<br>AAAA   | 60.1                             | 553                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_2164101   | Ca6                                     | 2164101                       | GTATATATATATATATATATATAT<br>ATATA/GTATATATATATATATATATA<br>TATATATA                   | CTCCTGCTAGATCACG<br>CCTC       | TGACTTTGCAGAGAAG<br>GAAAAA | 60.1                             | 557                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_21739441  | Ca6                                     | 21739441                      | AATATATATATATATATATATATAT<br>ATATATATAT/AATATATATATATATA<br>TATATATATATATATATATATATAT | TGAAGAACCATGGTCA<br>TATTAGACA  | AAACAAGGCTTCAACC<br>CTGA   | 59.8                             | 569                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_21769271  | Ca6                                     | 21769271                      | TTTATTAATTATTAAATTATTAA/TT<br>TATTAAATTATTAA                                          | AATTTCTTTGGAGGTT<br>CGC        | CCAAGCCCGCATATGA<br>TAGT   | 60.4                             | 814                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')         | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                 |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_21780461  | Ca6                                     | 21780461                      | T/TCG                                                         | GGTCGTTGATGCGA<br>ATTTT         | AAAACAAATGACCAAT<br>CGAAA   | 59.0                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21782816  | Ca6                                     | 21782816                      | TTTTATTT/TTTT                                                 | TAATGAGTTGGGACGG<br>GAGA        | ATGCAAACGCTACCCA<br>ATTCT   | 60.5                             | 782                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_2179226   | Ca6                                     | 2179226                       | CTTAGGGTTAGGGTTAGGGTT/CTT<br>AGGGTTAGGGTTAGGGTTAGGGTT         | GGGCAAAAAGGTGAGT<br>GAAA        | TAAACCGTGCTTGCTC<br>TTGA    | 60.1                             | 368                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21797693  | Ca6                                     | 21797693                      | ATTTAA/ATTTAATTTAATTTTAA                                      | TTGCTAATATACTTAAC<br>CCAATCTCAA | AAAGATGACACAAATC<br>GGGG    | 58.7                             | 166                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21799195  | Ca6                                     | 21799195                      | GAAAAA/GAAAAA                                                 | CAAAAGCATGTGCTCA<br>AAGG        | AATGGCAATCCAAATG<br>CTTC    | 59.5                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21801686  | Ca6                                     | 21801686                      | GA/GAA                                                        | TCTTGAACCGATACCC<br>TTTTT       | GACGGATGAGCATCGG<br>TTAT    | 57.7                             | 311                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21812932  | Ca6                                     | 21812932                      | TGA/TGAGA                                                     | GATGACACGGACCAAA<br>CCTT        | TTCAGCAGCAAAACCA<br>TCAG    | 59.8                             | 154                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21822725  | Ca6                                     | 21822725                      | ATTTTTTT/ATTTTTT                                              | CGAAGGTTTGTGCATC<br>TGAA        | TGAATTCACATGATTTT<br>GAGCA  | 59.8                             | 241                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21901902  | Ca6                                     | 21901902                      | TAAAAAAAAAAAAA/TAAAAAAAAAAA<br>A                              | CACCAGAAACAGTGGC<br>AAAA        | CCCGGATCTATGACCT<br>GCTA    | 59.7                             | 265                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_21927352  | Ca6                                     | 21927352                      | TCACACACACACACACACACAT<br>CACACACACACACACACACAC<br>A          | AAGGGAGGAGGAGAAA<br>GCTG        | CAACAAATTTATTACC<br>GCTCAAA | 60.0                             | 232                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                        | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                      |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_21988310  | Ca6                                     | 21988310                      | GAATAATAATAATAATAATAATA<br>ATAATA/GAATAATAATAATAATA<br>ATAATAATA                                                                     | TGAAATTCGTACCTCAT<br>GCTT   | AATGAGATAACCCGTG<br>CGTC   | 57.4                             | 391                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_22034371  | Ca6                                     | 22034371                      | AATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTA/AATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTA | CGCCCAATTTTCGTAAG<br>TAGC   | CTGGCCCAAGTGACCT<br>CTTA   | 59.7                             | 378                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_22082431  | Ca6                                     | 22082431                      | TTATATATATATATATATATA/TTA<br>TATATATATATATATATATA                                                                                    | TATGAATTTTGC GTTGCG<br>GAG  | GAGTTTGCGAAGAAT<br>TCACA   | 59.8                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_22099449  | Ca6                                     | 22099449                      | ATTTTTTTTT/ATTTTTTTTTTT                                                                                                              | TGTGTTGCTTCTTGCG<br>TTTG    | ACGTGTGGGTTTCAGG<br>TCTC   | 60.0                             | 620                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_22124013  | Ca6                                     | 22124013                      | TTCTCTCTCTCTCTCTCTCT/TTCT<br>CTCTCTCTCTCTCTCT                                                                                        | ATTCCAACGATCCAAG<br>ATGG    | TGCTCCAATGATGTTA<br>GAAACG | 59.8                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_22128416  | Ca6                                     | 22128416                      | CTTTTTTTTT/CTTTTTTTTT                                                                                                                | CACACACACAAAGA<br>GGGG      | ATAGGACCTGCTGCCT<br>GAGA   | 60.0                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_22410012  | Ca6                                     | 22410012                      | ATTT/ACACAAACATGACTCTTT                                                                                                              | TTTCATGTATCGGGCC<br>TAGC    | CTCTGGATCAAAGGG<br>TCAA    | 60.1                             | 688                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_22477290  | Ca6                                     | 22477290                      | GTATATATATATATATATAT/GTAT<br>ATATATATATATATATAT                                                                                      | AATTGAGTGAGTGGAA<br>TGAACA  | GGTCTTCCACCAACCT<br>TTGA   | 57.2                             | 805                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_23064745  | Ca6                                     | 23064745                      | C/A/C                                                                                                                                | TGGGTTGATTTCCCA<br>CATT     | TCTCGAGCAAATCAC<br>AGTTAAA | 60.0                             | 571                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_23065041  | Ca6                                     | 23065041                      | TGG/TG                                                                                                                               | TTTCGAATGCCTATCTA<br>ATTGGT | AAAAATCCGCAGGAAA<br>GGTT   | 59.1                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                 |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_23078754  | Ca6                                     | 23078754                      | TGG/TGGG                                                                        | TGGACAATCGCCCAAA<br>TTAT    | TCTCGAGCAAATCACG<br>AGTTA   | 60.2                             | 716                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_23078938  | Ca6                                     | 23078938                      | T/TC                                                                            | TGGACAATCGCCCAAA<br>TTAT    | TCTCGAGCAAATCACG<br>AGTTA   | 60.2                             | 716                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_23090578  | Ca6                                     | 23090578                      | AC/A                                                                            | GCCAAGCTTGTTTGT<br>GGTT     | TGTGTGCACATGTTGT<br>TCGT    | 60.2                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_23365057  | Ca6                                     | 23365057                      | ATTTTTTTTTT/ATTTTTTTTT                                                          | CCATATGCGAGAAGGA<br>CGAT    | GCAAGCCTTTTGCTA<br>TGAC     | 60.1                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_233746    | Ca6                                     | 233746                        | TTATTTATTTATTTATTTATTTA<br>TTTAT/TTATTTATTTATTTATATTT<br>ATTTATTTATTTATTTATTTAT | CGGATCCCACCACTTG<br>ATAA    | TTGATCGTTGGGTGA<br>TGAAAT   | 60.7                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_23409253  | Ca6                                     | 23409253                      | CTTTTT/CTTTTT                                                                   | TGCCGTATAAAATGGG<br>CTTC    | CTTGCTCTTCCTTCGTT<br>GCT    | 59.9                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_23655687  | Ca6                                     | 23655687                      | AATATATATATATATATATA/AATA<br>TATATATATATATA                                     | CAAGTTGAATTCATTAA<br>GACGCC | GATTGATCGCAGGGAC<br>AAGT    | 60.0                             | 294                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_23741801  | Ca6                                     | 23741801                      | GTATATATATATATATATAT/GTAT<br>ATATATATATATATATATATATA<br>TATAT                   | TAGTGCTCTGCATTG<br>TCCG     | TGAAGGACGATGAATT<br>CCTAAAA | 60.0                             | 768                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_2382805   | Ca6                                     | 2382805                       | ATTTTTTTTT/ATTTTTTTTT                                                           | TTACGGCCACCTATCG<br>AATC    | AAAATGGAGCGTTGTT<br>GGAC    | 59.9                             | 932                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_2384865   | Ca6                                     | 2384865                       | TTAATAATAATAATAATAATAAT<br>AATAATAATAA/TTAATAATAATAA<br>ATAATAATAATAATAATAATAA  | AGATTGCCCCACTTCA<br>AAAA    | TAACCTGCCAAAGAGG<br>AGGA    | 59.5                             | 866                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                   |                           |                            |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_23873936  | Ca6                                     | 23873936                      | CAT/CATCCTTTAAT                                                   | GAGCATAGTTCCTTT<br>CACGG  | AATTTTGGTCCCAAC<br>AGA     | 58.8                             | 441                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_24186567  | Ca6                                     | 24186567                      | AATATATATATATATATATAT/AAT<br>ATATATATATATATATATATAT               | CCGTTGGGAGTTTGGA<br>AGTA  | CCCTAACCTAACCTAA<br>ACCA   | 60.0                             | 844                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_24232847  | Ca6                                     | 24232847                      | TTATATATATATATATATAT/TTATAT<br>ATATATATATAT                       | TGAGGTGCTGTCCAAA<br>TTGT  | ATAAATCCGCAACCG<br>ATCA    | 59.1                             | 521                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_24252379  | Ca6                                     | 24252379                      | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATA<br>TAT     | TTGCCTGGCATTITAT<br>ATGAG | TTCGGGTCGTGTTGAT<br>TGTA   | 59.1                             | 598                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_24296638  | Ca6                                     | 24296638                      | CATATATATATATATATATATA/CA<br>TATATATATATATATATATATA               | GAGAAGGAGGGAAAA<br>TGGC   | ATGTTTTGGATTTGGC<br>TCG    | 60.0                             | 421                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_24305629  | Ca6                                     | 24305629                      | AATATATATATATATATATATATAT<br>ATATA/AATATATATATATATATAT<br>ATATATA | CGTCATTTTCAACAAA<br>CCTCA | TGACACCGTCGTAACC<br>TCAA   | 60.0                             | 648                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_24309703  | Ca6                                     | 24309703                      | AATATATATATATATAT/AATATATAT<br>ATATATATAT                         | TGATGTGGTTGACCTG<br>TGTG  | CTAGGCCCATGTGAAG<br>GAAA   | 58.9                             | 441                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_24637049  | Ca6                                     | 24637049                      | TTTCTTCTTCTTCTTCTTCTTCT<br>TCT/TTTCTTCTTCTTCTTCTTCT<br>TCT        | TGTTTTGGTGAAACG<br>TGGA   | AGGATGAATGTGGTGT<br>TGAAGA | 60.0                             | 376                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_24744388  | Ca6                                     | 24744388                      | TACACACACA/TACACA                                                 | TTTGATTTTGACTCG<br>GAGG   | AATGGAGGAAGGAGGG<br>AGAA   | 60.0                             | 384                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_24872220  | Ca6                                     | 24872220                      | TAAAAAAAA/TAAAAAAAAA                                              | TCCGATGCATCTAAAAT<br>TCG  | GGGAAAAATTCGTTC<br>AAATCA  | 58.7                             | 535                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_25002657  | Ca6                                     | 25002657                      | AATATATATATATATATAT/AATATAT<br>ATATATATATATATAT               | CTACATATGCAAAAGC<br>GGCA   | GGATGTGTTTTCCCT<br>TCAA   | 59.9                             | 400                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_2501071   | Ca6                                     | 2501071                       | TAACAACAACAACAACAA/TAAC<br>AACACAACAACAA                      | CCCACCAACCCAAATT<br>AAAA   | TCACCATCGTGTGATG<br>GACT  | 59.5                             | 305                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_2525217   | Ca6                                     | 2525217                       | TT/TTGCAT                                                     | AGTAACCGACCAGCCA<br>ATCA   | CAAAATTTGGTCACATT<br>CCG  | 60.5                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_2525428   | Ca6                                     | 2525428                       | TAAAAAAAAA/TAAAAAAAAA                                         | CCTGAAATTTGATTCTG<br>CGT   | CAAATTTGGTCACATT<br>CCG   | 57.8                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_2528953   | Ca6                                     | 2528953                       | AATAT/AAT                                                     | TGGGTCAATGTTAAGA<br>GGGC   | CGTCAACGTCGTGCAT<br>TTAC  | 59.9                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_25356142  | Ca6                                     | 25356142                      | TA/TAAA                                                       | GCCGCTTCCAAATTAG<br>TTCA   | TCGATTTGTACAGGG<br>ATCA   | 60.2                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_25495130  | Ca6                                     | 25495130                      | AGGTTTTAG/AGGTTTTAGGGTTTTA<br>G                               | TTCGTTCAAAATGCAA<br>AAGTC  | CCAAAAACCAAAATGAC<br>CAAA | 59.3                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_25583382  | Ca6                                     | 25583382                      | TAGGGTTCAGGGTTCAGGGTTCAG<br>GGTT/TAGGGTTCAGGGTTCAGGGT<br>T    | GGGTTTAGGGTTTTGG<br>GATT   | AAAAACCAAAATGACCC<br>AACA | 59.0                             | 377                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_25692899  | Ca6                                     | 25692899                      | AT/ATATCT                                                     | ATTCCAAACCAAAACC<br>CTCC   | AAATTGGTCCACTAGC<br>ACCG  | 60.0                             | 883                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_257739    | Ca6                                     | 257739                        | CATATATATATATATATATATATA/<br>CATATATATATATATATATATATA<br>TA   | CGACACATGTGCTATT<br>TAGCCT | ATGGGTTGCAGTTAGC<br>TTGG  | 59.3                             | 799                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                 |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_2598910   | Ca6                                     | 2598910                       | ATAATAATAA/ATAATAATAATAA<br>TAGTAATAATAA                                                        | CAGTCCCAACGAAAA<br>GCAT     | ATGGGACAAAACACCA<br>GAGC   | 60.1                             | 430                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26044857  | Ca6                                     | 26044857                      | GTTTTTTTTT/GTTTTTTTTT                                                                           | CAATGGAAAGTGTGGT<br>TCCC    | AAAAGGCGCGCTATAA<br>AATG   | 60.2                             | 929                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26084259  | Ca6                                     | 26084259                      | AATATATATATATATATATATATAT<br>ATATATATATATA/AATATATATATAT<br>ATATATATATATATATATATATATA<br>TATATA | TTGGGTCTTGTA<br>GAGAA       | CATTGTGCGGCTACTC<br>TTCA   | 57.4                             | 184                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26152782  | Ca6                                     | 26152782                      | G/GA                                                                                            | TCTTGCGATTCACTGT<br>TGC     | CAGTTTGGTCCCCCT<br>ATT     | 60.0                             | 703                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26263542  | Ca6                                     | 26263542                      | ATTTTTTTTT/ATTTTTTTTTT                                                                          | TTAGGGGCGAGTGT<br>GAATA     | CGCATACCAATTTACAT<br>GATGC | 60.5                             | 409                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26277672  | Ca6                                     | 26277672                      | T/TG                                                                                            | TTAGGTGCGCTTGACT<br>GATG    | GTTTGGCGTTGGTTT<br>CACT    | 60.0                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26382209  | Ca6                                     | 26382209                      | A/AGC                                                                                           | GGCCTTCTCCTCTCAA<br>TCCT    | TGGTTGGGATTTTGG<br>GTTA    | 59.8                             | 870                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26391440  | Ca6                                     | 26391440                      | CTATATATATATATATATATATAT<br>AT/CTATATATATATATATATATAT<br>AT                                     | GAGAAATGCATTGATG<br>TATCGAG | TTGGTCGCAATGCTTAT<br>TTTT  | 58.7                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_2639909   | Ca6                                     | 2639909                       | CTT/CT                                                                                          | AGCTGAAGCAATTTTC<br>GCAT    | GCAATGCAGCAGCAAT<br>AAAA   | 60.0                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26433995  | Ca6                                     | 26433995                      | AATATATATATATATATATAT/AAT<br>ATATATATATATATATAT                                                 | AGCCTAAATGTAGGTG<br>CATGG   | CACAAATGAGCCATGG<br>TGAG   | 59.1                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                    | Forward primers (5'-3')       | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                  |                               |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_26438751  | Ca6                                     | 26438751                      | ATTTTTTTTT/ATTTTTTTTTT                                                                                                                           | TCAGACACTACCCAGC<br>ATCAA     | CTTAGGCCGCCACAAA<br>ATA         | 59.3                             | 960                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26498886  | Ca6                                     | 26498886                      | TTATATATATATATATAT/TTATAT<br>ATATATATATAT                                                                                                        | AAATTCCATCTTTATTG<br>GTTTGAGA | TCAGCACATCACAATCA<br>TCTG       | 59.3                             | 343                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26545231  | Ca6                                     | 26545231                      | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATAT<br>ATA                                                                                    | TTTGATGATCCTTCATT<br>TTTAGG   | TGGTGAAATAAACATTA<br>TCATATCGTG | 59.4                             | 753                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26559767  | Ca6                                     | 26559767                      | CCATGATGAGCAGCCTCA/CCA                                                                                                                           | AGGAAAATCTGACGGT<br>GGTG      | TGCTGCTGCTGGTCAT<br>ATTG        | 60.0                             | 240                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26560475  | Ca6                                     | 26560475                      | CTA/CGTATA                                                                                                                                       | GTCTTTTGAGCATCCC<br>GTGT      | AGATGTTTGTTCG<br>GTCC           | 60.1                             | 331                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_2662582   | Ca6                                     | 2662582                       | AAGAGAGAGAGAGAGAGAGAGAGA<br>GAGAGAGAG/AAGAGAGAGAGAGA<br>GAGAGAGAGAGAGAGAGAGAG                                                                    | TTGGGTGCAGCAACAA<br>GTAG      | CCATACTTTAACCTCG<br>CCA         | 59.9                             | 257                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26686344  | Ca6                                     | 26686344                      | T/TATA                                                                                                                                           | CTAGTGCGAATGGCAG<br>ACAA      | GATTATGGCCAGCTT<br>TTGA         | 60.0                             | 358                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26790864  | Ca6                                     | 26790864                      | GAAAAAAAA/GAAAAAAAA                                                                                                                              | CCGAAAATTTGAAAATC<br>CGA      | CAAGTACAGGTGGAGT<br>GGCA        | 59.9                             | 728                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26804449  | Ca6                                     | 26804449                      | AATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTAT/AATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>T | CCACCTCCACCATCAG<br>TTTT      | CTACCACCAAACGGAC<br>CATA        | 59.8                             | 959                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_26834295  | Ca6                                     | 26834295                      | ATTTTTTTTTT/ATTTTTTTTTT                                                                                                                          | GAAATTAAGTTAAGGG<br>ACCGCA    | TGGTTTTGGGCTATAAT<br>GGG        | 59.5                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_26931819  | Ca6                                     | 26931819                      | TTATATATATATATAT/TTATATAT<br>ATATATATATATAT                   | GTACCACATTGCCGAG<br>GTTT  | GCTTGCCAAAATAAATG<br>GCT   | 59.9                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_2695274   | Ca6                                     | 2695274                       | ATTTTTTTTT/ATTTTTTTTT                                         | TTCAAAAACATATACCG<br>CACG | TTTAACACGGTTTGTC<br>ATGA   | 58.6                             | 250                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_27009865  | Ca6                                     | 27009865                      | TT/TGTTATAT                                                   | CGTGTGAGAAAACCTC<br>GACA  | ATTTTGCAAACCCAAGT<br>TCG   | 59.9                             | 314                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_27037809  | Ca6                                     | 27037809                      | TTTATTATTATTATTATT/TTTATT<br>ATTATTATTATT                     | CGTCCAGACTCGCCTT<br>TCTA  | ATTTTTCATCTGCGCGA<br>TTT   | 60.5                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_27165011  | Ca6                                     | 27165011                      | ATATTATTATTATTATTATTATTA<br>TT/ATATTATTATTATTATTATTATTA<br>TT | CATTGTTTGATCCATGT<br>CGC  | CCATCATTGACACTCG<br>AAAGAA | 59.9                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_27264510  | Ca6                                     | 27264510                      | ATTTTTTTTT/ATTTTTTTTT                                         | AACGTCCCATTAAAGT<br>CGCA  | TGACAAATTGCCTTTGC<br>TTG   | 60.5                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_27289106  | Ca6                                     | 27289106                      | GATATATAT/GATATATATAT                                         | CAATTCCCACAGGTAC<br>GCTT  | AATTTCAAGGATTGGC<br>GAAG   | 60.0                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_27315680  | Ca6                                     | 27315680                      | GAGTTTTCAATTTTAGTTTCAATTT<br>TA/GAGTTTTCATTTTA                | CATGCATCGGAAGTTG<br>TGTT  | TCAGTGTGAGGAGAT<br>TTCC    | 59.6                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_27348230  | Ca6                                     | 27348230                      | ATTTTTTTTT/ATTTTTTTTTTT                                       | TTGATCCCATATCCTCC<br>CAA  | GACACCCAAATCAAAC<br>CCAC   | 60.1                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_27421945  | Ca6                                     | 27421945                      | TAAAAA/TAAAAAA                                                | CATCTCCAGATGCAAC<br>CTTCT | TAGAATGGGGTGTGTTG<br>CGAC  | 59.3                             | 179                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfI)             | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing temperature<br>(0C) | Expected amplified product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|----------------------------|----------------------------|-------------------------------|-----------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                           |                            |                            |                               |                                         | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | Tfs |
| Ca6_P4_27447919  | Ca6                                     | 27447919                      | ATTTTTTTT/ATTTTTTTT                                                       | CACCATGTGCCACTTC ATTC      | TGGGCGGCTATGTTAA AACT      | 60.0                          | 359                                     | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_27448301  | Ca6                                     | 27448301                      | TTATATATATATATATATATATATA TATATAT/TTATATATATATATATATA TATATATATATATATATAT | CACCATGTGCCACTTC ATTC      | CTAGTGCAAGGTCGCT CCTC      | 60.0                          | 629                                     | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_2763643   | Ca6                                     | 2763643                       | TA/T                                                                      | ATCGCGTTCAATGTGT TTGA      | TGCCATGAATATTTGAT AAATGTGA | 60.1                          | 358                                     | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_27691258  | Ca6                                     | 27691258                      | ATTTTTTTTTT/ATTTTTTTTTT                                                   | CACTCGGTTGAGACGT GAGA      | AGGTCGGCGTCATAAA CATC      | 60.0                          | 290                                     | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_27970080  | Ca6                                     | 27970080                      | C/CAAA                                                                    | GCATAGTGGGAAGAAG AGCG      | CGAATGCTATTAGGGG CGTA      | 60.0                          | 904                                     | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_28188243  | Ca6                                     | 28188243                      | AATATATATATATATATATAT/AATAT ATATATATATATATATATATAT                        | ATCCAACCTCAACCTC ACCA      | TTTGATGAATTAATAATG ATGCGA  | 60.4                          | 922                                     | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_28189675  | Ca6                                     | 28189675                      | TAAAAAAAA/TAAAAAAAAA                                                      | TTCATACTTCCATTAT ATTGACTGC | TGAATTGCATAGGGTTT AGGG     | 59.7                          | 553                                     | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_28190647  | Ca6                                     | 28190647                      | AA/AATAATAATAATA                                                          | AGGTCTCATACCAGAG ATGCG     | TGTGGTTGAGTAAATG TGCCA     | 59.3                          | 580                                     | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_28190835  | Ca6                                     | 28190835                      | ATATTATTATTATTATT/ATATTATTA TTATTATTATT                                   | AGGTCTCATACCAGAG ATGCG     | AAGTTAAGGGACCGCA AATG      | 59.3                          | 871                                     | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_28193559  | Ca6                                     | 28193559                      | AGGG/AGG                                                                  | AAGGACTAAGTCGGGA AGAAAAA   | GATGGTTTTTGTCCATT GAATTT   | 59.7                          | 131                                     | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                   | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                 |                             |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_28194024  | Ca6                                     | 28194024                      | ATTTTT/ATTTTTT                                                                                                                  | GGACCACGAATGTAAT<br>T TAGCC | TGCGAGCATTAGAAGT<br>T GTTG  | 59.7                             | 737                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28222145  | Ca6                                     | 28222145                      | TTTTCT/TT                                                                                                                       | CAAGAAGACAAAGGGG<br>GACA    | TGCTCGTACGTTGTGC<br>GATA    | 60.1                             | 597                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28222721  | Ca6                                     | 28222721                      | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTAT/ATATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTAT | TATCCGACAACGTACG<br>AGCA    | CCCTACCACGTCCGTT<br>AAAA    | 60.3                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28264967  | Ca6                                     | 28264967                      | AATATATATATATATATATA/AAATA<br>TATATATATATATATA                                                                                  | GAAAATAGATGAAGCG<br>GCCA    | GACCTTTACCGACCAC<br>CGTA    | 60.2                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28332319  | Ca6                                     | 28332319                      | ATTTT/ATTTT                                                                                                                     | TTTCAAAAAGTCCCAAT<br>CGC    | GGTTTGGAGAAGAAGA<br>CGAAA   | 60.1                             | 751                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28332406  | Ca6                                     | 28332406                      | GTTTT/GTTT                                                                                                                      | TTTCAAAAAGTCCCAAT<br>CGC    | GGTTTGGAGAAGAAGA<br>CGAAA   | 60.1                             | 751                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28332579  | Ca6                                     | 28332579                      | A/AG                                                                                                                            | GTCGGAGCTCTGCCAT<br>AAAA    | GGTTTGGAGAAGAAGA<br>CGAAA   | 60.4                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28332651  | Ca6                                     | 28332651                      | C/CT                                                                                                                            | GTCGGAGCTCTGCCAT<br>AAAA    | GGTTTGGAGAAGAAGA<br>CGAAA   | 60.4                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28332758  | Ca6                                     | 28332758                      | TAAA/TAAAA                                                                                                                      | TTTCGTCCTTCTCTCCA<br>AACC   | CCCAACATATTACCTGT<br>TACCCA | 58.4                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28332973  | Ca6                                     | 28332973                      | A/AT                                                                                                                            | TTTCGTCCTTCTCTCCA<br>AACC   | CGTGCAAAGTCGAAGC<br>GTAT    | 58.4                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_28336699  | Ca6                                     | 28336699                      | ATTTT/ATTT                                                    | TCTCCCATTTTACCATT<br>GCC   | TTTGCTTTGGTTGATT<br>CCT   | 59.8                             | 980                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28354937  | Ca6                                     | 28354937                      | GTAT/GT                                                       | TTTTATGTGACCCGCTT<br>TGC   | AGAACGGCATCCAGAG<br>AAGA  | 61.0                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28388573  | Ca6                                     | 28388573                      | CA/CAACTTTA                                                   | GTTGGCAACGATTTTG<br>TCCT   | GGAGAACGTTAAGGCA<br>GCAG  | 60.0                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28407890  | Ca6                                     | 28407890                      | ATTTTTTTTTT/ATTTTTTTTT                                        | GGTCCCTTGTGTAATG<br>TCTCG  | TTGAATGCCAAAATAAT<br>CGTT | 59.5                             | 724                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28443583  | Ca6                                     | 28443583                      | CTCTTTTGTGTGA/CTCTTTTGTG<br>TTATATCTTTTGTGTGA                 | AAAAACACCAAAAGCC<br>CCTC   | CATAAAATGCCATTGAT<br>CCCT | 60.3                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28444744  | Ca6                                     | 28444744                      | GATAATAATAATAATAAA/GATAAT<br>AATAATAATAATAATAATAAA            | TCCCAACAGCCTAAC<br>AACC    | CAACGCAATCTGAAC<br>AAAA   | 60.0                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28496437  | Ca6                                     | 28496437                      | TTGT/TTGTCGTTTATTTATGT                                        | ATGGGGAGAACAACAG<br>CAAC   | GAAACTGCAGACTCAA<br>GGGG  | 60.0                             | 427                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28513941  | Ca6                                     | 28513941                      | ANNNNNNNNN/ANNNNN                                             | TGAAGAAATTTAAAG<br>GGACGAA | GTGTTGCATCTCATTG<br>GTGG  | 59.2                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28520924  | Ca6                                     | 28520924                      | CAA/CAATTAAA                                                  | TTAGAAACAGGGACCC<br>CTCC   | TTGTCTGTGAACCGAA<br>GCTG  | 60.3                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28520971  | Ca6                                     | 28520971                      | TCTTGCCTTGCCTTG/TCTTGCCTT<br>G                                | TTAGAAACAGGGACCC<br>CTCC   | TTGTCTGTGAACCGAA<br>GCTG  | 60.3                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')    | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                               |                            |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_28521027  | Ca6                                     | 28521027                      | A/CATAG                                                                       | TCTCATTCTTGCCTTGC<br>CTT   | TTGTCTGTGAACCGAA<br>GCTG       | 60.0                             | 172                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28521076  | Ca6                                     | 28521076                      | AACAT/A                                                                       | TCTCATTCTTGCCTTGC<br>CTT   | TTGTCTGTGAACCGAA<br>GCTG       | 60.0                             | 172                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28851395  | Ca6                                     | 28851395                      | TAAAAAAAAA/TAAAAAAAAA                                                         | AATTAGCTTGGGAGCG<br>ACAA   | CGAAAAATGACACATCAA<br>AAGGA    | 59.8                             | 374                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28878487  | Ca6                                     | 28878487                      | T/TCA                                                                         | CTCCGTTTTCTGCACA<br>TCAA   | TGATGTTGCCTCTGTTT<br>TGC       | 59.8                             | 396                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_28977511  | Ca6                                     | 28977511                      | ATTTTTTTTT/ATTTTTTTTT                                                         | TCCAAAATGTTTAAGAC<br>GATCC | TGATTCCACCCCTTGGA<br>TTTT      | 58.1                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_29231459  | Ca6                                     | 29231459                      | AAAGTCTCAAGTCTCAAGTCTCAA/<br>AAGTCTCAAGTCTCAAGTCTCAAGT<br>CTCAA               | ACTCCACACACCTCA<br>AAGG    | TTTCAAGTCTAGTCGAA<br>GTTTCATCA | 60.0                             | 834                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_29244002  | Ca6                                     | 29244002                      | ATTTTT/ATTTTT                                                                 | TGGCCATTATCCCTCA<br>TTTG   | ATTTTGTCTCCTTCACC<br>CCC       | 60.7                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_29259303  | Ca6                                     | 29259303                      | AATATATATATATATATATATATAT<br>ATATATATAT/AATATATATATATATA<br>TATATATATATATATAT | GGAATCCAAATTCCCA<br>ACAA   | TGTCCACATGCTTCGC<br>TTAG       | 59.6                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_29314280  | Ca6                                     | 29314280                      | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATAT                         | ATGTACCAATGCGTCG<br>TCAA   | CCACCCAGATTTCGCT<br>CTTA       | 60.0                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_29475109  | Ca6                                     | 29475109                      | CATATATATATATATATATATAT/CAT<br>ATATATATATATATATATATAT                         | AAATGAATGGAGATGA<br>AGGCA  | CACGCATCTATCCGTC<br>AGC        | 59.5                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                               | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                             |                          |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_29669016  | Ca6                                     | 29669016                      | T/TC                                                                                                        | GCCCTCAGATGAGAGT<br>CAGG | AATGGCCAGATGAAAT<br>CGAG     | 59.9                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_29815012  | Ca6                                     | 29815012                      | GAAAAAAAAA/GAAAAAAAAA                                                                                       | TGACAGTCAGAGTGCG<br>ATCC | TGCAGATAAATGGCCA<br>AACA     | 60.0                             | 807                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_29832986  | Ca6                                     | 29832986                      | CATATATATATATATATATATAT/C<br>ATATATATATATATATATAT                                                           | ACGCTCCATGGTAGTT<br>CCAA | TTGTGAGGGTTTTATTC<br>GGC     | 60.5                             | 153                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_29915132  | Ca6                                     | 29915132                      | AATATATATATATATATATAT/AAT<br>ATATATATATATATATAT                                                             | AAATGTGCAATTTGTTG<br>GCA | TCATTCCAACCTGCAG<br>TTACC    | 60.0                             | 632                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_29955539  | Ca6                                     | 29955539                      | ATTAT/ATTATTTTAT                                                                                            | TCAGCCAGAAAGCTGA<br>TGTG | TTGTGCAGAGAATATT<br>ATGTCGAT | 60.1                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_29969559  | Ca6                                     | 29969559                      | TAAAAAAAAA/TAAAAAAAAA                                                                                       | CTGTCGTGTCCAGTTT<br>GTCC | TGTTTCACCGTCACGTT<br>CAT     | 59.2                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_30102387  | Ca6                                     | 30102387                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                                                                   | TTGGGAGATGCATGTA<br>TTGG | TTAGACGTAACCCACC<br>TTGGA    | 59.4                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_30125014  | Ca6                                     | 30125014                      | TTATATATATATATATATATATATA<br>TATATATATATATATATA/TTATATAT<br>ATATATATATATATATATATATATA<br>TATATATATATATATATA | GGAAAAGGAAGGGAAT<br>CACG | TGCATGCACAAATTAGA<br>CACTTT  | 60.8                             | 854                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_30186365  | Ca6                                     | 30186365                      | TATTGATTGA/TATTGA                                                                                           | CCGTTGTCAACCTCAA<br>ATCC | ATCCCGCGACTCAAAA<br>TTC      | 60.4                             | 811                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_30358500  | Ca6                                     | 30358500                      | A/AT                                                                                                        | GCAATAAAGCACATGC<br>AGGA | CCCTGTGAGGACTCAA<br>CCAT     | 59.8                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)              | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                            |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_30456247  | Ca6                                     | 30456247                      | AATTAT/AAT                                                                 | GCGTTTCGACACAATT<br>TTCC  | AAAATAACGGGCAAGC<br>CTTT    | 60.5                             | 882                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_30621500  | Ca6                                     | 30621500                      | ATGAAAGTTTTGAAAGTTTTGAAA/<br>TGAAAGTTTTGAAA                                | ATTTTCGAACCTTTCGC<br>CTT  | TTTGAAAGTGTGATAA<br>AATCCCA | 60.1                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_30646917  | Ca6                                     | 30646917                      | CTTTTT/CTTTTT                                                              | TGTTTGCATCAAGATG<br>GGTT  | GCGACTTCCCACGTGA<br>TATT    | 59.0                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_30698837  | Ca6                                     | 30698837                      | GTTATTTATTTATTTATTTATTT<br>ATTTATT/GTTATTTATTTATTT<br>ATTTATTTATTTATTTATTT | CGTTTTCGGTTTCAGG<br>GTAA  | CCCATACCTATTACCCA<br>CGC    | 60.0                             | 949                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_30724309  | Ca6                                     | 30724309                      | AATATATATATATATATATAT/AAT<br>ATATATATATATATATATATAT                        | CCGTTGGGAGTTTGG<br>AGTA   | TGCGTATGCTTCAACG<br>TCAT    | 60.0                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3073674   | Ca6                                     | 3073674                       | AATATATATATATATATATATA/AA<br>TATATATATATATATATATATAT<br>ATATA              | CACCCATTTGCTTTG<br>GTCT   | CCTTTCCTCCAGCCAT<br>ACA     | 60.0                             | 164                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_30832584  | Ca6                                     | 30832584                      | AATATATATATATATATATATAT<br>AT/AATATATATATATATATATATA<br>TAT                | TTTTTGAATTGGTGATC<br>CAGA | TTCTAGATTTACCGCA<br>TGTGT   | 58.1                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3093515   | Ca6                                     | 3093515                       | ATT/AT                                                                     | GCGGCAAGCTTTTCTT<br>TATG  | TCGAACCGTTCATT<br>CCTC      | 60.0                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_31051947  | Ca6                                     | 31051947                      | TTAATAATAATAATAATA/TTAATA<br>AATAATA                                       | ACCCATTACTCTTGCA<br>CGG   | TCTCCAATGATTGTTT<br>TGTGG   | 60.0                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3108108   | Ca6                                     | 3108108                       | AT/ATAATAATAATATT                                                          | CACCAGTGCCAATCA<br>CCCT   | CGTCTCATGTTCTCC<br>AGGT     | 60.8                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |







| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                              | Forward primers (5'-3')         | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------|---------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                            |                                 |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_31939689  | Ca6                                     | 31939689                      | G/GAT                                                                                                                      | CTGCGGTTCTTGCTGA<br>TGTA        | AGGCAGCTTGATTCTT<br>GGA  | 60.0                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_31944698  | Ca6                                     | 31944698                      | TAAAAA/TAAAAAA                                                                                                             | GATCATCGAGTTTCCC<br>GTGT        | ACCATGCAAAGACATC<br>CACA | 59.9                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32308001  | Ca6                                     | 32308001                      | CTTATTTATTTATTTATTTATTT<br>ATTTATTTATTTATTTATTTATTTAT/<br>CTTATTTATTTATTTATTTATTTATTT<br>ATTTATTTATTTATTTATTTATTTAT<br>TAT | ATCCTTTGCACAATGG<br>TTCC        | TTTCCCTTCTTAGGCA<br>GCA  | 59.8                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32309196  | Ca6                                     | 32309196                      | AATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATATA<br>TATAT                                                          | CGTTATCGCGAACCA<br>CAAT         | TGTGGGTGATAAGGG<br>TTGT  | 60.9                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32350907  | Ca6                                     | 32350907                      | AATTATTATTATTATTATTAT/AA<br>TTATTATTATTATTAT                                                                               | TTGATATTTTCTACAAT<br>TGATCATACG | GAATGCCCTACTTTTGG<br>GCA | 57.8                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32371063  | Ca6                                     | 32371063                      | TGAT/TGATCGAT                                                                                                              | TGAAATCCATGGAGCA<br>AACA        | CCTTTGTCCACAAAT<br>TGC   | 60.0                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32372827  | Ca6                                     | 32372827                      | CAA/CA                                                                                                                     | GAATACGCGGCTGATT<br>CATT        | CGCCCCGTTTTAACTC<br>ATTA | 60.1                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32372986  | Ca6                                     | 32372986                      | ATTTTT/ATTT                                                                                                                | GAATACGCGGCTGATT<br>CATT        | CGCCCCGTTTTAACTC<br>ATTA | 60.1                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32373522  | Ca6                                     | 32373522                      | AATA/ATATA                                                                                                                 | TAATGAGTTAAACGG<br>GGCG         | TTGGTCCAACACGAAG<br>AGA  | 60.0                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32391786  | Ca6                                     | 32391786                      | AATATATATATATA/AATATATATA<br>TATATATA                                                                                      | CGCTATGCCCCATTAG<br>ATGT        | TTTGATTGACTCATTGC<br>GTG | 59.9                             | 294                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_32476687  | Ca6                                     | 32476687                      | TAGAAG/TAGAAGAAG                                              | TGCCTCAAGATCTCAT<br>GGTG  | CCGCTTCCTTTGTCTTT<br>GTC   | 59.8                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32519592  | Ca6                                     | 32519592                      | AG/A                                                          | CGCATGCCACTCACTC<br>TAAA  | CGCTGCCACTTTCTAC<br>ATCA   | 60.0                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32521477  | Ca6                                     | 32521477                      | GACATGATAC/GAC                                                | TTGCCAACGTGTCAAT<br>CACT  | TTTTCCCTACTATTTTG<br>CAGCC | 60.2                             | 259                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32522263  | Ca6                                     | 32522263                      | CA/CAA                                                        | TTGTTCATTTTGGTCG<br>TTCA  | CCTTGGCGGATATAGG<br>GAAT   | 59.0                             | 347                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32539826  | Ca6                                     | 32539826                      | TAAAAAAAAA/TAAAAAAAAA                                         | TATGAGCCTCTGCCAG<br>CTTT  | GTCCGCGTCCATTGAT<br>AAAC   | 60.1                             | 562                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32540172  | Ca6                                     | 32540172                      | TTATATATATATATAT/TTATATATAT<br>ATATATATATAT                   | GTTTATCAATGGACGC<br>GGAC  | TTCCCTAAAAACGGTT<br>GTG    | 60.3                             | 341                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32540257  | Ca6                                     | 32540257                      | TACATAA/TACATAAGAAACATAA                                      | GTTTATCAATGGACGC<br>GGAC  | TTCCCTAAAAACGGTT<br>GTG    | 60.3                             | 341                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32540480  | Ca6                                     | 32540480                      | GTTTTTTT/GTTTTTTT                                             | CACAACCGTTTTTAGG<br>GGAA  | GAGGATTGCTATGGAC<br>AACCA  | 59.8                             | 214                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32540585  | Ca6                                     | 32540585                      | AATATATAT/AATATAT                                             | CACAACCGTTTTTAGG<br>GGAA  | AAGGAGAACCAGTCAA<br>CCACA  | 59.8                             | 278                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3255826   | Ca6                                     | 3255826                       | AATATATATATATAT/AATATATAT<br>ATATATATAT                       | TGGCTTGTTTGATTTA<br>GGACA | ATTGCAATGATCAGTTG<br>CCC   | 58.3                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                            | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                          |                              |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_32617100  | Ca6                                     | 32617100                      | AAA/AAATAA                                                                               | GAACGGTCCATGCAAA<br>AGTT     | CCCCCGATCCTTATAC<br>GACT    | 60.0                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32629991  | Ca6                                     | 32629991                      | TAATGCA/TA                                                                               | CGCTCTCAATCGTGCA<br>ATAA     | TAGTGATTGGAAAGGA<br>CGGC    | 60.0                             | 719                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32630101  | Ca6                                     | 32630101                      | TTAAA/TTAAATAAA                                                                          | TTTGAGGGAGGGAATT<br>AGGG     | TAGTGATTGGAAAGGA<br>CGGC    | 60.3                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32630376  | Ca6                                     | 32630376                      | AGGGG/AGGGGGG                                                                            | GCCGTCCTTTCCAATC<br>ACTA     | ATCGGGAAGAGGTTAG<br>GGAA    | 60.1                             | 123                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32929483  | Ca6                                     | 32929483                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATT/TTTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>T | TTCAGTGCCAACAATA<br>CCCA     | ACTAGATGGTCGCATC<br>CTGG    | 60.0                             | 765                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_32971894  | Ca6                                     | 32971894                      | CTTTTTTTTTT/CTTTTTTTTTT                                                                  | TTAACCTACCAATTCTGA<br>ATACCA | TTAATGCATCTTGATGG<br>TGG    | 57.7                             | 257                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_329954    | Ca6                                     | 329954                        | C/CGT                                                                                    | GCAGTTTGATCCTTAG<br>GCTGAT   | TTGACCACACAACCATA<br>AAGAAA | 59.8                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_33094621  | Ca6                                     | 33094621                      | ATTT/ATT                                                                                 | TCAAAATGTAGCGGGT<br>TTCC     | AAGCCTTCCTCAAAATC<br>CAA    | 59.9                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_33094845  | Ca6                                     | 33094845                      | CAAAAA/CAAAAAA                                                                           | TCAAAATGTAGCGGGT<br>TTCC     | AAGTTGGACAAAATTG<br>GGGT    | 59.9                             | 950                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_33094956  | Ca6                                     | 33094956                      | ATTTTTTT/ATTTTTT                                                                         | AATTGGATTTTGAGGA<br>AGGC     | AAGTTGGACAAAATTG<br>GGGT    | 58.1                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                 | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                               |                            |                           |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_33113807  | Ca6                                     | 33113807                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATT/TTTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATT | AGAGGCAAACAAGAAC<br>CGAA   | TTGTGGCATTTCCTCA<br>TCA   | 59.9                             | 433                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_33210738  | Ca6                                     | 33210738                      | AACGTAC/AAC                                                                                                   | CATGCAGTCCTTTGTT<br>GCAT   | TTTTCCGATGTCAACT<br>TTCG  | 59.7                             | 595                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_33229272  | Ca6                                     | 33229272                      | GAAAA/GAAA                                                                                                    | TGTTGACGGTGTGTTT<br>TTAAGG | AAATTTTAGACCGCGA<br>CACG  | 59.9                             | 477                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_33229296  | Ca6                                     | 33229296                      | TG/TGG                                                                                                        | CGGTGTGTTTTTAAGG<br>ATTGG  | AAATTTTAGACCGCGA<br>CACG  | 59.4                             | 471                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_33229523  | Ca6                                     | 33229523                      | AAAAACGAAAA/AAAAA                                                                                             | CGGTGTGTTTTTAAGG<br>ATTGG  | GCGGATATCGTAGGGT<br>GCTA  | 59.4                             | 644                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_33229803  | Ca6                                     | 33229803                      | TAAAAAAA/TAAAAA                                                                                               | AAGCAAGCCAAAAACG<br>AAAA   | GCGGATATCGTAGGGT<br>GCTA  | 59.9                             | 382                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_33229847  | Ca6                                     | 33229847                      | T/TC                                                                                                          | AAGCAAGCCAAAAACG<br>AAAA   | GCGGATATCGTAGGGT<br>GCTA  | 59.9                             | 382                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_33231576  | Ca6                                     | 33231576                      | AT/ATT                                                                                                        | TGGTGTATTGGGTGCT<br>GATG   | GACCCATCGATTTGAA<br>GCAT  | 60.4                             | 975                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_33233620  | Ca6                                     | 33233620                      | G/GAA                                                                                                         | CCGCCCACTAAAAAGT<br>TGAA   | AATCGCCATAACTTGAA<br>ATGC | 60.1                             | 935                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_33240261  | Ca6                                     | 33240261                      | A/AAAGAG                                                                                                      | GTTTGGTATTGGGCTC<br>CCTT   | CACAATTCCTCCCTCTC<br>CAA  | 60.2                             | 314                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                  | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_33240380  | Ca6                                     | 33240380                      | A/AG                                                                           | GTTTGGTATTGGGCTC<br>CCTT    | CGAAACTCACCCCTTG<br>TTGT | 60.2                             | 750                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_33240742  | Ca6                                     | 33240742                      | AA/AATATA                                                                      | TTGGAGAGGGAGGAAT<br>TGTG    | CGAAACTCACCCCTTG<br>TTGT | 60.0                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_33285610  | Ca6                                     | 33285610                      | CATA/CATATA                                                                    | CAAAATGTCAATTGTTG<br>CACG   | ATTGTTTCCTCGTGCTT<br>TTG | 60.0                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_33293827  | Ca6                                     | 33293827                      | TGGG/TGGGG                                                                     | CCAAGGCTATGAGACC<br>TATCTGA | TGAAAACCCCTTGAAG<br>GTGC | 59.8                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3330798   | Ca6                                     | 3330798                       | AATTATTATTATTATTATTATTAT<br>TATTATTATT/AATTATTATTATTATT<br>ATTATTATTATTATTATT  | TCAATTGATTTTCGGTA<br>TCCTTC | GACCTCCCAAAGGCAT<br>TTTT | 59.3                             | 406                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3331064   | Ca6                                     | 3331064                       | TAAAAAAA/TAAAAAA                                                               | CAAATTGAAAAGTGGG<br>GCAT    | TTAAAGTTGGGAGACC<br>ACCA | 59.8                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_33334768  | Ca6                                     | 33334768                      | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>A                    | TTTTGTGTGCAGAGGC<br>TATGA   | GGGTTCAAGCTAATGG<br>CAGA | 59.5                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3340164   | Ca6                                     | 3340164                       | ATTTTTTTTT/ATTTTTTTTTT                                                         | AGGACAATGGGCAAG<br>ACAC     | TCATCACCTCAACCAAT<br>CCA | 60.0                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3346050   | Ca6                                     | 3346050                       | AATATATATATATATATATATATAT<br>ATATAT/AATATATATATATATATAT<br>TATATATATATATATATAT | ATAAATCACGGCCCAA<br>CAAC    | CCATTGCACATTTGGTT<br>TTC | 59.7                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_33506970  | Ca6                                     | 33506970                      | AAAAGTTAA/AAA                                                                  | CCATTGTATCTGCAAC<br>ATTGA   | GAAAAGGGGTGATTTG<br>GGAT | 59.5                             | 273                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                  | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                          |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                |                         |                         |                                  |                                               | Sequence components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_3351662   | Ca6                                     | 3351662                       | GATATAT/GATATATATAT                                                                                            | CGAAATGGAAAACACCACC     | TCGAGTTGCGTAACTGACATAG  | 60.2                             | 687                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_3351712   | Ca6                                     | 3351712                       | ATTTTTTTT/ATTTTTT                                                                                              | GGTTGATTTAGGCCTCACGG    | TCGAGTTGCGTAACTGACATAG  | 59.6                             | 580                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_3351745   | Ca6                                     | 3351745                       | CATATTATATATA/CATA                                                                                             | GGTTGATTTAGGCCTCACGG    | TCGAGTTGCGTAACTGACATAG  | 59.6                             | 580                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_3352912   | Ca6                                     | 3352912                       | AATTA/AA                                                                                                       | AAAGTGGGTGGCAATT AACG   | TTATCCAATTCCGTTGCAACA   | 59.9                             | 247                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_33535351  | Ca6                                     | 33535351                      | AATATATATATATATATATATATATATATAT/AATATATATATATATATATATATATATATATATAT                                            | CTTGCTCTTGGTCACATCCA    | TTGGAAGAAGCCATCCAAG     | 59.8                             | 954                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_33539008  | Ca6                                     | 33539008                      | AAAAATAAAATAAAATAAAATAAAT<br>AAAAATAAAATAAAATAAAATAAATA/<br>AAAAATAAAATAAAATAAAATAAAT<br>AAAAATAAAATAAAATAAATA | GTGGGAACGTTAAGCCAAAA    | GGAGTCAAGTTTCGAGGACG    | 60.0                             | 424                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_3355103   | Ca6                                     | 3355103                       | GCTATTGATCAATCTATTGAT/GCTATTGAT                                                                                | TGAATAGATGTGCGCGAGAC    | TCCACGGGAGTGAGAGAGAT    | 60.0                             | 401                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_3355875   | Ca6                                     | 3355875                       | CTTT/CTTTT                                                                                                     | AATTTGCCCTATTGGCTTT     | AGAAACGGAATGAGTCAACGG   | 59.8                             | 709                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_3374594   | Ca6                                     | 3374594                       | TTAA/TTAAATAA                                                                                                  | GAAACTTCAGCAAAAA CCGC   | TGTGATATCCCAATCCGCTT    | 59.9                             | 806                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_3375268   | Ca6                                     | 3375268                       | TAAA/TA                                                                                                        | GATCAGTTGACCCGCGTAGT    | CCATTGAACATTTGGTTTCA    | 60.1                             | 680                                           | INTERGENIC                                     | --                               | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_3377584   | Ca6                                     | 3377584                       | CTTTTT/CTT                                                    | ATGCGGTGATGGTGAT<br>ATTG | TATGGCGAATATGGAT<br>GGGT    | 59.2                             | 745                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3378118   | Ca6                                     | 3378118                       | GAGAA/GA                                                      | ACCCATCCATATTCGC<br>CATA | TTTGCCATCCTCTCTTT<br>TTCA   | 60.0                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3382708   | Ca6                                     | 3382708                       | AA/AAGGGTTGGA                                                 | ATCACCGACCACTCAC<br>CTTC | TCAATTTTCTTCGTG<br>ACGG     | 60.0                             | 787                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3382789   | Ca6                                     | 3382789                       | CTTTTT/CTTT                                                   | ATCACCGACCACTCAC<br>CTTC | GTTCAATCAGTGCAGC<br>GTGT    | 60.0                             | 810                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3382946   | Ca6                                     | 3382946                       | CAAAAA/CAAAA                                                  | TAACCACCAACATTCT<br>GCCA | TGTTCCGTCCCACTCA<br>TACA    | 60.0                             | 927                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3387211   | Ca6                                     | 3387211                       | CTG/CTGGTGTAGTG                                               | ACCCCTGAACGATGTA<br>AACG | CGCTCTTATCCTGTTG<br>GCTC    | 59.9                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3387853   | Ca6                                     | 3387853                       | AGTACGTA/AGTA                                                 | GAGCCAACAGGATAAG<br>AGCG | GAAAATTGAGTTCCAT<br>GACGTTT | 60.0                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3387937   | Ca6                                     | 3387937                       | A/AG                                                          | GAGCCAACAGGATAAG<br>AGCG | GAAAATTGAGTTCCAT<br>GACGTTT | 60.0                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3388065   | Ca6                                     | 3388065                       | GATATATATAT/GATATATATAT                                       | GAGCCAACAGGATAAG<br>AGCG | TTGTCTTCACTTCTTT<br>TTCCG   | 60.0                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3392451   | Ca6                                     | 3392451                       | T/TGTAAG                                                      | TGATTGCAAAGGTGTT<br>CTCG | ATAATGAGTTGCGGGA<br>AGGC    | 59.8                             | 378                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_3392779   | Ca6                                     | 3392779                       | CTTTT/CTTT                                                    | AGATTACTCTGCCTTC<br>CCGC  | TGACGAAAAAGCTTGG<br>AGATG | 60.7                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3393664   | Ca6                                     | 3393664                       | CAAAAAA/CAAAAAA                                               | CATTTTGCCCATCTAAA<br>ACGA | TGGAAAAATAACGTTG<br>CCC   | 60.0                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3394112   | Ca6                                     | 3394112                       | GT/GTAT                                                       | CCATCCAGAGCACCTG<br>AAAT  | TCAATTGCCTTGCATGT<br>TGT  | 60.1                             | 371                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3394137   | Ca6                                     | 3394137                       | AT/ATT                                                        | CCATCCAGAGCACCTG<br>AAAT  | TCAATTGCCTTGCATGT<br>TGT  | 60.1                             | 371                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_33981637  | Ca6                                     | 33981637                      | ACTACATTTATATCCCTA/ACTA                                       | CTTTGATCTCTGCCAC<br>CCAT  | TCCCAATAAGAGCTG<br>CCTC   | 60.1                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34004073  | Ca6                                     | 34004073                      | TAATAAATAAAATAAATAAA/TAA<br>TAAATAAAATAAATAAATAAATA<br>AAAA   | TGTGTAATCTGATGGG<br>CGAA  | AAATGATCTGCACCCA<br>AAGC  | 60.1                             | 696                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34039542  | Ca6                                     | 34039542                      | AATATATATATATATATAT/AATATAT<br>ATATATATAT                     | TTTGATGCGCATGATA<br>AGAAA | CTTAACATCAGTCGAG<br>CGCA  | 59.3                             | 411                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34132247  | Ca6                                     | 34132247                      | C/CT                                                          | AATTATCGATCATCGGT<br>GCC  | CCGAGCCAAATCCAA<br>AATA   | 59.8                             | 700                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34162137  | Ca6                                     | 34162137                      | A/AGC                                                         | ATGGAAAGTTTGGTGC<br>CTTG  | AAAAACGCACGCGTTA<br>AAAT  | 60.0                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34164737  | Ca6                                     | 34164737                      | CCCACCAC/CCCAC                                                | CCACTTTGTTGGGAAA<br>AACC  | AGAAGAACGGTTGCCA<br>AAGA  | 59.3                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                  | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_34177096  | Ca6                                     | 34177096                      | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>A                                                                    | TCCTTGGGTATTGTGA<br>AACCA | TCATCAACACCAATAT<br>TTTCCA | 60.2                             | 434                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3420698   | Ca6                                     | 3420698                       | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATAT                                                                          | TAGCCGACAACATTGG<br>AACA  | TGAACTCGCACATTG<br>AGGA    | 60.1                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34235790  | Ca6                                     | 34235790                      | TAGAGAGAGAGAGAGAGAGAGAGA<br>GAGAGAGAGA/TAGAGAGAGAGAG<br>AGAGAGAGAGAGAGAGAGA                                                    | TGTTGCTGCTGAGGTA<br>GGTG  | TTCAATCGGGTTTTCGA<br>TTC   | 60.0                             | 863                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34320971  | Ca6                                     | 34320971                      | CATATATATATAT/CATATATATAT<br>AT                                                                                                | AGACGTTTGGTGTGTC<br>TTGC  | GCACATCATGTCAAGA<br>ACCAA  | 58.8                             | 889                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34540623  | Ca6                                     | 34540623                      | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATT/ATATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATT | GTCAAAGTGCCTCAAC<br>CCAT  | GTTTTCACCGAGAGT<br>TGGA    | 60.0                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34684404  | Ca6                                     | 34684404                      | GAAAAA/GAAAAAA                                                                                                                 | CCCTGAGACTCACGAA<br>GAGG  | CCCCCTTTTGCATAAG<br>TGA    | 60.0                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34728984  | Ca6                                     | 34728984                      | TTATATATATATATATATATAT/TTAT<br>ATATATATATATATATATAT                                                                            | TAGGCACATCAAGTCA<br>ACCG  | TCAGACCATCCGATAG<br>AGGC   | 59.7                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34748246  | Ca6                                     | 34748246                      | ATTTTTTTTT/ATTTTTTTT                                                                                                           | GCCTGCTTGAAACAAA<br>CACA  | ATAATGGTGACCCGAG<br>TTGC   | 59.9                             | 227                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34816135  | Ca6                                     | 34816135                      | ATTTT/ATTTT                                                                                                                    | ATGCAATGCGTATATG<br>CCAA  | GTGTTTTGGTGTGGAT<br>CGTG   | 59.9                             | 872                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34827878  | Ca6                                     | 34827878                      | CATATATATATATATATATATATA<br>TATATA/CATATATATATATATATA<br>TATATATATA                                                            | AAGTTTCGGGGTAGAG<br>CGAT  | TGTAGCATTCTCATGG<br>CGAG   | 60.1                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                      | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                    |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_34831881  | Ca6                                     | 34831881                      | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATATAT<br>ATATATATATATATA                                                        | GAGGAACCAAGAACC<br>AATTTT | TCAC TTATGCAATTCAC<br>GTTCC | 58.5                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34838549  | Ca6                                     | 34838549                      | CAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAA/CAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAA                               | CACGTTTGATGTTGGA<br>TCAGA | ATGTGGATGGAACGTG<br>GTTT    | 59.6                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34859064  | Ca6                                     | 34859064                      | GATATATATATATATATATATATA/<br>GATATATATATATATATATATATA<br>TA                                                                        | GAAAGAGTTTGTAGCC<br>ACGG  | AAGTCCAATCTCGGTC<br>AACTT   | 59.9                             | 625                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34893967  | Ca6                                     | 34893967                      | GAATCAAACACATAGAAATCAAACA<br>CATAGAAATCAAACA/GAATCAAACA<br>CATAGAAATCAAACA                                                         | TCAGACCGAACCAATG<br>GAAT  | TATCACTTGACTCCCC<br>CTGC    | 60.3                             | 804                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_34982866  | Ca6                                     | 34982866                      | ATT/AT                                                                                                                             | ATCACTGCATCACCGA<br>AACA  | TCAGTGTGTTCTTGC<br>CAAA     | 60.1                             | 751                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_35048353  | Ca6                                     | 35048353                      | CTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAA/CTAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAA | CATTGCTGCCCAAAG<br>TATT   | AGCGAGAGTCACGGAG<br>AAAG    | 60.0                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_35093227  | Ca6                                     | 35093227                      | GAGTGTGACTTTTTCA/GAGTGT<br>GACTTTTTTCATAGTTTGACTTTTT<br>CA                                                                         | AACCGCTATTGGGCTA<br>GGTT  | CTCTGATATGCGTGGC<br>AAGA    | 60.0                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_35161798  | Ca6                                     | 35161798                      | TATA/TAAATATAAAATA                                                                                                                 | AGGAAGAGTGGAGTTG<br>CGAA  | CGGTTGAGAACCAAGG<br>ATGT    | 60.0                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_35169658  | Ca6                                     | 35169658                      | GTATATATATATATATATATATAT<br>A/GTATATATATATATATATATATA<br>TATATATATATA                                                              | AGGAAGAGTGGAGTTG<br>CGAA  | TATTTTGATTTTGGCT<br>CGG     | 60.0                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_35246739  | Ca6                                     | 35246739                      | CAAAAA/CAAAA                                                                                                                       | GCCTCTCGAGGCTCTG<br>AGTAT | AAAGCTCGCAATGCAA<br>AGAT    | 60.1                             | 881                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                 | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_3539767   | Ca6                                     | 3539767                       | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATA/AAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAA | AACCCCTTGACCATCT<br>TTCC  | CTAGGTGGGAGACAAA<br>ACGC     | 60.2                             | 339                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_35399219  | Ca6                                     | 35399219                      | GGA/GGAGA                                                                                     | GAAGCTCAGATGGCAC<br>ACAA  | AAACACCTAGTGTGGG<br>CTGG     | 60.0                             | 302                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_35399356  | Ca6                                     | 35399356                      | GTTT/GAATTT                                                                                   | TTGAAGCTCAGATGGC<br>ACAC  | CTCCCCCTTTTGGCAT<br>AAT      | 60.0                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_35616799  | Ca6                                     | 35616799                      | C/CCTT                                                                                        | GTTTCTGAGGCAAAAT<br>CCCA  | TGCATTGTCTTCCCAT<br>TGA      | 60.1                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_35800993  | Ca6                                     | 35800993                      | CTTTTTTTTT/CTTTTTTTTT                                                                         | CTTCATAAGCCGCAT<br>TGTT   | GGGCCAACGACCTCTA<br>AGTA     | 60.1                             | 234                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_35802672  | Ca6                                     | 35802672                      | TTTCT/TT                                                                                      | GAGCCTTAGAGTTGGG<br>AGCA  | ACCCAATTGTGCAAC<br>CAAC      | 59.6                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_35810337  | Ca6                                     | 35810337                      | C/CT                                                                                          | TCATCGATTGCAACTT<br>GCTT  | CCCTAAAATTTGTGG<br>GCTT      | 59.4                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_35832130  | Ca6                                     | 35832130                      | TTCTCT/TTCT                                                                                   | TCGCCTTCTCGAAATT<br>AAGTC | AAAAGATTGGTTGGATT<br>AAAAAGA | 59.9                             | 147                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3589483   | Ca6                                     | 3589483                       | CG/CGG                                                                                        | CTAATCAGCCACCCTT<br>CTCG  | GGATGAAGATCCTCG<br>TTGA      | 59.8                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3589752   | Ca6                                     | 3589752                       | AC/ACC                                                                                        | ATGCAACAGCAATGAG<br>CATC  | TTTAGTCAAGCTCCGC<br>CACT     | 59.8                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_36789650  | Ca6                                     | 36789650                      | C/CT                                                                          | CACAAGAGGGCAACAA<br>GGAT   | TGATCCGAGAGTTGCA<br>CTTG | 60.1                             | 201                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_36898169  | Ca6                                     | 36898169                      | AATATATATATAT/AATATATATATAT<br>AT                                             | AAGAGAGGTCACCTTG<br>GCGA   | CAATTCCACAGGTAC<br>GCTT  | 60.0                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_37110970  | Ca6                                     | 37110970                      | ATAAATTAAAGT/ATAAATTAAAGTAA<br>ATTAAAGT                                       | GCTGCGCTCGTACTCA<br>TTTT   | ATCTTGACACTTCCGAT<br>GCC | 59.3                             | 652                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_37202118  | Ca6                                     | 37202118                      | CATATATATATATATATATATATATA<br>TA/CATATATATATATATATATATATA<br>TA               | GCGAAAATGGAAATGG<br>AAGA   | TTTGTTTTGAACTCG<br>GAGG  | 60.0                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_37221968  | Ca6                                     | 37221968                      | CCTAAT/CCTAATCTAAT                                                            | AACCCATTTGAGGTGA<br>CTGC   | CCGATCTTCCAATCGTT<br>GAT | 60.0                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3742101   | Ca6                                     | 3742101                       | A/ATTATTATT                                                                   | TGAAAGTTTAGCGGCA<br>ATCA   | AATTGTTGGCACGCTTT<br>TTC | 59.4                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_37640608  | Ca6                                     | 37640608                      | CAAAATTTAAAAATTTAAAAATTTAA<br>AA/CAAAATTTAAAAATTTAAAAATTT<br>AAAAATTTAAAA     | TTTGCGTAGTGTGAC<br>TTGC    | CTCGTGAGGGGAAGCA<br>TAAG | 59.9                             | 308                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_37741039  | Ca6                                     | 37741039                      | CAAA/CAA                                                                      | AGGGTGAGTGATCCGT<br>TGTC   | CCACGAGTTCAGGGTT<br>TCAT | 60.0                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_37798672  | Ca6                                     | 37798672                      | TTATATATATATATATATATATATATA<br>TATAT/TTATATATATATATATATATA<br>TATATATATATATAT | GGACGTGAACAACGAG<br>TCAA   | GATGCAGTGGCCAAAG<br>AAAT | 59.7                             | 684                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3780129   | Ca6                                     | 3780129                       | CTTTTT/CTTTTTT                                                                | GCGTTGTCAAATTAC<br>AAATTCA | TTATTTGAATCCCCAA<br>AACA | 59.1                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                       | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                     |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_37902107  | Ca6                                     | 37902107                      | TT/TTGATAT                                                                                          | GTTTGTGACAGGCCCA<br>ATAA  | ATGGTGGTTCGGTCAC<br>ATTT | 59.9                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_37981298  | Ca6                                     | 37981298                      | A/AATGTC                                                                                            | GCTGCTCCTTTTGAAC<br>TTTCC | TATTGCCTCAAAGTGG<br>CTGA | 60.4                             | 402                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_37981463  | Ca6                                     | 37981463                      | GAAA/GA                                                                                             | CCAATTGGAACAAGGT<br>TGGA  | TATTGCCTCAAAGTGG<br>CTGA | 60.7                             | 243                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_37981858  | Ca6                                     | 37981858                      | TAAA/TAA                                                                                            | TGCAATGACCTTGAAA<br>TTCC  | CTTTAGCCTTCATCGC<br>CAG  | 59.7                             | 817                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_37982172  | Ca6                                     | 37982172                      | AATGAT/AAT                                                                                          | GGTACACTTCCCATC<br>AGCAA  | CTTTAGCCTTCATCGC<br>CAG  | 60.0                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_38201434  | Ca6                                     | 38201434                      | GTTTTTTT/GTTTTTTT                                                                                   | GGTTCGTAATGGATGG<br>GATG  | AAGGCCTTTTACAACG<br>CTCA | 60.0                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_38202225  | Ca6                                     | 38202225                      | CT/CTGAT                                                                                            | AAGCTCAACATGCAAA<br>ACCC  | CAATGTGAATGCCAC<br>CAAG  | 60.1                             | 691                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_38220530  | Ca6                                     | 38220530                      | TTATATATATATATATAT/TTATAT<br>ATATATATATATATAT                                                       | GGGTGGGAAAAAGCTA<br>GACC  | GATAGTTTTTCGACCG<br>CGAG | 59.9                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_38385351  | Ca6                                     | 38385351                      | CC/CCCTCTGTCCAGATCTC                                                                                | CGAAGCCTTGTCCTC<br>CAAC   | GGAAAAAATGCCTCC<br>AAGA  | 60.0                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3855737   | Ca6                                     | 3855737                       | GATATATATATATATATATATATAT<br>TATATATATATATATATAT/GATATAT<br>ATATATATATATATATATATATATAT<br>TATATATAT | GTTTCCAAGTTCATG<br>GTCG   | TTTTTCAGTGTGCAAA<br>ACAA | 60.4                             | 770                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')         | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                 |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_38677967  | Ca6                                     | 38677967                      | TA/TATACACACA                                                 | AACACCCCAAACGAC<br>ACTC         | TCGAAGAGAAGGTTGC<br>CACT      | 59.9                             | 948                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_38718082  | Ca6                                     | 38718082                      | GT/GTATCAGTAT                                                 | TTGAGGATTTCCAGAA<br>ACGG        | CCCCAATTCACACCAAA<br>TTC      | 60.0                             | 291                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_38908988  | Ca6                                     | 38908988                      | AT/A                                                          | CGGTGTCTCCATGAAT<br>GTTG        | CCATCTCTTCCTTTTGC<br>TCG      | 60.0                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_39127532  | Ca6                                     | 39127532                      | GAGTATA/GA                                                    | CGGTCAAATCTGAAGC<br>AACA        | ACCAACTGGTTGGCTA<br>CGTC      | 59.8                             | 615                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_39250014  | Ca6                                     | 39250014                      | ANNNNNNNNNNN/ANNNNNNNN<br>NNNN                                | CTCGAGGGGCGTAAAT<br>CATA        | GGGTGGTTCCATGAGT<br>TGAT      | 60.1                             | 172                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3937441   | Ca6                                     | 3937441                       | ATTTTTTTTT/ATTTTTTTTT                                         | TGAAGGAAGATGATCC<br>ACGA        | CAAATTCAGCAGCACT<br>GGA       | 59.2                             | 733                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_39446229  | Ca6                                     | 39446229                      | GAA/GAAA                                                      | CTTCACCTTGAGTCCC<br>CTTG        | TTGGCCAGACCACTTT<br>TACC      | 59.7                             | 815                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_39450071  | Ca6                                     | 39450071                      | CTTTTT/CTTTTT                                                 | TTTCAGAACACATATAG<br>TAAACGTTGG | TGATTTCACTTTTGGTG<br>AGTAATGA | 59.8                             | 313                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_39465065  | Ca6                                     | 39465065                      | ATTTTTTT/ATTTTTTTTT                                           | TAAGGTACGGGATTTT<br>CCCC        | TCACCAATCCCCAAG<br>ACTC       | 60.0                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_39467723  | Ca6                                     | 39467723                      | TAAA/TAA                                                      | GGGAATCAAACCCGGT<br>AACT        | TCCTAAACACATGCGT<br>CCAA      | 60.1                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                               | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                             |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_3977548   | Ca6                                     | 3977548                       | TC/T                                                                                        | AACTCAGAAGGCCGAG<br>TTGA   | TGATCGGCCTTTGTAC<br>TCTG  | 60.0                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_3977816   | Ca6                                     | 3977816                       | ATTTTTTTTTTT/ATTTTTTTTTTT                                                                   | AACTCAGAAGGCCGAG<br>TTGA   | TGATCGGCCTTTGTAC<br>TCTG  | 60.0                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_39791831  | Ca6                                     | 39791831                      | T/TC                                                                                        | CTCGTGTTTCGTTCTGTG<br>AGAA | CAGGGTACGAACCGGT<br>AAGA  | 60.0                             | 869                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_39811005  | Ca6                                     | 39811005                      | AATACATAC/AATAC                                                                             | ATATGACACGTGGCAG<br>TCCA   | GAGTCGGTCCAACAAA<br>TTCAA | 60.0                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_39829036  | Ca6                                     | 39829036                      | CTTTC/CTTTCCTCTTTTC                                                                         | CCCACAATCATATTCC<br>CCTG   | CGCTCCAAGAGTCAAT<br>GTCA  | 60.0                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_39831963  | Ca6                                     | 39831963                      | CATATATATATATATATATATATA<br>TATATATATATAT/CATATATATATAT<br>ATATATATATATATATATATATATA<br>TAT | TTGGAAGGAGCCCTTA<br>CCTT   | ATGTCAATTCAGTTGC<br>GACG  | 60.1                             | 492                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_39879844  | Ca6                                     | 39879844                      | GA/GAA                                                                                      | ATCAACCCGCCCTTTA<br>CTTT   | CGGCGGCTCTTTATTT<br>AGTG  | 59.8                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_39931353  | Ca6                                     | 39931353                      | ATTT/A                                                                                      | TGGTGCTCCACTTATC<br>CCTC   | GCATGTTCCATGGTGT<br>GAAT  | 60.1                             | 249                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_40031841  | Ca6                                     | 40031841                      | T/TA                                                                                        | TGAGAAACTTTTCCGC<br>TGCT   | CTATTAGCGTTGGCTC<br>TCGG  | 60.1                             | 411                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_40508760  | Ca6                                     | 40508760                      | GAAAA/GAAAAA                                                                                | AATTGACGTCGAACCC<br>TGTC   | CGTAGCGAAGTCGGAT<br>GAAT  | 60.0                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                            | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                          |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_40594605  | Ca6                                     | 40594605                      | AC/A                                                                                                     | TCTGATCAGCTCTATG<br>CCTCC  | GGATGGTTGTTGAGT<br>GGCT    | 59.5                             | 158                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_40699134  | Ca6                                     | 40699134                      | GATATATATATATATATATAT/GAT<br>ATATATATATATATAT                                                            | TGGATTTGAGCCTCGT<br>AACC   | AAGCACGTGTCAAATC<br>GTGA   | 60.1                             | 743                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_40730901  | Ca6                                     | 40730901                      | AATATATATATATATATATA/AATATA<br>TATATATATATATATA                                                          | TCCCGAATTCTTTTCATT<br>GTTG | TAGCGATCCATTCCCA<br>AAAC   | 59.9                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_40803495  | Ca6                                     | 40803495                      | ATTT/ATTGTTT                                                                                             | ATGAATGGAAGACGTG<br>ACGA   | TGGACAAATTGCGTATT<br>GACA  | 59.1                             | 862                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_41128605  | Ca6                                     | 41128605                      | TAAAAAAAAA/TAAAAAAA                                                                                      | AATGGGCGCTGTAAA<br>TGTC    | GGGAGCTGATACCACA<br>GCAT   | 60.0                             | 702                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_41168319  | Ca6                                     | 41168319                      | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATT/AT<br>ATTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATT | TTGAATCGTGAGGGTG<br>TCAG   | TGATTTCAAAGCAATG<br>TCAAAA | 59.7                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_41197274  | Ca6                                     | 41197274                      | TAAAAAAAAA/TAAAAAAA                                                                                      | AGCATTGGTGGTGTAG<br>GAGG   | TGCAACGAAACAGATT<br>GGAG   | 60.0                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_41464281  | Ca6                                     | 41464281                      | CTTTGATTTGA/CTTTGA                                                                                       | AAGCAGAAGGTAGTGG<br>CGAA   | GTACGTGGTCCTTCCC<br>TGAA   | 60.0                             | 395                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_41464328  | Ca6                                     | 41464328                      | GAAA/GAAAA                                                                                               | AAGCAGAAGGTAGTGG<br>CGAA   | GTACGTGGTCCTTCCC<br>TGAA   | 60.0                             | 395                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_41498708  | Ca6                                     | 41498708                      | AATATATATATATATATATATATAT<br>ATATATATATATATAT/AATATATATA<br>TATATATATATATATATATATATAT                    | TTCTCCCTTGAGAACC<br>ATGC   | TGTCGCAAGTAATTTCC<br>AAGC  | 60.2                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_41574227  | Ca6                                     | 41574227                      | CATAATAATAATAAAT/CATAATAA<br>TAATAATAATAAT                    | TGATTAATCGCAAATTG<br>TCCA     | TTTTTGGGGTCGTTTGA<br>TGC  | 59.0                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_41574282  | Ca6                                     | 41574282                      | TTTATTATTATTATTATT/TTTATTATT<br>ATTATTATTATT                  | TGATTAATCGCAAATTG<br>TCCA     | TTTTTGGGGTCGTTTGA<br>TGC  | 59.0                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_41659483  | Ca6                                     | 41659483                      | CAAAA/CAAAAA                                                  | CCATCAGAACTGGGA<br>TGGT       | TGGCCCTTCATTTTCA<br>ATC   | 59.8                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_41668275  | Ca6                                     | 41668275                      | AATATATATATATATATATA/AAATA<br>TATATATATATATATATATATATA<br>ATA | TCAAAACAGAACAGAT<br>CATGTGG   | GTAAATGAAGCGCTT<br>TCGC   | 60.0                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_41669222  | Ca6                                     | 41669222                      | AA/AAAGGACTTGGA                                               | AATGGGCGCTGTAAA<br>TGTC       | AGGGGTGATGAAGAAA<br>TTCG  | 60.0                             | 265                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_41669872  | Ca6                                     | 41669872                      | ATT/ATTT                                                      | TGTAGAATCCACCAAT<br>GTCCA     | ACCAATCATGTTTCGTG<br>GAA  | 58.8                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_41777270  | Ca6                                     | 41777270                      | GT/GTT                                                        | CTTGGGTTGACTTGGG<br>ACTC      | TTGAACAACATGGGAG<br>AGGA  | 59.5                             | 696                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_418262    | Ca6                                     | 418262                        | GTTTTTTTT/GTTTTTTTTT                                          | AACGCTCCTCTTCCTT<br>CAAA      | TCTTCACTTGTTGGTT<br>CCAA  | 59.1                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_41874600  | Ca6                                     | 41874600                      | AAGA/AA                                                       | TGTAGTTACGTTTCTT<br>TTTGAATTT | CATTTAAGATTTGCGG<br>CATTT | 57.0                             | 347                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_41903041  | Ca6                                     | 41903041                      | TTATATATATATATA/TTATATATA<br>TATATATATA                       | TCGGTATTTCGAACTT<br>GGGT      | AGCCCCAAAAAGTGGC<br>TATT  | 59.4                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                        | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                                      |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_41903127  | Ca6                                     | 41903127                      | TTTGGATT/TTT                                                                                                                                                         | TCGGTATTTTCAACTT<br>GGGT    | AGCCCCAAAAAGTGGC<br>TATT   | 59.4                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_42130307  | Ca6                                     | 42130307                      | GAAAA/GAAAAA                                                                                                                                                         | CGAATACACTTGGCCA<br>CTGA    | CCGAAGCGACTGGA<br>TTAG     | 59.7                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_42269920  | Ca6                                     | 42269920                      | AC/A                                                                                                                                                                 | CCAAGAAATTAGAATC<br>GACATCA | TTTCACGTGGGACAAC<br>AAAA   | 59.5                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_42308665  | Ca6                                     | 42308665                      | CTTATTATTATTATTATTATTATT<br>ATTATTACTATTATTATTGTTATT<br>ATTATTATTATTATTATTATTATT<br>/CTTATTATTATTATTATTATTAT<br>TATTATTATTACTATTATTATTGT<br>TATTATTATTATTATTATTATTAT | CTGAATCGCGAAAGAA<br>GTCC    | ATGGAGATGCGACAAT<br>GTGA   | 60.0                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_42360169  | Ca6                                     | 42360169                      | TC/TCCCAAAAAGC                                                                                                                                                       | AGAACAGAGGGAACGC<br>AGAA    | CAGCGCTTATTTGGGA<br>AAAG   | 60.0                             | 625                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_42398678  | Ca6                                     | 42398678                      | ATTTTTTT/ATTTTTT                                                                                                                                                     | GGTTTGGGAGAGAAAA<br>AGGAA   | TGGTTAAAACTCATTGG<br>TCCC  | 59.6                             | 900                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_42418850  | Ca6                                     | 42418850                      | ATATTATTATTATTATT/ATATTA<br>TTATTATTATT                                                                                                                              | CCGACGTCTCTATTC<br>TCAA     | AACGACAACCTTCAACC<br>CATTT | 59.0                             | 686                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_42464964  | Ca6                                     | 42464964                      | A/AT                                                                                                                                                                 | GGTGAGTTTTCCACAA<br>GCGT    | GCTTCAATGAAATTTGG<br>CGT   | 60.2                             | 982                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_42480728  | Ca6                                     | 42480728                      | A/AT                                                                                                                                                                 | CACAAACATCACGTG<br>AACC     | GATATGGGCAGACAG<br>GTAAA   | 60.0                             | 885                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_42608436  | Ca6                                     | 42608436                      | ATTT/ATTTT                                                                                                                                                           | CCTCGGATGCATTCT<br>CTAA     | TGGGAACGTGTATTCT<br>ACAA   | 60.2                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_43017644  | Ca6                                     | 43017644                      | ACATCAT/ACATCATCAT                                            | GGAAGGATTTGAAGA<br>AACCA | GCCGTGCCTTTTAAAT<br>GTGT     | 58.1                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_43043105  | Ca6                                     | 43043105                      | CA/C                                                          | TGATTTGGTCGCAACA<br>GCTA | AAAAATTGTGCCAAAGT<br>TATGTGA | 60.4                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_43064353  | Ca6                                     | 43064353                      | A/AACTG                                                       | CGCCACAACCTCTACT<br>CCTT | GAGGTGCGACAACAGA<br>TGAA     | 59.4                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_43064766  | Ca6                                     | 43064766                      | ACC/ACCC                                                      | GCACCAAGGTTTACG<br>TTCA  | GCCGATGACACATCAA<br>AATG     | 58.7                             | 719                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_43138332  | Ca6                                     | 43138332                      | GAAAA/GAAA                                                    | GTTCCCTTTGGAATGC<br>TTGA | TCTTTGGGCCAGTGAA<br>AATC     | 60.1                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_438370    | Ca6                                     | 438370                        | A/AG                                                          | AACCATTGCTTTCATT<br>CGT  | ATGGACCCCATACAAG<br>ACCA     | 59.4                             | 850                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_43909185  | Ca6                                     | 43909185                      | TTGAAG/TTGAAGCAAGTACAACCTC<br>ATGAAG                          | TGATTGGGTTTGGGTT<br>CATT | ACATAGATGCCGCCTT<br>CATT     | 60.0                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_43909507  | Ca6                                     | 43909507                      | CTTTTTTTTT/CTTTTT                                             | GAAGCGGCATCTATG<br>TGTT  | GGCTTTTGAATCACCG<br>AAAA     | 60.1                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_43921995  | Ca6                                     | 43921995                      | TAAA/TAA                                                      | GGTGTGCTGTGTGTT<br>GCGT  | GCTTAATTCTAGGGAG<br>GCGG     | 60.7                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_44134697  | Ca6                                     | 44134697                      | GGTGGCC/GGTGGCCGTGGCC                                         | GAGGCTGGATGGAAGA<br>GAGA | AGGTTGCTGTTGTGCA<br>GATG     | 59.5                             | 197                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)  | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                |                           |                            |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_44263063  | Ca6                                     | 44263063                      | TTATATATATATATATATATATATAT<br>T/TTATATATATATATATATATATATA<br>T | CCCTTCCTCCACCATC<br>ACTA  | TTTAAAATTCGGCCGT<br>GAAG   | 59.9                             | 643                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_44292405  | Ca6                                     | 44292405                      | TAA/TAAA                                                       | AACACTAGAACTCGC<br>GCAAA  | CCAATCTACATGATGCA<br>CGG   | 60.1                             | 304                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_44301191  | Ca6                                     | 44301191                      | CTTTTT/CTTTTT                                                  | TGCACATTTTACAGCG<br>CTTC  | TGAAATTATGGGTGGG<br>CATT   | 60.0                             | 254                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_4433303   | Ca6                                     | 4433303                       | TAAAAAAAAA/TAAAAAAAAA                                          | TGGAGAGACTTCGGTT<br>GCTT  | CCACTCGTACTCCCTG<br>AGATTC | 60.0                             | 911                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_443925    | Ca6                                     | 443925                        | TTATATATATATATATATATATA/TTA<br>TATATATATATATATA                | GGACTTTGAGGAGAAT<br>CGAGG | TGCTCACAAATATGCAT<br>TCCA  | 60.2                             | 500                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_44636710  | Ca6                                     | 44636710                      | CTATATATATATATATATATATAT<br>ATAT/CTATATATATATATATATAT<br>ATAT  | CGCAGTCGTGCTTTCA<br>ATAA  | TGTCCAGAGCAATCTT<br>CGACT  | 60.0                             | 637                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_44637030  | Ca6                                     | 44637030                      | GATATATATATATATATATA/GATATA<br>TATATATATATATATA                | AATCCAAAAGTTGAAC<br>CCGA  | CAATAAGTGGTTTTTCC<br>CGC   | 59.4                             | 577                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_44845775  | Ca6                                     | 44845775                      | GAAA/GAAAA                                                     | GTGTTGCCTGATGAAT<br>GTGG  | ATCGTGTGATTGGGAG<br>GAAG   | 60.0                             | 641                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_449509    | Ca6                                     | 449509                        | TAAAAAA/TAAAAA                                                 | ATGGTGTTGGGAACA<br>CATT   | GTCAATCCGACCCCTAT<br>GCTA  | 60.0                             | 468                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_44977370  | Ca6                                     | 44977370                      | CCTTCTATTT/CCTTCTATTTCTT<br>TTCTTTCTATTTTC                     | GTTGGTTCCTAGCAC<br>CGTA   | TGGATATTGGCTCAGA<br>GGCT   | 60.0                             | 623                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                 |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_45282323  | Ca6                                     | 45282323                      | TCCTTTT TAGAAAGTAC/TC                                           | TGTTGGAGAGGCTCTG<br>CTTT    | CGTTTTTCTGCACTCTG<br>CAA | 60.1                             | 214                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_45290500  | Ca6                                     | 45290500                      | AT/A                                                            | GGCACGCTATGGAAAG<br>AGTC    | TGAAATTCCATAGGAA<br>GCGG | 59.8                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_45329060  | Ca6                                     | 45329060                      | T/TTTAAAA                                                       | TTTTTGCTATTTTATTC<br>TCGTGG | TCGATTATGCGTAGGG<br>AAGG | 57.6                             | 762                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_45329314  | Ca6                                     | 45329314                      | TC/T                                                            | GGGAGATACGTAGGAG<br>CACG    | TCGATTATGCGTAGGG<br>AAGG | 59.7                             | 242                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_45585418  | Ca6                                     | 45585418                      | G/GCTCGGT                                                       | AAAAGGGGAGCTCAA<br>CGAT     | CTTCGAATGGTGTGG<br>TCCT  | 60.1                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_4559660   | Ca6                                     | 4559660                       | AATATATATATATATATA/AATATA<br>TATATATATATATATA                   | GCCAGGTTGCTGATAT<br>TTTCAT  | ATCACGCCAATATCGC<br>TGTA | 60.3                             | 935                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_45895264  | Ca6                                     | 45895264                      | TTATATATATATATATATA/TTATATA<br>TATATATATA                       | TTGAAAGAACCAAACG<br>AGGG    | TTTGAGAAATCCCCATT<br>GGA | 60.1                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_45900035  | Ca6                                     | 45900035                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATAT                 | TCCGACACATTGCACA<br>AAAT    | TCCAAGTTTCAAATGG<br>GGAT | 60.0                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_45908144  | Ca6                                     | 45908144                      | CATATATATATATATATATATA<br>TATATAT/CATATATATATATATAT<br>ATATATAT | AAAGGAGCTGGCATAT<br>CGAA    | GATGTGGGTACGACGG<br>ATCT | 59.8                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_46305635  | Ca6                                     | 46305635                      | CTTTTTTTTT/CTTTTTTTTTT                                          | AATGAAGGGAAGGGCA<br>TTTT    | TGGTCGTTTTTCGTTTG<br>TTG | 59.8                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                        | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                      |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_46346578  | Ca6                                     | 46346578                      | TTATGAATAT/TTAT                                                                                                      | TAACCCAAAAATCCCA<br>CCA   | ACTTGGGAACCCGAAG<br>AAGT  | 60.0                             | 466                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_4635371   | Ca6                                     | 4635371                       | GT/GAGAAAAATTCGGTT                                                                                                   | CCAAAGCCAACGGCTA<br>TAAT  | ATGAATTGAGGGGGTA<br>AGGG  | 59.1                             | 302                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_46399842  | Ca6                                     | 46399842                      | T/TCA                                                                                                                | TAACCTTGATGGGGA<br>AAAG   | TTATGGTGTTCCTTG<br>GCA    | 59.9                             | 619                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_4649762   | Ca6                                     | 4649762                       | AATAAGT/AATAAGTATAAGT                                                                                                | GGTCGAACCACTTGAG<br>GTGT  | AATCCACTCCCACTCC<br>ACTG  | 60.0                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_465128    | Ca6                                     | 465128                        | TTTTATTTATTTATTTATTT/TTTT<br>ATTTATTTATTTATTT                                                                        | TGAGCGAAAAATCATG<br>AAAGG | TTTGGGTTTTGTTTTCC<br>TCG  | 60.2                             | 986                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_46525735  | Ca6                                     | 46525735                      | TTTATTATTATTATTATTATTATT<br>ATTGTTATTATTATTATTATTATT<br>/TTTATTATTATTATTATTATTAT<br>TATTATTGTTATTATTATTATTAT<br>TATT | AGAAGAGATGGTTGCT<br>GTCCA | GCATAATTGATCCTAC<br>GGTCC | 59.9                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_46772986  | Ca6                                     | 46772986                      | A/ATT                                                                                                                | GATTATTCTGCCTCCC<br>GTCA  | AAACGCAATCCTTGAG<br>TTCG  | 60.0                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_46790016  | Ca6                                     | 46790016                      | TATTCATT/TATT                                                                                                        | AAAGCTGTCATACTCA<br>GCCCA | TTGCTCCTACGTATCTC<br>CCG  | 59.9                             | 895                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_46827577  | Ca6                                     | 46827577                      | AATATATATATATATATATATA/AA<br>TATATATATATATATATATATATA                                                                | TGCATCGTTACCCCCA<br>TTAT  | GGGGACCACTCTATCT<br>TTTCG | 60.0                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_4699610   | Ca6                                     | 4699610                       | CG/CGG                                                                                                               | TTCTCTTCAAAGCGTG<br>AGCA  | TTCTTGTCCCATCTCC<br>ATC   | 59.9                             | 304                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                              |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_47001052  | Ca6                                     | 47001052                      | A/AG                                                                                         | GAAGCGTACTTCCCA<br>TTGA  | GTTTACAATGTGGGGA<br>CGAG  | 60.1                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_47036359  | Ca6                                     | 47036359                      | TTGTGTGT/TTGTGT                                                                              | TCTTGATCGTGTGAGG<br>CATT | TGTGTGGGGCATTACT<br>TTGA  | 59.2                             | 384                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_47040606  | Ca6                                     | 47040606                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTAT/TTTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTAT | TATCATCACCTCACCC<br>CCAT | TCCAGTCAATGTGCAA<br>AAACA | 60.0                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_4713516   | Ca6                                     | 4713516                       | CAAAAAAAAA/CAAAAAAAAA                                                                        | TGGAGAGGTGTGTGCA<br>AGAG | GAGGCAAGAGCGACGA<br>ATAG  | 60.0                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_47141352  | Ca6                                     | 47141352                      | CAAAA/CAAA                                                                                   | TATGTCAGAATCCCGA<br>TCCC | AAACATTTGGCTACAAG<br>GCG  | 59.7                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_47299841  | Ca6                                     | 47299841                      | AACATATTCA/AACATATTCATATAC<br>ATATTCA                                                        | TTGCGCGCTTGTATA<br>CTTG  | GCATGCTGCAAGGGAT<br>AGTT  | 60.0                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_47312521  | Ca6                                     | 47312521                      | GTT/GTTT                                                                                     | TATCTGTGGTCGTGTG<br>GGAA | TCACGGGTCAACACGA<br>TTTA  | 60.0                             | 822                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_47527023  | Ca6                                     | 47527023                      | GAAAAAAAAA/GAAAAAAAAA                                                                        | AACGAGAAAACGGAGA<br>GCAA | CCCACAAAACATGACT<br>GCAC  | 60.0                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_47615563  | Ca6                                     | 47615563                      | GAAAAA/GAAAAA                                                                                | GGATTATTAATTCGCG<br>GGGT | AAATCTGGTCGCTGAA<br>TTGG  | 60.0                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_47701039  | Ca6                                     | 47701039                      | CAAA/CAAAA                                                                                   | TGTCCTGAGTATTCC<br>GGTC  | ATGTGACAAACCTTTTC<br>GGG  | 59.9                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_4771733   | Ca6                                     | 4771733                       | TTATATATATATATATATAT/TTAT<br>ATATATATATATATAT                 | GGGCCACATGTATTTG<br>TGTTT    | GGAGGCAAGGCAATAA<br>ATCA     | 59.6                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_47787286  | Ca6                                     | 47787286                      | TT/TTAT                                                       | AGGAAACAAACGAAGG<br>CAGA     | CCGCTTTGCATCCTCA<br>TAAT     | 59.9                             | 226                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_47790346  | Ca6                                     | 47790346                      | TTATATATATATATATATATAT/TTATATATATATATATATATAT                 | GCAAGATCGCATTCTT<br>GTCA     | CGGGTATAAGGCTCCA<br>CTCA     | 60.0                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_4781527   | Ca6                                     | 4781527                       | TA/TACTCTCCGA                                                 | GATTTCTCGCTTCCC<br>TTCT      | CCTTGTCCAGTTGTC<br>CCAT      | 59.8                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48011269  | Ca6                                     | 48011269                      | GATATATATATATAT/GATATATATAT<br>ATATAT                         | TTTGTTCGTAATGTT<br>GTTGA     | TAGCTGTTGCGACCA<br>ATCA      | 59.2                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_4801698   | Ca6                                     | 4801698                       | TGG/TGGG                                                      | ATAACCGACACAGACG<br>AGGC     | GTTGTTGCTTCTGCTC<br>CTCC     | 60.1                             | 278                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48063867  | Ca6                                     | 48063867                      | AAGA/AA                                                       | CGTTTTATTTCGGGAC<br>TGGA     | CTGCGAGGAACATTTC<br>AACA     | 59.9                             | 325                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48143669  | Ca6                                     | 48143669                      | ATTTT/AT                                                      | TAAACGGATGGAGGG<br>ATCA      | TGAACGAGGATTTTGG<br>AAGG     | 60.3                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_4823285   | Ca6                                     | 4823285                       | GTATATATATATATATATAT/GTAT<br>ATATATATATATATAT                 | CATCTTGCAAAACAAAC<br>AAATG   | TCCACTAACAAGTACTC<br>CAAAACG | 58.3                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_4823723   | Ca6                                     | 4823723                       | TAA/TAAA                                                      | CGTTTTGGAGTACTTG<br>TTAGTGGA | ACAACCATCAAACCGAT<br>TCC     | 59.6                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                      | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                    |                              |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_48260819  | Ca6                                     | 48260819                      | GAAAATTAATAAAATA/GAAAATTAA<br>TAAAATAAAATTAATAAAATA                                                                | GTGGATGGTGGGGAAT<br>AGTG     | CTGAGGTCCCAAGCTA<br>CGTC     | 60.1                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48267774  | Ca6                                     | 48267774                      | ATTTTTTTTT/ATTTTTTTTT                                                                                              | GACATAAGAATGGAGG<br>CGGA     | TTTCTTCGCGTTTGACT<br>AATG    | 60.0                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48271447  | Ca6                                     | 48271447                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTAT/TTTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>AT | TGACTAATTGGTCGCC<br>CTTC     | GGATGCGATCATGTGA<br>AGAA     | 60.1                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48279466  | Ca6                                     | 48279466                      | G/GA                                                                                                               | AACCAGATACTAACCC<br>GCGA     | TCTGGAAGTTTCTTGAC<br>CGTG    | 59.6                             | 620                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48279626  | Ca6                                     | 48279626                      | ATTTTTTT/ATTTTTTT                                                                                                  | AACCAGATACTAACCC<br>GCGA     | TCTGGAAGTTTCTTGAC<br>CGTG    | 59.6                             | 620                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48280097  | Ca6                                     | 48280097                      | GAAAAAAA/GAAAAAAA                                                                                                  | GACACGGTCAAGAAAC<br>TTCCA    | TGCGTTGACTCTTCAAT<br>ACACA   | 60.1                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48280225  | Ca6                                     | 48280225                      | GTAT/GT                                                                                                            | GACACGGTCAAGAAAC<br>TTCCA    | TGTGGCACATTCCAAA<br>TTTAT    | 60.1                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48280286  | Ca6                                     | 48280286                      | ATTTTTTTTTTTTTTT/ATTTTTTTTT<br>TT                                                                                  | GACACGGTCAAGAAAC<br>TTCCA    | TGTGGCACATTCCAAA<br>TTTAT    | 60.1                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48280545  | Ca6                                     | 48280545                      | ATT/ATTT                                                                                                           | TGTGTATTGAAGAGTC<br>AACGCAT  | AAAAGTTGTGCCAAAG<br>TTATGTGA | 59.7                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48280766  | Ca6                                     | 48280766                      | TCTA/TCTAAACTA                                                                                                     | TGTATTGATGAGTCGT<br>TGAATGAT | GGAGACGTTAAAGTCC<br>CACA     | 58.5                             | 902                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                           |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_48281397  | Ca6                                     | 48281397                      | TAAAAAAAA/TGAAAAAAAA                                                                      | GGGACTTTAACGTCTC<br>CAATACA | CTTGAGAACGATCTGC<br>CACA  | 59.4                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48281570  | Ca6                                     | 48281570                      | TA/TAATTAAA                                                                               | TAGGGCAATTGTGCAC<br>ATGA    | CTCCAGGTAACGGTTG<br>TGGT  | 61.1                             | 335                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48373786  | Ca6                                     | 48373786                      | GTTTCACCACTCT/GT                                                                          | TCACACGACGTTCAAC<br>ATTT    | TCCATCAAGGTAGGCC<br>ATTC  | 60.0                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48385345  | Ca6                                     | 48385345                      | G/GA                                                                                      | GGCTTTTGCAATGGTT<br>GTTT    | TGCACTCACTCGCCAT<br>TTAC  | 60.0                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_4843264   | Ca6                                     | 4843264                       | A/ATGCAAT                                                                                 | CACACATCAATCGACC<br>CAAG    | ACACGGTATTTCCAATT<br>CGC  | 60.0                             | 748                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48821438  | Ca6                                     | 48821438                      | AATATATATATATATATATATATAT<br>ATATATATAT/AATATATATATATATA<br>TATATATATATATATATATATATAT     | CTACGTTCCGTCGATT<br>CCAT    | CCAGTATGCGACAAGC<br>TGAA  | 60.0                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48850339  | Ca6                                     | 48850339                      | CTT/CT                                                                                    | TTGAGGGGTGTGATTA<br>GCAA    | TGGGGACCATAACTGA<br>GGAG  | 59.1                             | 846                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48891611  | Ca6                                     | 48891611                      | TAAA/TAAAA                                                                                | TGTGTCCAAAACATCA<br>AGGA    | GCTGCCTCCCCTCTCT<br>AACT  | 59.1                             | 773                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_48905387  | Ca6                                     | 48905387                      | GAAAAA/GAAAAAAA                                                                           | CACGGTCCCTAGAGCC<br>AATA    | ATCGACTCCCGAACTC<br>AAAA  | 60.1                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_49079894  | Ca6                                     | 49079894                      | TTAATAATAATAATAATAATAAAT<br>AATAATAATAATA/TTAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATA | AATACCTGGACGACTG<br>TGCC    | CCTCCATCTTTCTGAT<br>CAACC | 60.0                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                              | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                            |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_49218883  | Ca6                                     | 49218883                      | TAAAAAA/TAAAAAAA                                                                                                           | CCCCTTCATATGCTTC<br>CAGA   | GTGCTTGCTTTTACTTC<br>GCC  | 60.0                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_49222205  | Ca6                                     | 49222205                      | T/TG                                                                                                                       | CCTGCGGAATTCCTA<br>ATGA    | AGGTAACACGGCAGGT<br>AACG  | 60.0                             | 197                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_4941032   | Ca6                                     | 4941032                       | GATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAAT/GATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAAT | TATGACCCGAGATCCG<br>CTAC   | GGTTCTCGCACACAAC<br>AAAA  | 60.1                             | 318                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_49437012  | Ca6                                     | 49437012                      | TG/T                                                                                                                       | CCGTTGAGAAGTTAAT<br>GGCG   | TTGAAGCGGTAGTTGA<br>CGAA  | 60.6                             | 248                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_49497029  | Ca6                                     | 49497029                      | AATATATATATATATATATATAT<br>/AATATATATATATATATATATAT                                                                        | GTTTTTGGCACGCAAT<br>TTGT   | TGACCTTCAACTGATC<br>GCAC  | 60.9                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_49611302  | Ca6                                     | 49611302                      | AAG/AAGCTAG                                                                                                                | CATTGAAGGCAACCA<br>TGTG    | CTGTAGGCCACACAAA<br>ATGC  | 60.0                             | 951                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_49619550  | Ca6                                     | 49619550                      | ATTTTTTTTTTTTT/ATTTTTTTTT<br>TTTT                                                                                          | CCGATGAAGGTGGTTT<br>ATTTTT | AAACCCACTGAATTGAA<br>ACCT | 59.3                             | 816                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_4964508   | Ca6                                     | 4964508                       | TAAAAAAAA/TAAAAAAAA                                                                                                        | GACAGAAGCGACATGG<br>TTGA   | AGTTGCTTAGTTGGCA<br>ACCC  | 59.8                             | 767                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_49686510  | Ca6                                     | 49686510                      | T/TCAA                                                                                                                     | CATGTCGTTATTGCGA<br>CCAC   | AAGCCGTGAAATGGTT<br>TTTG  | 60.0                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_49733827  | Ca6                                     | 49733827                      | TCC/TC                                                                                                                     | TTGCAATCTCATCAACT<br>CGG   | GTAATGAAGCGCTT<br>TCGC    | 59.8                             | 810                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                              | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                            |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_49749941  | Ca6                                     | 49749941                      | TATAATAATAATAATAATAATAA<br>AAATAATAATAATAATAATAATA<br>ATAA/TATAATAATAATAATAATA<br>ATAATAATAAAATAATAATAAT<br>AATAATAATAATAA | GACGCACGGTTACAC<br>ACTA   | ATGTGGATGGTGACGT<br>ACGA   | 59.6                             | 299                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_49863050  | Ca6                                     | 49863050                      | TAAAAA/TAAAAA                                                                                                              | ATCTTCCCTCTCCCGA<br>GTTC  | TTGGATTGTCACCTTCA<br>GACA  | 59.6                             | 727                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_49920252  | Ca6                                     | 49920252                      | AC/A                                                                                                                       | AAGCGAGGAGCAAAAA<br>CGTA  | TCAACACGTAGACTCG<br>ACCG   | 60.0                             | 326                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_49998830  | Ca6                                     | 49998830                      | GTTTTTTT/GTTTTT                                                                                                            | AAGAGAGGTCACTTTG<br>GCGA  | TTGCATTCTCCAAAC<br>ACA     | 60.0                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_50002097  | Ca6                                     | 50002097                      | CT/CTGTGAAAAATT                                                                                                            | CGATCACCATGTTTGT<br>CGTC  | CGAACCCAGATGAAT<br>TGTT    | 60.0                             | 337                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_5025748   | Ca6                                     | 5025748                       | T/TATATA                                                                                                                   | TGTGGATCATGACTCG<br>GAAA  | CACCTTCGGTCTAAGC<br>CATTG  | 60.0                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_5031791   | Ca6                                     | 5031791                       | ATTTTTTT/ATTTTTT                                                                                                           | TGATGTCGCATGGGTA<br>TTGT  | AAAAAGTTGAGGCCCA<br>AAGG   | 59.8                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_50349238  | Ca6                                     | 50349238                      | GAA/GAATTGTTTATTTAAA                                                                                                       | CATCACAAAATCCAC<br>ACACT  | GCAATTGCGCAAATAC<br>AAAA   | 58.3                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_50467177  | Ca6                                     | 50467177                      | TTATATATATATATATATATATA<br>TAT/TTATATATATATATATATATA<br>TATATATAT                                                          | TGATGTGGCACGTCTA<br>ACAAA | ATGCTTGCTAAATGGC<br>ACAA   | 60.2                             | 280                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_50528740  | Ca6                                     | 50528740                      | TAAAAA/TAAAA                                                                                                               | TGGGTTTATCCCTTCTT<br>TGC  | TGGATCCAACCTTTGAG<br>ACACC | 59.0                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                              |                              |                             |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_50797014  | Ca6                                     | 50797014                      | ATTTTTTTTTTTTTTT/ATTTTTTTTT<br>TTTTT                                         | GGAGAATGCGATAGCT<br>GGAG     | TGGCGTTCTTTTAGC<br>CTGT     | 59.9                             | 827                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_50938274  | Ca6                                     | 50938274                      | TTTATTATTATTATTA/TTTATTATTA<br>TTATTATTA                                     | ACACGTTTTGTTTGTG<br>GCAA     | AGTTGGCTTTTGTACC<br>CCCT    | 60.1                             | 396                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_50968923  | Ca6                                     | 50968923                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                                | TCCCTTTCAGTCCCTT<br>CTCA     | CACTGCACCGTTGCTT<br>AAAA    | 59.8                             | 557                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_51039137  | Ca6                                     | 51039137                      | ATGTGTGTGTGTGTGTGTGTGT/ATGTGTGTGTGTGTGTGTGTGT<br>GT                          | TAAATGGATGGTGGGG<br>ATGT     | AATTTTGAATTGTGTG<br>CGA     | 59.9                             | 740                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_51142833  | Ca6                                     | 51142833                      | CTTTATTTATTTATTTATTTATTT/CT<br>TTATTTATTTATTTATTTATTTATTT                    | TTGCTTTGCTTTTGAAAA<br>CCC    | CCACTTGTGCATAACA<br>ACTCAAA | 60.2                             | 637                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_51270485  | Ca6                                     | 51270485                      | AATATATATATATATATATAT/AAATAT<br>ATATATATATATATATATAT                         | AAAACCGAATATGTGG<br>CTGC     | TTTCCCTCCAAACACAC<br>ACA    | 60.0                             | 534                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_51350130  | Ca6                                     | 51350130                      | GATAAAT/GATAAT                                                               | CAATCCAATCAACGGT<br>GCTA     | TTTTAAAGTCACGAGG<br>AACCAAA | 59.5                             | 543                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_51391817  | Ca6                                     | 51391817                      | CTATATATATATATATATAT/CTAT<br>ATATATATATATATATATAT                            | TATTTTTATGTCGGCCA<br>CCC     | AAACAAATCGCAAAA<br>CGG      | 59.7                             | 340                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_51433841  | Ca6                                     | 51433841                      | AAATAATAATAATAATAATAATAATA<br>ATAATA/AAATAATAATAATAATAATA<br>ATAATAATAATAATA | GCGAAAGAGCAGCAAA<br>AGAC     | TGCATGGATGTAAATC<br>AAACAA  | 60.3                             | 771                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_51482572  | Ca6                                     | 51482572                      | TAAAAAAAA/TAAAAAAAA                                                          | TGCACAATTGTTTATGA<br>TGTTTTT | ACACTCCCAAAATCGT<br>CCAG    | 58.5                             | 552                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                              |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_51482605  | Ca6                                     | 51482605                      | TAAAAAAA/TAAAAA                                                                              | TGCACAATTGTTTATGA<br>TGTTTT | ACACTCCCAAAATCGT<br>CCAG | 58.5                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_51746046  | Ca6                                     | 51746046                      | TTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAAT/TTAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAAT | GACGAAATTCCTTTAAG<br>AGGGG  | TTTATGGCACAACACCA<br>TCG | 58.3                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_51772881  | Ca6                                     | 51772881                      | ATTTTTTTTT/ATTTTTTTT                                                                         | CTGGGGATACGTAGGA<br>GCAA    | CTTAGGTTTGCACTCA<br>GCCC | 60.1                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_51775849  | Ca6                                     | 51775849                      | GATTTTTTATTT/GATTT                                                                           | TGATGTGCTACCCATA<br>CCGA    | GAGAGCATGCGTTTGT<br>TTCA | 59.9                             | 205                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_51785881  | Ca6                                     | 51785881                      | GTTTTTTTTTT/GTTTTTTTTT                                                                       | AACATTGTTGCGGCCT<br>AAAA    | CAGAAGATCACTCGTG<br>CCAA | 60.5                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_51816063  | Ca6                                     | 51816063                      | TTATATATATATATATATATATATA<br>TA/TTATATATATATATATATATAT<br>ATATATATATA                        | ATTGGAGACAACGGGA<br>ACAG    | GCACAGGCACCTAACC<br>AAAT | 60.0                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_5191855   | Ca6                                     | 5191855                       | TTATATATATATATATATA/TTATATA<br>TATATATATA                                                    | ATCAACAATTCAAGGC<br>CAGG    | CAAGTCATGCAATTTGA<br>CGG | 59.9                             | 807                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_51978058  | Ca6                                     | 51978058                      | TTATATATATATATATATAT/TTATAT<br>ATATATATATATATAT                                              | AAAAACCTTTGGGAAA<br>TCGG    | CCAAATTTCAAATGGC<br>GACT | 60.2                             | 211                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52087568  | Ca6                                     | 52087568                      | GT/GTTTTAATCT                                                                                | GCCAGCCATTCGATAA<br>CACT    | GAAGCAAGGATTACCG<br>ACCA | 60.1                             | 244                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52107130  | Ca6                                     | 52107130                      | CAA/CAA                                                                                      | TGGCCCTGTCCTCATA<br>AATC    | AAAGGCTATTTGCTCG<br>TGGA | 59.9                             | 911                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_52329133  | Ca6                                     | 52329133                      | CTTATTTATTTATTTATTTATTTATTT/<br>CTTATTTATTTATTTATTT           | TCACCCATAATCAAG<br>GTGAA       | TTGCGTTCTCTTACGCA<br>TCA   | 60.2                             | 990                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52486383  | Ca6                                     | 52486383                      | GTTTTTTTTTTTTTTTTT/GTTTTTTT<br>TTT                            | GTTCCATGCTGCCTTT<br>TCAT       | AGAGGAAGCAGCCACT<br>GTGT   | 60.1                             | 271                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52486696  | Ca6                                     | 52486696                      | ATTTTTTTTTTT/ATTTTTTTT                                        | AGGCCATCACATTCCT<br>TTTG       | CACTTTGGGACGTCA<br>AGTT    | 59.9                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52657541  | Ca6                                     | 52657541                      | AATATATATATATATATATA/AATA<br>TATATATATATATATATA               | TGGTTAGCATGTGTTT<br>GGGA       | TTGTGGTGCAATTCTCA<br>TCC   | 60.0                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52774565  | Ca6                                     | 52774565                      | AATATATATATATATATATAT/AAT<br>ATATATATATATATAT                 | CGGTGAATCCTTTACG<br>GAGA       | GCGAGTCAATCCGGTA<br>AAAA   | 60.1                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52787964  | Ca6                                     | 52787964                      | CG/C                                                          | TTCTCACGAACGAACA<br>CGAG       | GTGGCACCTCGGTAA<br>CAGT    | 60.0                             | 667                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52848807  | Ca6                                     | 52848807                      | ACTCGCT/A                                                     | CTGCCAAATACTGCGA<br>CTCA       | TCAATTTTGCTTGTAAG<br>ATGGA | 60.0                             | 381                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52850074  | Ca6                                     | 52850074                      | ACTAATTTCTAATT/ACTAATTTCTAA<br>TTTCTAATT                      | TCTGATTCGTTAATGAC<br>AACCTTT   | CGTGGGAGCAATTATG<br>TCCT   | 59.1                             | 218                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52850184  | Ca6                                     | 52850184                      | TA/T                                                          | AGGACATAATTGCTCC<br>CACG       | TCCATCTCCAACAACAT<br>CAAA  | 60.0                             | 305                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52854746  | Ca6                                     | 52854746                      | CATATATATAT/CAATATATATAT                                      | TGAGAATAAAGAAATTT<br>GTTGCTAAA | AGGTCAACGTACAACA<br>TTTGC  | 57.9                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_52856262  | Ca6                                     | 52856262                      | TG/T                                                          | CCGGACCTAACACGTC<br>CTAA  | TTCAGTGACAACTCCAT<br>GTGC  | 60.0                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52858291  | Ca6                                     | 52858291                      | AAAATAA/AAA                                                   | CACATGCTGCAAAATT<br>GAATG | CCACAAAAATGGTGTT<br>GCAG   | 60.1                             | 190                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52858643  | Ca6                                     | 52858643                      | GTATCTATCTATCTAT/GTATCTATC<br>TATCTATCTAT                     | CTGCAACACCATTTTTG<br>TGG  | TTTGCTGAAAGCATGTT<br>TGTTT | 60.0                             | 689                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52859170  | Ca6                                     | 52859170                      | CTTTCTTTTT/CTTT                                               | AAGTGAATTCCACCTT<br>CCCA  | CGAGCCTCCAACCTCT<br>CTTG   | 59.4                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52859293  | Ca6                                     | 52859293                      | ATATATTATATT/ATATATT                                          | AAGTGAATTCCACCTT<br>CCCA  | CGAGCCTCCAACCTCT<br>CTTG   | 59.4                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52862596  | Ca6                                     | 52862596                      | T/TTATAA                                                      | ACATGAAGGCTTGGGT<br>TGAC  | GAGGAGCATGATAGCA<br>AGGC   | 60.0                             | 193                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_5287896   | Ca6                                     | 5287896                       | TAAA/TA                                                       | CCGAAGAAAAGAAAGC<br>AACG  | AGTGCGGAGCGAGGAT<br>ACTA   | 60.0                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52889876  | Ca6                                     | 52889876                      | ATT/ATTT                                                      | TAAAGGACCAAGTCGG<br>GAAA  | TGCTCATGGAGTTAGA<br>AGCAA  | 59.5                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52890200  | Ca6                                     | 52890200                      | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATA<br>T   | TAAAGGACCAAGTCGG<br>GAAA  | TTATTTGGGTGCATGA<br>GCAA   | 59.5                             | 863                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52935026  | Ca6                                     | 52935026                      | CATATATATATATATATATATATA<br>T/CATATATATATATATATATATAT<br>ATAT | CTTTGTGTGCTTCCCA<br>TCAA  | TGCACGAACCTGTGTA<br>TGAAAA | 59.7                             | 888                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_5295925   | Ca6                                     | 5295925                       | TTTATTATTATTA/TTTATTATTATT<br>ATTATTATTA                      | TTGACATTTCAAACCG<br>GTCTAT | TGGAAAAGACTCCTGA<br>ATATGGA | 58.5                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52960258  | Ca6                                     | 52960258                      | A/ACCTT                                                       | TTGTCCCAAGCAACA<br>ATTA    | GTTTGGGGTGGTGATT<br>CTCA    | 59.0                             | 607                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_52997933  | Ca6                                     | 52997933                      | G/GCC                                                         | CCAAGGAAGGACGAAA<br>ATGA   | GAGACCATTTGAACAAT<br>TATGCC | 60.0                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_53017362  | Ca6                                     | 53017362                      | GATATATATATATAT/GATATATAT<br>ATATAT                           | TTCTCTTCAGTCCCCTT<br>CTCC  | GTCACCTTGTCGTGA<br>CCCA     | 59.8                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_53311252  | Ca6                                     | 53311252                      | AT/ATT                                                        | GATGGTGGCCATTGAA<br>GAGT   | CAACAGTGTATGCACC<br>TGCC    | 59.9                             | 721                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_53312302  | Ca6                                     | 53312302                      | AAAAATAAAATAAAATAAAATAAA/A<br>AAAAATAAAATAAAATAAAATAAA<br>AAA | ATAGCAATTGGTGCAT<br>CCCT   | ATGACCAAGGCATTGA<br>GGAC    | 59.4                             | 761                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_53359449  | Ca6                                     | 53359449                      | TAAAAAAAAAAAAAAAA/TAAAAAAA                                    | GTTCGAATCTCTCAGG<br>CGAC   | ACGCGAGAAAAGAGGAG<br>ATGA   | 60.0                             | 239                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_53363665  | Ca6                                     | 53363665                      | TAAAAA/TAAAAA                                                 | AGGCTTCTGTGGGATA<br>CAAA   | TTGGAGATTGGGACTT<br>GGAG    | 57.3                             | 297                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_53413835  | Ca6                                     | 53413835                      | ATT/ATTT                                                      | CGTCATTGGGGGACT<br>AAAA    | GAGTTCGGGAGTAGGG<br>AAGG    | 59.8                             | 978                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_53493467  | Ca6                                     | 53493467                      | CATATATATATATATA/CATATATA<br>TATATATATATA                     | TCAACAGCAGAACCTT<br>AGCG   | TTGTTAGCTTTTCAATT<br>GTCGC  | 59.2                             | 117                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                                 |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_54069955  | Ca6                                     | 54069955                      | TAAAAA/TAAAA                                                  | ACAAGAGGCCGTGGTA<br>ATTG     | TTTTGGTGGGTCCAC<br>TTTT         | 60.0                             | 751                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54070088  | Ca6                                     | 54070088                      | ATT/ATTT                                                      | GCAATTGTCGTGATTTT<br>ATTTTGT | TTTTGGTGGGTCCAC<br>TTTT         | 59.8                             | 379                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54070236  | Ca6                                     | 54070236                      | TAAAA/TAA                                                     | TTTCTTTCTCATGCTT<br>TAGAGG   | TTTTGGTGGGTCCAC<br>TTTT         | 59.1                             | 123                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_5410706   | Ca6                                     | 5410706                       | ATTTTTTTTT/ATTTTTTTTT                                         | TTTGAAAAAGTGAGGG<br>GTGG     | CTTTGGTGGTGGTCAG<br>AGGT        | 59.9                             | 956                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54108101  | Ca6                                     | 54108101                      | TAATAAAATAAAATAAAATAAAAT/TA<br>ATAAAATAAAATAAAAT              | TTTGTGCTACATGGGT<br>GAGTG    | AATCCGTGCATTTAGA<br>GCATT       | 59.6                             | 838                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54143290  | Ca6                                     | 54143290                      | ATTTTTTTTTTTTTTT/ATTTTTTTTTT<br>T                             | GGGATCGAAAATCACG<br>AGAA     | GAAATTAAGGGATGTA<br>TTAAGTCCAAA | 60.0                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54143384  | Ca6                                     | 54143384                      | T/TAA                                                         | CCAAGAGATATACGGG<br>GCAA     | TGAAAGTCTGATCCGA<br>TCTAATAGT   | 59.9                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54143529  | Ca6                                     | 54143529                      | CTTTTTTT/CTTTTTTTTT                                           | CCAAGAGATATACGGG<br>GCAA     | GCGGCCGATAAGTAAG<br>ACAT        | 59.9                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54143698  | Ca6                                     | 54143698                      | CAAAATAAAATAAATAAA/CAAAATAAA                                  | CCAAGAGATATACGGG<br>GCAA     | TATGTCCACCCGACAA<br>AACA        | 59.9                             | 917                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54144071  | Ca6                                     | 54144071                      | ATTTT/ATTT                                                    | GCCGCCGAATCTTATA<br>TTACC    | CGTGCATTAAACATCGA<br>CAGG       | 59.8                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_5414443   | Ca6                                     | 5414443                       | ATAAACTAA/ATAAACTAACTAA                                       | TGTTTTGTCGGGTGGA<br>CATA     | CGTGCATTAAATCGA<br>CAGG    | 59.8                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54160745  | Ca6                                     | 54160745                      | ATTGCTTG/ATTG                                                 | GCGAGTTAGAAGATAT<br>GAGGGG   | CGAAAAAGTTCCAAAG<br>ATGGAC | 59.2                             | 818                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54160778  | Ca6                                     | 54160778                      | GA/GACATTAA                                                   | GCGAGTTAGAAGATAT<br>GAGGGG   | CGAAAAAGTTCCAAAG<br>ATGGAC | 59.2                             | 818                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54161011  | Ca6                                     | 54161011                      | TGAGAGA/TGAGA                                                 | TTGATTTGACAATTTTC<br>ATTGCTT | TCAGTTTTCCGGTTTCT<br>TGC   | 59.9                             | 703                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54163818  | Ca6                                     | 54163818                      | CTTTTTTTTT/CTTTTTTTTT                                         | CACACGTTGGTAGTCG<br>TTCTG    | TTTGTGGCGTGTGT<br>TGTT     | 60.2                             | 809                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54192734  | Ca6                                     | 54192734                      | ATTTTTTTTT/ATTTTTTTTT                                         | GGACGGCGAAAATAAA<br>ACAA     | TTGAAAATGGCTAAGG<br>CAAAA  | 59.9                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54193024  | Ca6                                     | 54193024                      | GTATATATATATATATATA/GTATA<br>TATATATATATATA                   | GGACGGCGAAAATAAA<br>ACAA     | TGGAGAGCGTTGAAGA<br>TGAA   | 59.9                             | 918                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54320493  | Ca6                                     | 54320493                      | CTTTTTTT/CTTTTTTTTT                                           | CTCCAATATTCCTCTCG<br>GCA     | TGACACGAGAAATGTC<br>CCAA   | 60.2                             | 724                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54343914  | Ca6                                     | 54343914                      | CTTTTT/CTTTT                                                  | ACGTCGTCGCTTTTGA<br>GAGT     | GCCGTTTTCCATTGTG<br>ACTT   | 60.1                             | 214                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54359904  | Ca6                                     | 54359904                      | AC/A                                                          | CCTTGAACCCATTTTCT<br>GGA     | CCATTCCAACGACCAC<br>TCTT   | 59.9                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                             | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                           |                             |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_54364730  | Ca6                                     | 54364730                      | TAAAAAAAAAAAAA/TAAAAAAAAA                                                                                                 | TGTTCCAATTTAGGGA<br>GAACA   | ATTTTCCTCGATCCCTT<br>GCT    | 59.4                             | 395                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54666936  | Ca6                                     | 54666936                      | GTATATATATATATATATAT/ATATATATATATATAT                                                                                     | GTGCGCATGTGTTTGT<br>CTTT    | GGGGAGAGAGAGGGA<br>CAGAG    | 59.8                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54683653  | Ca6                                     | 54683653                      | TTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAA/TTAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAA | TAGTCTCATGCTGACA<br>CGCC    | TGCCGAGAGAGAAGAAG<br>GAGG   | 60.0                             | 219                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_5469396   | Ca6                                     | 5469396                       | CATATATATATATATATAT/CATATATATATATATAT                                                                                     | GGAATAACGGCTGGCA<br>TAGA    | CAAAATGCAGCGCCTA<br>AAA     | 60.1                             | 335                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54754837  | Ca6                                     | 54754837                      | GCCAAATCGATTT/GCCAAATCGATTTCCAAATCGATTT                                                                                   | GTAAAGGCCACCAATC<br>GAAA    | TTGTCCGTGAGAGACT<br>GCAC    | 59.9                             | 939                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_54952283  | Ca6                                     | 54952283                      | TTATATATATATATATATATATATATAT/TTATATATATATATATATATATATATATATAT                                                             | CCATTGTAAACCCCCA<br>AATTTTA | TTTCTCCATTTCTTCG<br>TGG     | 59.9                             | 937                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_55143076  | Ca6                                     | 55143076                      | A/AAAGAGTGTAAGGTAAT                                                                                                       | ATAAAGCCTCGCGATG<br>AAGA    | CACCCAATACGGGTTA<br>CGTC    | 59.9                             | 466                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_55445634  | Ca6                                     | 55445634                      | TAAAAAAAAAAAAA/TAAAAAAAAA                                                                                                 | AATCACGCGAATCCAC<br>AAAT    | AATTCTACCCTCCCCA<br>CAC     | 60.3                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_55446083  | Ca6                                     | 55446083                      | AG/A                                                                                                                      | TGAGAGTGTGGGGAG<br>GGTAG    | TTCATGTGAATAAATGA<br>CGTTGC | 60.1                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_55446463  | Ca6                                     | 55446463                      | AACA/AACACA                                                                                                               | AAGGTCCTAACACCTG<br>CCTT    | TCGGTGAAAACATAG<br>GGCG     | 57.8                             | 285                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_55471469  | Ca6                                     | 55471469                      | AAGA/AA                                                                 | CTTTCACTTTGCAGCT<br>CGTG   | GAAATTGTCCTTGCAT<br>GGCT    | 59.8                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_55490592  | Ca6                                     | 55490592                      | A/AC                                                                    | CAAAGAATGTGAGGG<br>GACAA   | CTCCAATGTGCGTCTC<br>TTCA    | 60.0                             | 179                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_55490894  | Ca6                                     | 55490894                      | T/TTAATAC                                                               | TGAAGAGACGCACATT<br>GGAG   | TGTCGGTTACTAAACAT<br>GATGGA | 60.0                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_5551268   | Ca6                                     | 5551268                       | TAAAAAAAAA/TAAAAAAAAA                                                   | ACGTCACATTACCCAT<br>GCAA   | TAACAAACGGGCTCTT<br>GACC    | 59.8                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_55769150  | Ca6                                     | 55769150                      | C/CT                                                                    | TCGATTATGCGTAGGG<br>AAGG   | TTTTTCCTTTGTAGGCC<br>CAA    | 60.1                             | 943                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_55771133  | Ca6                                     | 55771133                      | GTC/GTCTTC                                                              | GGAAACGTGTGAACGG<br>AAGT   | GGTAACCAATCCGAAG<br>ACGA    | 60.0                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_55771190  | Ca6                                     | 55771190                      | TAT/TATCGTCTTCGGAT                                                      | TTACCGATGCATTGAT<br>CGAC   | GGTAACCAATCCGAAG<br>ACGA    | 59.5                             | 143                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_55771649  | Ca6                                     | 55771649                      | TAAAAAAAAA/TAAAAAAAAAAAAA<br>A                                          | GGATTGATTATCCGAT<br>GCGT   | GAACGCGAGATATTGG<br>GTGT    | 59.8                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_55847701  | Ca6                                     | 55847701                      | ATTT/ATT                                                                | AGCCCATACGGATGCT<br>CTAA   | TGGGAAGATTGACTTG<br>GAGG    | 59.7                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_55867824  | Ca6                                     | 55867824                      | GTTATTATTATTATTATTATTATT<br>ATTA/GTTATTATTATTATTATTATTA<br>TTATTATTATTA | GGATAGATACCCATCC<br>AATCCA | CTTGGAACCAACCCCT<br>ATTA    | 59.9                             | 275                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical positions (bp) | InDels ( <i>Kabuli</i> reference genome- CDC Frontier/PfII)                           | Forward primers (5'-3')  | Reverse primers (5'-3')       | Annealing temperature (0C) | Expected amplified product size (bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------|---------------------------------------------------------------------------------------|--------------------------|-------------------------------|----------------------------|--------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                         |                                                                                       |                          |                               |                            |                                      | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | Tfs |
| Ca6_P4_55987809  | Ca6                                     | 55987809                | AATATATATATATATATATATATATATATATATATATATAT/AAATATATATATATATA TATATATATATATATATATATATAT | TTCAAGG TTCATTACA CAACG  | AAAGT TGACTCATATCA AAACCCA    | 59.0                       | 390                                  | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_56061377  | Ca6                                     | 56061377                | AATATATATATATATATATATATATATAT ATATA/AATATATATATATATATATAT ATATATATATATATATATATATA     | TTTG GTTGACGCATGT GTTT   | ACCAA CGCCATTTTCAT TGT        | 60.0                       | 737                                  | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_56087656  | Ca6                                     | 56087656                | CTTT/CTTTT                                                                            | TTGTG AGCATGAGAAG TTGTTG | TGAAAA ATTATTGAAAA AGTTACTTCC | 59.0                       | 737                                  | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_56139090  | Ca6                                     | 56139090                | A/AAACACAAATT                                                                         | ACCCT CTCACCCCTCT TGAT   | TCCTCAT CATTCCCTCC TTG        | 59.9                       | 387                                  | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_56191156  | Ca6                                     | 56191156                | C AAAATAAATAAATAAATAAATAAATA A/CAAAATAAATAAATAAATAAATAA                               | TCGATTATGCGTAGGG AAGG    | TCCTTGAGTTTTGGGA CACA         | 60.1                       | 482                                  | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_56304604  | Ca6                                     | 56304604                | AC/A                                                                                  | TTGTCGTGCTTCCATC AGAG    | CAACTCAGAACTGCCG TCAA         | 60.0                       | 431                                  | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_56410876  | Ca6                                     | 56410876                | ATTGTTTTGTGTTTGTGTTTGTGTTT/ATT GTTTGTGTTTGTGTTT                                       | CGTTT CTGCCATTTT CAT     | TCAATTTTGGCATTCT TTCA         | 60.1                       | 745                                  | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_5645292   | Ca6                                     | 5645292                 | CTATATATATATATATATATAT/CTAT ATATATATATATATATATATAT                                    | GTA AACCCAAGAGAGG TGCG   | TTCTAAATGGCGACTTT CCA         | 59.7                       | 923                                  | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_56503513  | Ca6                                     | 56503513                | CAAAAA/CAAAAAA                                                                        | CTCACAA ACATTGGG GGAC    | GACCATCCGACTTTGC ATTT         | 60.2                       | 568                                  | INTERGENIC                                  | --                               | --                    | --  |
| Ca6_P4_56503742  | Ca6                                     | 56503742                | C/CCACTTATCT                                                                          | GTTGGCGCAA ACTCTT CTTC   | CGGGTAACATGACCC TTG           | 60.0                       | 273                                  | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                        | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                      |                           |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_56503979  | Ca6                                     | 56503979                      | AAACAA/AAA                                                                                           | GTTGGCGCAAACCTT<br>CTTC   | TGCAACTTTCAGGTCC<br>CTTT     | 60.0                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_56504001  | Ca6                                     | 56504001                      | ATTTTT/ATTTT                                                                                         | GTTGGCGCAAACCTT<br>CTTC   | TGCAACTTTCAGGTCC<br>CTTT     | 60.0                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_56504140  | Ca6                                     | 56504140                      | AAAAGAAA/AAAA                                                                                        | AAATGCAAAGTCGGAT<br>GGTC  | TGCGAAGAAGAATGAT<br>CACG     | 59.9                             | 896                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_56504753  | Ca6                                     | 56504753                      | ATTTTTTTTTTTTT/ATTTTTTTTTT                                                                           | CGTGATCATTCTTCTT<br>GCA   | TCGGTCACCAAGTTAC<br>CACA     | 59.9                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_5650524   | Ca6                                     | 5650524                       | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAA/AAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAA | CCCCACCTTTATGCAG<br>TACC  | TGTGGACTTTTTACCAA<br>ATTCTTG | 59.3                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_56505598  | Ca6                                     | 56505598                      | AC/A                                                                                                 | TGTTAACTTGGTGACC<br>GACA  | AATTTTGCAGAAGAAA<br>GAAAAAG  | 60.0                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_56506826  | Ca6                                     | 56506826                      | TAAAAAAA/TAAAAAAA                                                                                    | GGGCACCTTGTTAGCAT<br>TTCC | TGCGAAGAAGAATGAT<br>CACG     | 59.6                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_56507452  | Ca6                                     | 56507452                      | TATCA/TA                                                                                             | CGTGATCATTCTTCTT<br>GCA   | ATCCAACATTGGCCAT<br>TTC      | 59.9                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_56507723  | Ca6                                     | 56507723                      | GTTTTTTTTTTTTT/GTTTTTTTTT<br>TTTTT                                                                   | CGTGATCATTCTTCTT<br>GCA   | CTCCCAATTGCAGTG<br>TCCT      | 59.9                             | 966                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_56507798  | Ca6                                     | 56507798                      | CA/CAA                                                                                               | AAATTCAAGTCTCGAC<br>GCAAA | CTCCCAATTGCAGTG<br>TCCT      | 59.9                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')   | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|---------------------------|--------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                     |                           |                                |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_56578763  | Ca6                                     | 56578763                      | AATATATATATATATATATATA/AA<br>TATATATATATATATATATATA                 | GAATGCCCTATGTGAC<br>ACGA  | GTAAGCAAAACGGGT<br>CGAA        | 59.5                             | 855                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_56713561  | Ca6                                     | 56713561                      | ATT/ATATTT                                                          | TTCACGTTGGAACCTTG<br>CTTG | TTTTGTGATTCAAGGTG<br>GCA       | 59.9                             | 833                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_56727392  | Ca6                                     | 56727392                      | TAA/TAAA                                                            | AGGCAAAACATGTTCC<br>CTCA  | AATGTTAGTGACCGT<br>GTCG        | 60.5                             | 706                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_56748962  | Ca6                                     | 56748962                      | ATTTTTTTTTTT/ATTTTTTTTTT                                            | TTTCGTGCTGTGATTG<br>AAGC  | TTTTCAAGTGCAAGCC<br>AAT        | 60.0                             | 725                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_56767873  | Ca6                                     | 56767873                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAA<br>A                                   | TCATGGATTCAACCAG<br>ATGC  | TTCATCTTTCAAACCTG<br>AGACTCG   | 59.5                             | 188                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_57039572  | Ca6                                     | 57039572                      | TAAAAAAAAA/TAAAAAAAAA                                               | GGTGTAGTGGATCGGT<br>CTTGA | ATAGTGCCGAAGGAAG<br>CAAA       | 60.0                             | 334                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_57117976  | Ca6                                     | 57117976                      | AATATATATATATATATATATATAT<br>ATATATA/AATATATATATATATAT<br>ATATATATA | TTTCATGTGCGTGTGA<br>GTGA  | TCAACCAATTCAACAAT<br>TTGACA    | 59.9                             | 519                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_57460927  | Ca6                                     | 57460927                      | CAAAAAAAAAA/CAAAAAAAAAA                                             | GTTGTGGGATGAACGT<br>ACCC  | GTTGGAATTCCTTTTG<br>GCAC       | 60.2                             | 848                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_5746619   | Ca6                                     | 5746619                       | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATAT                   | TTGCTAGTATGCGCTG<br>ATGG  | GGATCAATTAATGCC<br>ATCCT       | 60.0                             | 575                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_57648762  | Ca6                                     | 57648762                      | CATATATATATATATATATATAT/C<br>ATATATATATATATATATATATA<br>T           | AACATTGTGAGAGT<br>GTGACAA | CAGTTAACGCAACTAAT<br>AGTGTTTCA | 57.3                             | 320                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                       | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                     |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_5765272   | Ca6                                     | 5765272                       | TTTTTTATTTTTATTTTTATTTTTAT/<br>TTTTTTATTTTTATTTTTATT                                | CTCTTGGACATGTGGT<br>GGTG   | TCCCTTTCGTTTTGGTT<br>GAC     | 60.0                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_57935713  | Ca6                                     | 57935713                      | CATATATATATATATATATATATATA/<br>CATATATATATATATATATATATATA<br>TATA                   | AACACTGCATTCTCC<br>AAAAA   | GTGGAGAAAGCCATTG<br>GAGA     | 59.6                             | 736                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58204126  | Ca6                                     | 58204126                      | GAAAAAAAAA/GAAAAAAAAA                                                               | GGGACATTTACTTCCC<br>TCCC   | TTCAACCACGTTATAAT<br>TCCAAAA | 59.6                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58296268  | Ca6                                     | 58296268                      | ATATTTAT/ATAT                                                                       | ACGGTTGTCTGTGTTT<br>ACCA   | TTGATCTGAACACCTT<br>CCC      | 60.0                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58313547  | Ca6                                     | 58313547                      | TNNNNNNNNNN/TNNN                                                                    | TACAAGCCTGAGCCTG<br>ACCT   | TTAACGTTGTGCTTGT<br>CGC      | 60.0                             | 340                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58373671  | Ca6                                     | 58373671                      | GATATATATATATATATATATA/GA<br>TATATATATATATATATATATATA                               | TCACGCAAAAGATTCA<br>TAAAGA | AGTTTGTAGCTGTGC<br>GTCG      | 58.9                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_5846506   | Ca6                                     | 5846506                       | TAAAAAAAAAAAAA/TAAAAAAAAA                                                           | TGATTAGGCCTGAATT<br>GTGGT  | GCAAGTTGCCAAGAAA<br>AAGC     | 59.4                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_5852510   | Ca6                                     | 5852510                       | TAATAATAATAA/TAATAATAATAAT<br>AATAATAA                                              | TGACGTATGTTGCACT<br>TTGGA  | CCAATTCATGAAATCCG<br>TCC     | 60.2                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_5853411   | Ca6                                     | 5853411                       | GTATTATTATTATTA/GTATTATTATT<br>ATTATTATTA                                           | TCGAACATAACACCTC<br>GCAG   | TCCGGTTACATTCCTTC<br>TTTTG   | 59.9                             | 467                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58539579  | Ca6                                     | 58539579                      | CATATATATATATATATATATATA<br>TATATATATAT/CATATATATATATAT<br>ATATATATATATATATATATATAT | CGAGCCTAATAGTCGA<br>CCCA   | AACGGGTCAACCAATC<br>ACAT     | 60.2                             | 258                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_5854308   | Ca6                                     | 5854308                       | TAAAAAAAAA/TAAAAAAAAA                                                         | CACGTGGTCATACTTC<br>CATCA | TGTCAATTCCAAATGCA<br>TCAA    | 59.4                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58615933  | Ca6                                     | 58615933                      | GTAGTT/G                                                                      | CAAATTGTCCGTGCAA<br>TCAC  | GAAGAATGGTAGGCGG<br>AACA     | 60.0                             | 227                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58627027  | Ca6                                     | 58627027                      | AATATATATATATATATATATATAT<br>ATATA/AATATATATATATATATATAT<br>ATATATATATATATATA | CCAAAATCGAGCCTTC<br>ACAT  | TGTGTGTAGCACGGTT<br>CTCTC    | 60.1                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58758402  | Ca6                                     | 58758402                      | ATTTTTTTTT/ATTTTTTTTTT                                                        | TGGTCTGGCCTATTCT<br>CACC  | GATCCGTC AAGTCCCT<br>CGTA    | 60.1                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58781669  | Ca6                                     | 58781669                      | T/TG                                                                          | GGACCTCATTTAGTCG<br>GAGG  | TGTTGGGATTGTAGG<br>TGGT      | 58.6                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58782759  | Ca6                                     | 58782759                      | TC/T                                                                          | TTGAAATCGTGATTTTG<br>GCTT | CGTTGGCAATTTTGG<br>TCTT      | 59.6                             | 225                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58782804  | Ca6                                     | 58782804                      | T/TC                                                                          | TTGAAATCGTGATTTTG<br>GCTT | CGTTGGCAATTTTGG<br>TCTT      | 59.6                             | 225                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58783805  | Ca6                                     | 58783805                      | ATTTTTTT/ATTTTTT                                                              | TCGGTATAAGTGCTTT<br>GCCA  | AAACAAAACATGGGAC<br>AAACAT   | 59.3                             | 218                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58784094  | Ca6                                     | 58784094                      | A/AT                                                                          | TCGGTATAAGTGCTTT<br>GCCA  | AAGCATCGGAAAAAGT<br>ACAAAAA  | 59.3                             | 887                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58784343  | Ca6                                     | 58784343                      | ATTT/ATT                                                                      | CAATGTTTGTCCCAT<br>GTTTTG | GCTCTCTTCAATATTAA<br>GCATCGG | 60.1                             | 709                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_58784829  | Ca6                                     | 58784829                      | ATTTTTTT/ATTTTTTTT                                            | TTTTGTACTTTTCCG<br>ATGCTT    | CCGTAATTTTGCTATGG<br>AGC  | 59.2                             | 795                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58790530  | Ca6                                     | 58790530                      | GTTTTTTTT/GTTTTTTTT                                           | GGCGACGTGTTTTCA<br>TTTT      | TTTGGCGGTGTGCAA<br>AT     | 60.0                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58791052  | Ca6                                     | 58791052                      | ATAA/ATAAGTAA                                                 | TTTAAATTGCACACC<br>GCC       | GAGCCGTCTTCATTC<br>AATCTT | 60.8                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58805367  | Ca6                                     | 58805367                      | AAATTAATT/AAATT                                               | AAGTCGAACAAAGGGA<br>GGGT     | AAAATGAAATTTGGTG<br>GCGA  | 60.0                             | 116                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58806728  | Ca6                                     | 58806728                      | AAA/AAATTAA                                                   | GGCTCGAAAGATGGTT<br>GAAG     | ATTATATGAGTGCGG<br>GGCA   | 59.8                             | 885                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58808278  | Ca6                                     | 58808278                      | T/TC                                                          | TGGTGCGTCCACTATT<br>CAAA     | ATTTTCCCATGGACT<br>GGT    | 60.1                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58815507  | Ca6                                     | 58815507                      | CT/C                                                          | ATTCCTCGACCAGTTG<br>AAAA     | CATCAATCATGTTGCAT<br>GGC  | 57.2                             | 242                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58817752  | Ca6                                     | 58817752                      | AATAT/AATATTAT                                                | AACGGATATGATTGATT<br>GATTGTG | CTCCTAACGGATTGCT<br>GGAT  | 60.0                             | 700                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58818339  | Ca6                                     | 58818339                      | A/AT                                                          | ACGAAGCCGGAATTAA<br>AACA     | TCAATTTTGTGCGCTC<br>AAC   | 59.6                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58851448  | Ca6                                     | 58851448                      | AG/A                                                          | CTTGATTGCGGATGG<br>ATT       | TTAAAGCGCTCCCATC<br>AACT  | 59.9                             | 896                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')      | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                 |                              |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_58872310  | Ca6                                     | 58872310                      | GTTTTTTTTT/GTTTTTTTTT                                           | CCGATTGGTTGGTTGA<br>GTTT     | AAAATGGTGATGAAGT<br>GTTAATTTTT | 59.8                             | 828                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58872639  | Ca6                                     | 58872639                      | TAAAAAAAAA/TAAAAAAAAA                                           | CGAACTCAAGTACAAC<br>TTTTTGGA | TGCATTCTCTCTTGACT<br>TTCAAT    | 59.7                             | 865                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58873196  | Ca6                                     | 58873196                      | GATATATATATATATATATATATA<br>TATA/GATATATATATATATATATA<br>TATATA | TTGAGCGAGAATGTAG<br>AGAGAATG | AGAGCAAGCTTAAGCC<br>GACA       | 60.0                             | 233                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_58874492  | Ca6                                     | 58874492                      | GTATATATATATATATATATATAT<br>A/GTATATATATATATATATATATA           | TCTCAATGTGATTTTAA<br>TGTTCCC | GCCTCCTCATGCTGAT<br>TCAC       | 59.3                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_59059948  | Ca6                                     | 59059948                      | CT/CTTT                                                         | ATAGGACGCAAGAAAA<br>GCCA     | TCCACAACACCTACG<br>TCCA        | 59.8                             | 263                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_59066187  | Ca6                                     | 59066187                      | TAAAAAAAAA/TAAAAAAAAA                                           | TGTTTGTCACTTTTCA<br>AATCCA   | TGTGGGCTGATGTTGG<br>TTTA       | 60.4                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_59072971  | Ca6                                     | 59072971                      | CTT/CTTT                                                        | TGCGAGTCTTGTTTCT<br>CCCT     | ATTTGGTCACTCGAGG<br>TTGC       | 60.0                             | 869                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_59074556  | Ca6                                     | 59074556                      | TTTC/TTTCTTC                                                    | TGGAAATGATGAGCAA<br>TGGA     | CGTTGTCAAGAGAATT<br>CACGC      | 60.0                             | 723                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_59093194  | Ca6                                     | 59093194                      | ATTTTTTTTTT/ATTTTTTTTTT                                         | GGAGGCAACCCAACCT<br>TATG     | TCGCATAATTGGAACG<br>TCAA       | 59.6                             | 271                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_59133166  | Ca6                                     | 59133166                      | GTATATATATATATATAT/GTATATAT<br>ATATATAT                         | TAATCATTTTCGCGCG<br>CTAC     | GCATGCTCAATTTTGG<br>TGA        | 60.1                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                           | Forward primers (5'-3')         | Reverse primers (5'-3')  | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------|---------------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                         |                                 |                          |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_59190908  | Ca6                                     | 59190908                      | TTATATATATATATATATATATATATATATAT<br>T/TTATATATATATATATATATATATAT                                                                        | TTAATTATCGTCTATCC<br>TTCAATTTTT | TCGGACTTGGTTTAATT<br>GCC | 57.3                             | 932                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_59273311  | Ca6                                     | 59273311                      | TA/T                                                                                                                                    | TTTTTGGGCTGAAGCC<br>ATAC        | GGTGGAGAATGAAACG<br>GAGA | 60.1                             | 359                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_59349983  | Ca6                                     | 59349983                      | AATATATATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATATATATAT<br>ATATATATATA                                                       | TTTCATTGCACTCACT<br>CCA         | CCTATCATGGCCTGAC<br>CTGT | 60.2                             | 777                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_59384361  | Ca6                                     | 59384361                      | AATATATATATATATATA/AATATATA<br>TATATATATATA                                                                                             | CGGCCTTATCCTAAAG<br>ACCC        | AAAATAGGAGACCAA<br>TTTCG | 59.9                             | 393                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_59406741  | Ca6                                     | 59406741                      | ACTTCTTCTTCTTCTTCTTCTTCTTCTTCT<br>TTCTTCTTCTTCTTCTTCTTCTTCTTCTC/A<br>CTTCTTCTTCTTCTTCTTCTTCTTCTTCT<br>TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT | AATCAAAACCATCCAA<br>CCA         | TTGGCGAGGAAGTTGA<br>AATC | 60.0                             | 254                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_59434628  | Ca6                                     | 59434628                      | CAAAAA/CAAAAAA                                                                                                                          | ACAGCAGCCTTGCAAT<br>CTCT        | TGTTGCCTCTGTTTTTG<br>CAG | 60.2                             | 374                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_6082681   | Ca6                                     | 6082681                       | TTATATATATATATATATATAT/TTAT<br>ATATATATATATATATATATAT                                                                                   | CGCACTAGACTAAATG<br>CGTGC       | GCCCTTTGACGTCCAA<br>CTAA | 61.0                             | 442                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_6089953   | Ca6                                     | 6089953                       | ATTTTTTTTT/ATTTTTTTTTT                                                                                                                  | CGAATATCAAGCACGC<br>ACAT        | GCAACGGCAAGGATTG<br>TTAT | 59.7                             | 921                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_6149697   | Ca6                                     | 6149697                       | AATATATATATATATATATA/AATATA<br>TATATATATATATATA                                                                                         | CGAAAACCAAAGTGGA<br>GGAA        | TGAATTGTTTTTGGTTG<br>GCA | 60.1                             | 550                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_6152979   | Ca6                                     | 6152979                       | AATATATATATATATATATATATATA/A<br>ATATATATATATATATATATATATAT                                                                              | CCATTAGTTGACCATC<br>GCCT        | GAGGACTAGAGGGAGT<br>GCCC | 60.0                             | 155                                           | INTERGENIC                                           | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                                 |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_6158112   | Ca6                                     | 6158112                       | GTATATATATATATAT/GTATATATAT<br>ATATATAT                       | GATGAGTGAAGGAGC<br>CAAA       | TGAAAGATAATCCAATT<br>TTAAATGAGT | 60.2                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_6303863   | Ca6                                     | 6303863                       | CAAAAAAAAA/CAAAAAAAAAAAAA                                     | TCTCATTTTACGGATAG<br>ATGTTCT  | GTGGATGTGCTTGCTT<br>CAAA        | 59.5                             | 293                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_6321313   | Ca6                                     | 6321313                       | A/ACCTTTTAAACG                                                | CATTTAAGGGCTCGTG<br>TTAAAGA   | GGAAATGGGTTTCAA<br>TTCG         | 59.7                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_6332755   | Ca6                                     | 6332755                       | AG/A                                                          | GCAACAGTTTCCCATG<br>GAGT      | AGGAAGTTGCGACAAA<br>GCAT        | 60.0                             | 189                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_6341110   | Ca6                                     | 6341110                       | AA/AATAATA                                                    | CAAGTCGTTTGTTTTG<br>GCAG      | TATGGAAGTACCACCC<br>GGAA        | 59.4                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_6409101   | Ca6                                     | 6409101                       | ATT/ATTT                                                      | TTTTGTGGGTGAATGA<br>TATTGC    | ATAACACAAGAGGCCG<br>TGGA        | 59.7                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_6411336   | Ca6                                     | 6411336                       | AAT/AATAT                                                     | ATCTCGTGGTGCAACA<br>ATCA      | TTTGGGAAGGGTCAAG<br>AAAA        | 60.1                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_6411394   | Ca6                                     | 6411394                       | TTATTTAT/TTATTATATATTAT                                       | ATCTCGTGGTGCAACA<br>ATCA      | TTTGGGAAGGGTCAAG<br>AAAA        | 60.1                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_6415040   | Ca6                                     | 6415040                       | TAAAAATTAATAAATAAATAAATAA<br>ATTAAAA                          | AATTTTCATTTTAGTTT<br>GGATTGAA | GGTCGCATTTTATCGT<br>GTG         | 57.4                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_6469039   | Ca6                                     | 6469039                       | ATT/ATTT                                                      | ATGGTTGAAGGATCGT<br>GGTC      | ATCATTATGTCATCG<br>GGT          | 59.8                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)                | Forward primers (5'-3')    | Reverse primers (5'-3')        | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                          |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                               |                            |                                |                                  |                                               | Sequence components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_697724    | Ca6                                     | 697724                        | CATATATATATATATATATATATA<br>TATAT/CATATATATATATATATAT<br>ATATATATATATATATATAT | GACTTGACATATTGG<br>GCCT    | TGACAAAAGAGTGAAA<br>AAGGAAAA   | 60.0                             | 586                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_7192124   | Ca6                                     | 7192124                       | TA/TGATATAAGGGAAA                                                             | GCATGGCAACGTTGTA<br>AGAA   | GAGAAAGACAAAATGC<br>GGCT       | 59.7                             | 362                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_7318576   | Ca6                                     | 7318576                       | TAAAAAAAAA/TAAAAAAAAA                                                         | GGCATGTAAACATCGCA<br>ACTG  | CGAGAAAGTGTTGGGG<br>AAAA       | 60.1                             | 739                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_7319973   | Ca6                                     | 7319973                       | AC/ACC                                                                        | TTTATGAGCTCGATGG<br>GTCC   | CGTCTGTAGAAGCAGG<br>GGAG       | 60.0                             | 613                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_7353319   | Ca6                                     | 7353319                       | CAAAAAAAAA/CAAAAAAAAA                                                         | AAGCTTGTGGAGGAGC<br>ACAT   | CCGGTGAGACCTTTGG<br>ATAA       | 59.9                             | 520                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_7360320   | Ca6                                     | 7360320                       | ATTTTT/ATTTTT                                                                 | CACCAAATGTGGGTTC<br>CATCA  | ATTACCCCCTCTTAG<br>GTGC        | 59.2                             | 614                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_7505796   | Ca6                                     | 7505796                       | CATATATATATATATATAT/CATAT<br>ATATATATAT                                       | AGGGCATTTGACGAAC<br>ACAT   | CATTAAGTCTATCACGA<br>GTTTAACCA | 60.4                             | 508                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_7587726   | Ca6                                     | 7587726                       | TC/T                                                                          | GTGTGATGAAGGATTC<br>GCCT   | GATGAGACTTTCCCTA<br>GCCTT      | 60.1                             | 842                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_7588189   | Ca6                                     | 7588189                       | TT/TTGCAT                                                                     | AAGGCTAGGGAAAAGT<br>CTCATC | GCTCTCAGTTGAATAG<br>CACGG      | 58.1                             | 504                                           | INTERGENIC                                     | --                               | --                    | --  |
| Ca6_P4_7588870   | Ca6                                     | 7588870                       | AAAG/A                                                                        | TATGAGCACCGCCAGT<br>TGTA   | CCAAAAATCTTCCCGAA<br>CAG       | 60.3                             | 227                                           | INTERGENIC                                     | --                               | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                 |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_7594302   | Ca6                                     | 7594302                       | A/AT                                                            | CACCAATTATTGCAAGT<br>CTCG | TGAAACGAGTTTGTATG<br>GCC    | 58.3                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7594709   | Ca6                                     | 7594709                       | TA/T                                                            | GGCAATCAAAACTCGT<br>TTCA  | TTGCTCTACGTTTATG<br>GGG     | 58.7                             | 299                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7595372   | Ca6                                     | 7595372                       | TTATAT/TTAT                                                     | CATGGGCATATTACAC<br>CACG  | ACGGTGTGGTGTTTC<br>TGGT     | 59.7                             | 847                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7612067   | Ca6                                     | 7612067                       | TTATATATA/TTATATATATA                                           | AATGTTTTAACGACGG<br>CGAC  | TGTGGAAGATGATGTA<br>CAACGG  | 60.0                             | 861                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7612342   | Ca6                                     | 7612342                       | AAAATAAATAAATAAATAAA/AA<br>AATAAATAAATAAA                       | TGGCTGTAAGTTTGC<br>TCTG   | AACACACCATCCATGC<br>AAAA    | 60.1                             | 762                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7612818   | Ca6                                     | 7612818                       | A/ACTATT                                                        | TTTTGCATGGATGGTG<br>TGTT  | GCAGTTTCTTTGGCAT<br>CCTC    | 59.8                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7631953   | Ca6                                     | 7631953                       | TATTTATTTTTAATTTATTTT/TATTT<br>ATTTTAAATTTATTTTAAATTTATTTT<br>T | TGCTTGCCTCTAGTTG<br>TTCG  | TGACAAAATCTTACTGC<br>ATGCTT | 59.2                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7634031   | Ca6                                     | 7634031                       | TT/TTCT                                                         | ACGAGGCACCGACATG<br>TAAT  | AATTTGCACATACACG<br>CCA     | 60.4                             | 506                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7636237   | Ca6                                     | 7636237                       | AG/A                                                            | CATGAGATACCGACAT<br>GCGA  | TGGGCGTCTTTAGCT<br>ATGC     | 60.7                             | 171                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7638969   | Ca6                                     | 7638969                       | CATAAAAAATAAAAAATAA/CATAAA<br>AAATAA                            | AACCACATTTGTTGTC<br>GCTG  | TTGGATGTCAACAATGT<br>ACACG  | 59.6                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_7641189   | Ca6                                     | 7641189                       | CT/C                                                          | TCTGTGTCGTCTCAACC       | AAGGGCCATTGAAGAGAAA     | 60.0                             | 808                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7641770   | Ca6                                     | 7641770                       | G/GA                                                          | AGCGAATCACTCGAGCAAAA    | AAGAACGAAGAAAGGTCGCA    | 61.1                             | 865                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7643275   | Ca6                                     | 7643275                       | TAAAA/TAAAA                                                   | TTGCATTCCATAAACACGGA    | TGATCAGATAGATATGTGACCGA | 59.9                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7643356   | Ca6                                     | 7643356                       | ATTTTT/ATTTTT                                                 | TTGCATTCCATAAACACGGA    | TGATCAGATAGATATGTGACCGA | 59.9                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7643618   | Ca6                                     | 7643618                       | ATGT/AT                                                       | CAATTGTCAACATGACCCTTAAA | TCATTGATTCAACCTCTGGTCTT | 58.9                             | 411                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7644876   | Ca6                                     | 7644876                       | ATGTGTGTGTGTGTGT/ATGTGTGTGTGTGTGTGT                           | GACTTCGTTTCGTGCTTCCTC   | GCCACCGTTGTGTTCTTAT     | 60.0                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7660694   | Ca6                                     | 7660694                       | GAATT/GAATTCATTCTAACAATT                                      | AGGACGAAGAGTTGAAGCCA    | AATGTCGTAAGGGGCACAAA    | 60.0                             | 766                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7660929   | Ca6                                     | 7660929                       | AATATATATATATATATATATATA/<br>AATATATATATATATATATATATATATA     | GCCCCAAAAGAGCCAATAACAA  | ACGAAAACGCCACTTACCTG    | 60.1                             | 788                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7670210   | Ca6                                     | 7670210                       | GTTTTTTTT/GTTTTTTTTTTTT                                       | TCCTTCAAACTCGTCCCTTG    | CTCCTCATGCGCTAACACAA    | 60.2                             | 264                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7670257   | Ca6                                     | 7670257                       | TTATATATATATATATATATA/TTATATATATATATATATA                     | TCCTTCAAACTCGTCCCTTG    | CTCCTCATGCGCTAACACAA    | 60.2                             | 264                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_7689057   | Ca6                                     | 7689057                       | TC/T                                                          | GGTGAGACAACCCATT<br>TGCT | AACCCTCCACCGAAAC<br>TTCT    | 60.0                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7689459   | Ca6                                     | 7689459                       | TA/T                                                          | AGAAGTTTCGGTGGAG<br>GGTT | TCCTTTGCAGGATGGG<br>TAAG    | 60.0                             | 733                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7691192   | Ca6                                     | 7691192                       | TTGTGT/TTGT                                                   | TGAAATGGGAGGAAG<br>GTTG  | TTTGAGTGTGTTGCAT<br>GGGT    | 59.9                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7708179   | Ca6                                     | 7708179                       | CTATA/CTA                                                     | CGTGTGGACATTGGTA<br>CGAG | TAAATCGCAATGGAAC<br>ACGA    | 60.0                             | 149                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7708884   | Ca6                                     | 7708884                       | AAGAG/AAG                                                     | CTCATCACACTGGGCA<br>AATG | TGTTCAATTCGAATGCC<br>AAA    | 60.1                             | 983                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7711932   | Ca6                                     | 7711932                       | ATTTTTTTTTT/ATTTTTTTTTT                                       | ATTAAGCGGGTGCAGG<br>TATG | TCAGTGCATGTACTCT<br>CTTGGG  | 60.0                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7712192   | Ca6                                     | 7712192                       | CA/C                                                          | CCCCACAATGGGTATG<br>GTAA | CCTGTCCTCATACTG<br>CGAT     | 60.3                             | 715                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7713878   | Ca6                                     | 7713878                       | TTATATATATAT/TTATATATAT                                       | CAAATCGTTTTGTCCCA<br>TTG | TACCGCACTTAGACGA<br>CGAG    | 58.9                             | 816                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7718474   | Ca6                                     | 7718474                       | A/AGT                                                         | ACATGTTGCATTTCACT<br>GCC | TTTGAAGGGGTGAATC<br>GAAG    | 59.6                             | 775                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7732809   | Ca6                                     | 7732809                       | CTAT/CTATAT                                                   | TGGGCAGAACCCACTA<br>ATT  | CCTCCACATGTTAATGT<br>CCTAGC | 59.4                             | 298                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_7733001   | Ca6                                     | 7733001                       | TATATA/T                                                      | AAGCGATGGTTTAAGT<br>GGCA  | TGGTGAACATATGGGG<br>TCTG    | 60.6                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7734369   | Ca6                                     | 7734369                       | GTTTTTTT/GTTTTTTT                                             | TCTCGAGGCATCTCAA<br>TCCT  | TCAATAAAATCACCGAC<br>TTGTGA | 59.9                             | 212                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7735386   | Ca6                                     | 7735386                       | ATATATTATATTATATTATATT/ATAT<br>ATTATATTATATT                  | TGATGAGTTCACCCCT<br>GTCA  | AAATTTCCATTGGCCAA<br>CAA    | 60.1                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7737928   | Ca6                                     | 7737928                       | TGA/T                                                         | AAATCCCATCAAACAAT<br>GGC  | TTCGCTTGAAATAACAA<br>CAAAAA | 59.6                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7773242   | Ca6                                     | 7773242                       | ATCTCTCCTTCTCTC/ATCTCTCCTT<br>CTCTCCTTCTCTC                   | CCTTTCCAACATCCAA<br>GCAT  | AAGCACAGGGAGAACA<br>AAGC    | 59.9                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7775563   | Ca6                                     | 7775563                       | ATTTTTTT/ATTTTTTTT                                            | CACAATTGCTCATGTG<br>GTCC  | TGGTCCCTTGACTTAAT<br>TTCAGA | 60.0                             | 372                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7781946   | Ca6                                     | 7781946                       | A/AATTT                                                       | GGGTAAGGGACGTGTC<br>ATTG  | CAAGTGCCTTACTTGT<br>TAAGGA  | 60.2                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7799591   | Ca6                                     | 7799591                       | TTATCTATCTAT/TTATCTATCTATCT<br>AT                             | ACAACTTAAATGGTGG<br>CTTCA | GACAATCTCAGGGGTC<br>TCCA    | 57.3                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7801585   | Ca6                                     | 7801585                       | AT/ATT                                                        | TGAGGGATGCATCAAC<br>ATTC  | CATTGAAGAGAGGAAC<br>CCCA    | 59.5                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7802935   | Ca6                                     | 7802935                       | ACA/ACATGCA                                                   | ATGTGGGCCCTTGAC<br>TATT   | TGCTAAAGGCTTCCCT<br>TCAA    | 60.6                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_7806679   | Ca6                                     | 7806679                       | TA/TACA                                                       | TCAAGGGATCCCCATA<br>ACAA   | TTCACATTCCCCATTAA<br>GCC | 60.1                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7806865   | Ca6                                     | 7806865                       | TC/TCC                                                        | TTCATCGCAGGTTTCA<br>GAGA   | TTCACATTCCCCATTAA<br>GCC | 59.5                             | 174                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7812857   | Ca6                                     | 7812857                       | GTA/GTAATGCTA                                                 | CATTGCCCAAATCCT<br>GAGT    | CCCCTCGTTTTCGCT<br>ATT   | 59.9                             | 798                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7814183   | Ca6                                     | 7814183                       | ATTTTTTT/ATTTTTTTT                                            | TGTGTTTGGCTGTGAA<br>CAGAA  | TACACCGCCAATGCAT<br>TTTA | 60.3                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7819596   | Ca6                                     | 7819596                       | GCACAC/GCACACAC                                               | TGACCATGCTTTACAG<br>GGGT   | AAGGGGGCAAGGATAC<br>AAGT | 60.4                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7859686   | Ca6                                     | 7859686                       | ACTC/ACTCTC                                                   | CAAAGCAACAAATTAA<br>AGCG   | TGGCGTCTTAATGGTC<br>ACTG | 57.7                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7860074   | Ca6                                     | 7860074                       | AC/ACC                                                        | CGACTCACACAGTGCA<br>ACAA   | GAGACTCTCCACCCTC<br>GTGT | 59.5                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7861129   | Ca6                                     | 7861129                       | TACCAC/TAC                                                    | CAAATATTCCAAGTGCA<br>ACCAA | ACGCTCTCGCTTTTATT<br>GAT | 59.9                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7869663   | Ca6                                     | 7869663                       | ATTTT/ATTTT                                                   | TGAACCATCGCAACAT<br>TCAT   | TCCATAAGTGGTTTCC<br>GACA | 59.9                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7870049   | Ca6                                     | 7870049                       | GAAAAA/GAAAA                                                  | TGTCGGAAACCACTTA<br>TGGA   | CCAGAAATGACTCCAC<br>CGTT | 59.0                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_7881252   | Ca6                                     | 7881252                       | CTTTATTTTATTTAT/CTTTATTTTA<br>TTTTATTTTAT                     | TTTCCGATCGTTGAC<br>GTTT    | AACGGGGTTCACCCTA<br>ACAT   | 60.5                             | 951                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7881359   | Ca6                                     | 7881359                       | TTTAAT/TTTAATTAAT                                             | CCACACCTCTCTCTCT<br>CTCTCC | AACGGGGTTCACCCTA<br>ACAT   | 59.6                             | 848                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7881668   | Ca6                                     | 7881668                       | ATATTATT/ATATT                                                | TTGGATGCCCTTAAC<br>TCTTT   | GTACCAATGATGGTGG<br>GAGG   | 60.0                             | 346                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7883319   | Ca6                                     | 7883319                       | ATTTGTTTGTT/ATTTGTT                                           | AAAAATGAATGAAAAG<br>GGGTG  | GAAAGAGGCATTGGGA<br>TTCA   | 58.0                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7883626   | Ca6                                     | 7883626                       | CT/CTTT                                                       | TGAATCCCAATGCCTC<br>TTTC   | TGAGAATTTTGTGCAT<br>CGC    | 60.0                             | 160                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7884565   | Ca6                                     | 7884565                       | AACACAC/AACAC                                                 | CACCAAAACCTGCAAT<br>TCCT   | GTTGAAAACCGACCCT<br>GAAA   | 60.0                             | 687                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7899205   | Ca6                                     | 7899205                       | ATTATTTTATTTTATTTT/ATTATTTTA<br>TTTTATTTTATTTTATTTT           | GCACGGGCACCTTATT<br>AGTTA  | CCGGATCACCGTATTG<br>AATC   | 59.2                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7899665   | Ca6                                     | 7899665                       | TAAAAA/TAAAAAA                                                | ATTAGGGTGGTGGTTG<br>ACGA   | TTCGCATGTTCTAAATT<br>GGTTG | 60.2                             | 723                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7903885   | Ca6                                     | 7903885                       | A/AAT                                                         | TAGGACCTCCCCACGT<br>TATG   | ACACCACAATCAATGG<br>AGCA   | 59.8                             | 877                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7911705   | Ca6                                     | 7911705                       | TAAAA/TAAAAA                                                  | CCTCAACCTTAAGTGC<br>TCCG   | GCATTTGATTGGAAC<br>GTGA    | 59.9                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                               |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_7921239   | Ca6                                     | 7921239                       | CTAATTTAATTTAATTTA/CTAATTTA<br>ATTTA                          | TGGAGTCGTTACCGTC<br>CTTC   | AAAAGTTTGCCATTAT<br>CAATTTT   | 60.1                             | 477                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_7922258   | Ca6                                     | 7922258                       | TT/TTTAT                                                      | TATCAACCAAATGCGT<br>CCAA   | AAAAGGATTTAACATAA<br>ACCGAGTC | 59.9                             | 566                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_7935468   | Ca6                                     | 7935468                       | ATTTT/ATTTT                                                   | TTGTTGTCATTTGCAGT<br>AAAGC | TTGTGCACACTCGTTAA<br>GTTGA    | 58.0                             | 428                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_7936124   | Ca6                                     | 7936124                       | TC/TCC                                                        | GGACAATTGCCCAATT<br>TCITT  | GCGTTGTGTTTGTTCG<br>TCAT      | 60.2                             | 421                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_7942841   | Ca6                                     | 7942841                       | ATT/AT                                                        | TCAAAGCTGGAATTTG<br>GACC   | TCAACAGAAGCCGGAA<br>CTCT      | 60.1                             | 508                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_7948620   | Ca6                                     | 7948620                       | CTT/CTTTTTT                                                   | GCGCGTTAAACTACTC<br>ACCC   | TCATTGCAATTCTCAGC<br>CTCT     | 59.8                             | 430                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_7948820   | Ca6                                     | 7948820                       | AATATATATATATATATAT/AATATAT<br>ATATATATATATATATATATATAT       | ATCCACCATGATAGCC<br>TCCA   | GGAGGGACACTGTTGA<br>AAGG      | 60.3                             | 765                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_7953411   | Ca6                                     | 7953411                       | AAAAA/AAAAAGAAAA                                              | CGCTTCTCCAAAGAGC<br>GATA   | ACTCAATGGTGCCGAG<br>TTGT      | 60.6                             | 635                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_7954309   | Ca6                                     | 7954309                       | TAAAAAA/TAAAAA                                                | CTAACGCGTATACATC<br>GGCA   | CACGGTACCACATTGA<br>CGAC      | 59.7                             | 580                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca6_P4_7954796   | Ca6                                     | 7954796                       | A/ATTT                                                        | TTTCGTGACCTCGAAA<br>GGAT   | TTTTCTCCGTATCTCA<br>CGG       | 59.7                             | 577                                           | INTERGENIC                                           | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_7970811   | Ca6                                     | 7970811                       | CTCTTCTTCTTCT/CTCTTCTTCTCTTCT                                 | GGGCACGGATCAGTTCTTTA     | GAGCAAAAGTTGGCAGGAAG         | 60.1                             | 311                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7972071   | Ca6                                     | 7972071                       | AT/ATT                                                        | TAGTTTCTGACTCGGC<br>GACA | ACGGATCCCAAGTCAATGAG         | 59.6                             | 786                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7972712   | Ca6                                     | 7972712                       | TAAAAAAAA/TAAAAAAAAAAAA                                       | CTCATTGACTTGGGATCCGT     | TCATTGCTTATGTGTAA<br>TTGTGC  | 59.9                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7972862   | Ca6                                     | 7972862                       | GTATATATATAT/GTATATATATATAT<br>AT                             | CTCATTGACTTGGGATCCGT     | GAGAAAAGGTGGATCC<br>TACATACC | 59.9                             | 921                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7973691   | Ca6                                     | 7973691                       | TTATAT/TTATATAT                                               | TGCCCATCTTTTCCTTCATC     | CGCCGTCGTCCTACTCTCTA         | 60.0                             | 438                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7976984   | Ca6                                     | 7976984                       | TAAAA/TAAAA                                                   | AGGCCAATCCTCCATT<br>TGTA | ATATGGATTGGGGTAGGGC          | 59.4                             | 230                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7989945   | Ca6                                     | 7989945                       | ATTT/ATT                                                      | CCACAAGGGGTGGTGT<br>AGTC | GTGGAGACTTTTGGGACCT          | 60.3                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7990379   | Ca6                                     | 7990379                       | ATTATGT/AT                                                    | AGGGTCCCAAAAGTCTCCAC     | TGAGCCTTGAGTGCAAAAGA         | 60.3                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7990494   | Ca6                                     | 7990494                       | CAAAAA/CAAAAAA                                                | AGGGTCCCAAAAGTCTCCAC     | TGAGCCTTGAGTGCAAAAGA         | 60.3                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7991799   | Ca6                                     | 7991799                       | T/TC                                                          | CCCGTGCAACACACTACTTC     | TTGTGCGGATCGTTTATTTG         | 59.2                             | 727                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_7995646   | Ca6                                     | 7995646                       | TTT/TTTGTT                                                    | TAACAATTGCGGCAAC<br>AAAA      | AAAAGAACTGGCCGTC<br>ACAC | 60.1                             | 254                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7995932   | Ca6                                     | 7995932                       | TTT/TTTGTT                                                    | TAACAATTGCGGCAAC<br>AAAA      | CCTGACGGATTCTTT<br>CTCAA | 60.1                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_7997168   | Ca6                                     | 7997168                       | AAAAAATTAT/AAAAAATTATGAAAA<br>TTAT                            | GCTTGCATTAGTCAG<br>ACCA       | GACACATGGTTGCAG<br>ATTCT | 60.0                             | 625                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8005951   | Ca6                                     | 8005951                       | T/TTA                                                         | TCACCGACCTTCATTA<br>GCAA      | AGGTTGACCTGGTTCA<br>TTCG | 59.3                             | 981                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8006058   | Ca6                                     | 8006058                       | AATATATATATATATATATATA/ATA<br>TATATATATATATATA                | TTTGTTTTGATGGAGT<br>TATTTCTTT | AGGTTGACCTGGTTCA<br>TTCG | 59.8                             | 748                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8022121   | Ca6                                     | 8022121                       | TAATTAAAAATTAAAAAT/TAATTAA<br>AATTAAAAATTAAAAAT               | TTTGTTTGCATGGCT<br>CATA       | TGTTTTCCGAGCGTA<br>CACA  | 60.2                             | 818                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8033661   | Ca6                                     | 8033661                       | ATAAATGTCGCT/AT                                               | AAAAATTGATGCCCTC<br>ACCA      | CAGCGATAAATATTTGC<br>CCA | 60.3                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8035204   | Ca6                                     | 8035204                       | GAAA/GAA                                                      | ACACCCACCAATTGT<br>GTTT       | GCATATGTGCTTGGC<br>CACC  | 60.0                             | 694                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8035617   | Ca6                                     | 8035617                       | AATATATATA/AATATATATATA                                       | CAAGCTTTATCTGTAA<br>CGCTG     | TGAGGTGTGCGGTAA<br>TCGT  | 59.1                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8044596   | Ca6                                     | 8044596                       | G/GAA                                                         | TAGATGATTACGCGG<br>AACC       | CCCTTATTTTGGGAGG<br>GAAA | 59.9                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_8048922   | Ca6                                     | 8048922                       | GTTTTTATTTTTA/GTTTTTATTTTT<br>TATTTTTTA                       | TGCTAGAACATGCTGC<br>TGCT      | CATTCTCAGCCCAGGA<br>AAAC    | 59.9                             | 438                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8064946   | Ca6                                     | 8064946                       | ATTTTTTT/ATTTTTTTTT                                           | ATCACGTTATTCTTTCT<br>ACGATGA  | CCCGTGACATACACAT<br>GGAA    | 57.1                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8098915   | Ca6                                     | 8098915                       | CATA/C                                                        | TTCCGGTTGTTATCCG<br>TTTT      | CAAGTGAAAATCCTCG<br>TTGACA  | 59.3                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8099378   | Ca6                                     | 8099378                       | ATTTTTTT/ATTTTT                                               | TGTCAACGAGGATTTT<br>CACTTG    | TGCCGCTTAACCTTCAC<br>CTTT   | 60.1                             | 167                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8100368   | Ca6                                     | 8100368                       | AAAAATAAAA/AAAAATAAAATAAA                                     | AGGTAGGAACTAATTG<br>CCTATTTTT | TTACATGGCAAAATCT<br>TTCA    | 57.3                             | 467                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8122786   | Ca6                                     | 8122786                       | TTTAAAGATTAAA/TTTAAAGATTAAA<br>GATTAAA                        | CACACGCGGTCTTTTA<br>ATTT      | GATTCAAGTGCCTTGC<br>CATT    | 60.0                             | 755                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8123635   | Ca6                                     | 8123635                       | TC/T                                                          | TGGTCATTTCGAAAGA<br>AAGAA     | TTGCAATCAAAAGCTCT<br>TAAAAA | 59.7                             | 286                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8131261   | Ca6                                     | 8131261                       | TACA/T                                                        | ATCCCAATTTCCCAA<br>GGTG       | CTCGGGGTTTTGTTGA<br>TGTT    | 60.9                             | 239                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8131551   | Ca6                                     | 8131551                       | CTTTTTTTTTTTTTTTTT/CTTTTT<br>TTTTTTTTTT                       | AACATCAACAAACCC<br>CGAG       | TTGCGTAACGTTTGG<br>ACAC     | 59.8                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8156312   | Ca6                                     | 8156312                       | AAA/AAATTCGTAA                                                | GTCTCCAGCAGAGCAA<br>AACC      | CGTTTGAACACGAAGC<br>TGAA    | 60.0                             | 874                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_8164226   | Ca6                                     | 8164226                       | GAAAAA/GAAAAAA                                                | CCTCCGCTCTACCAAC<br>TGAG  | TCGAATTTTCTTCAAT<br>GGG      | 60.0                             | 324                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8177320   | Ca6                                     | 8177320                       | G/GTATT                                                       | TTGTATAACTCGGCTG<br>ACGG  | AACCCTCATTGAGTC<br>CGTG      | 58.8                             | 408                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8178292   | Ca6                                     | 8178292                       | GTATA/GTA                                                     | AGTTGACGAACCAACA<br>TGTA  | CCATGACTTCGAAATG<br>CTCA     | 59.0                             | 971                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8181367   | Ca6                                     | 8181367                       | CAAAA/CAAA                                                    | GGTGACACAATAGTGGT<br>GTCG | AGCCTCTCTCACCCCA<br>AAAT     | 60.0                             | 400                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8182365   | Ca6                                     | 8182365                       | ATTTT/ATTTT                                                   | TGCTGATACAAATGTG<br>GGAAA | ACACTGAAACCAACCC<br>TTCG     | 59.0                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8200088   | Ca6                                     | 8200088                       | CTTTAAATTTAA/CTTTAAATTTAAAT<br>TTAA                           | AAGACACGGCGGTTAT<br>TACG  | AAATGGAATACGTCGA<br>GTTCAAA  | 60.0                             | 684                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8312848   | Ca6                                     | 8312848                       | ATTTTTTTTTTTTTTTTT/ATTTTTTTT<br>TTTT                          | GGATCTTTTGGCCGAA<br>ATCA  | TTTGTATGCACATTT<br>AGTCAATCA | 60.0                             | 753                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8410500   | Ca6                                     | 8410500                       | CAA/CA                                                        | AATCGATTGATTCAGC<br>CCAG  | TAATGCCCCGTTTTTCA<br>AAG     | 60.0                             | 795                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_850916    | Ca6                                     | 850916                        | TCC/TCCC                                                      | AATCAAGTGCAAAAGT<br>GGGG  | ACCACCCCATATCCA<br>GCAT      | 60.0                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8624865   | Ca6                                     | 8624865                       | AATATATATATATATATA/AATATA<br>TATATATATATATATATA               | ATTGGGTTGATTGCGA<br>AGAG  | TCCAAATCCAACTCCAC<br>GTA     | 60.1                             | 846                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                 |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_8640916   | Ca6                                     | 8640916                       | ATTTTTTTTTT/ATTTTTTTTTTT                                                        | CGAAAAAGTTAAACTC<br>CTGCGA | TTTTCCCGACTTGGTC<br>TTTT    | 60.7                             | 667                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8672001   | Ca6                                     | 8672001                       | AATATATATATATATATATATATA/<br>AATATATATATATATATATATATAT<br>A                     | TCATAGTTTGCCGCTA<br>GGCT   | AGAACTTTGATGCCATT<br>TTGTG  | 60.0                             | 115                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8705473   | Ca6                                     | 8705473                       | AAGAGAGAGAGAG/AAGAGAGAGA<br>G                                                   | GCTTGTGGGGATGTTA<br>AACC   | GAAGGGAATGAAATGC<br>GAAA    | 59.3                             | 492                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8771580   | Ca6                                     | 8771580                       | A/ATTCAATACAGTTACAAT                                                            | TGACACCACCTCCAAA<br>AACA   | GTCGCAAAATCGGAGA<br>AAAA    | 60.0                             | 733                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8834153   | Ca6                                     | 8834153                       | ATTTTTTTTT/ATTTTTTTT                                                            | TTGCAGATTTTGGAGAA<br>GTTCA | TTTGGTGGGTGATAGG<br>CAAT    | 57.7                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8849732   | Ca6                                     | 8849732                       | CTATATATATATAT/CTATATATATAT<br>ATAT                                             | AACTGGCCGAGATTCA<br>AAGA   | TCAAGAAATGATGGAC<br>AAACTCA | 59.8                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_8904663   | Ca6                                     | 8904663                       | GATATATATATATATATATATATA<br>TATATATATAT/GATATATATATATAT<br>ATATATATATATATATATAT | TGAATTGCTTCGAACC<br>TGTG   | TGCATTTCAAGCTCTCA<br>TGC    | 59.8                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_89501     | Ca6                                     | 89501                         | TAATATA/TAATATAAATATA                                                           | TCCGATAAAATCTCCG<br>TTCG   | GCATTCTACTGCAATG<br>CCAA    | 60.0                             | 820                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_9014214   | Ca6                                     | 9014214                       | CA/CAA                                                                          | TACTGGGGTGCTGGT<br>GTGA    | AGCTGCACGCAGACTG<br>TAAA    | 60.0                             | 441                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_9015636   | Ca6                                     | 9015636                       | AAGT/AAGTAGT                                                                    | TGAAACAAGTGCTGGC<br>AAAG   | ATCAACCCCAACAATCT<br>CCA    | 60.0                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                           | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                                         |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_9018972   | Ca6                                     | 9018972                       | TTAAATAAATAAATAAATAAATAA/TT<br>AAATAAATAAATAA                                                                                                                           | GTCTGTAATTCGTGC<br>GTCG   | ATTTCAGCGAGGAGA<br>AAAA     | 59.3                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_9239871   | Ca6                                     | 9239871                       | GTCTCT/GTCT                                                                                                                                                             | GAGGGGAACCCCAAAA<br>AGTA  | ATGGTCTCACCTTTATG<br>CCG    | 60.2                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_925681    | Ca6                                     | 925681                        | AATATATATATATATATATATATATAT<br>ATATAT/AATATATATATATATATATA<br>TATATAT                                                                                                   | CCGAGTTGGGTGAACC<br>AATA  | AACTGTGGTTTTTGC<br>GACC     | 60.7                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_9335470   | Ca6                                     | 9335470                       | AATATATATATATATATATATAT/A<br>ATATATATATATATATATATATATA<br>T                                                                                                             | GTGTGTGCTTAAATTG<br>GCCC  | TGAAATCCAAACCACA<br>TGC     | 60.4                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_9483877   | Ca6                                     | 9483877                       | GTTATTATTATTATTATTATTATT<br>ATTATTATTATTGTTGTTATTGTTAT<br>TGTTATTGTTATTGTTATTATTATTA<br>TTATTATTATTATTATTGTTATT<br>GTTATTATTATTCTTATTATTATT<br>ATTATTATTCTTATTATTATTATT | CAACTTCCTACGTTTTG<br>GCA  | CCCAATTGTTTCATCCCA<br>ATC   | 58.8                             | 717                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_9932385   | Ca6                                     | 9932385                       | CATATATATATATAT/CATATATAT<br>ATATAT                                                                                                                                     | CCCATCATTGACCGAA<br>GAAT  | CTTGTGGGGGTATGAG<br>GAAA    | 59.8                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_9947644   | Ca6                                     | 9947644                       | AAA/AAAGAGAA                                                                                                                                                            | ACATGACCATCACATC<br>ACGG  | CGAACTTTTTGGAATG<br>CAAC    | 60.3                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca6_P4_9998146   | Ca6                                     | 9998146                       | AATATATATATATATA/AATATATA<br>TATATATATATA                                                                                                                               | AGTGCATGTTCCATGA<br>CGTG  | CTCACTTACCCTCGCT<br>CCTG    | 60.6                             | 116                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10060696  | Ca7                                     | 10060696                      | CAAAAAAAAA/CAAAAAAAAA                                                                                                                                                   | GCTGACTCTACGAGGA<br>AAGGG | CAGATGACTAATGGTC<br>GACAACA | 60.4                             | 429                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10063869  | Ca7                                     | 10063869                      | CATATATATATATATATATATATA<br>T/CATATATATATATATATATATAT<br>ATATATAT                                                                                                       | CCATCCTCTCGCTGTC<br>ATTT  | TTGTATTTGGTTGCTGA<br>TCTCG  | 60.2                             | 204                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                   |                           |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_10168743  | Ca7                                     | 10168743                      | CTTTTTTTTTTT/CTTTTTTTTTTT                                                         | CGCGAAACAACGTATG<br>ATCT  | GCCACCAGAATGAAAT<br>ATACAAAA | 58.8                             | 344                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_1018745   | Ca7                                     | 1018745                       | C/CT                                                                              | TTGCAACATGATAGC<br>TGCC   | TTGTTGGCATTGTTGT<br>GGTT     | 59.8                             | 467                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_1018777   | Ca7                                     | 1018777                       | ATTGCAT/ATTGCATATTGCAT                                                            | TTGTTCCCGTAAAAGAT<br>CGC  | TTGTTGGCATTGTTGT<br>GGTT     | 60.1                             | 233                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10192729  | Ca7                                     | 10192729                      | TTTTTTCATATA/TTTTTTCATATA<br>ATGTTTTTTCATATA                                      | CCCATTCCGAATACATT<br>GCT  | GAGTTGGGTGCACGAT<br>TTTT     | 59.8                             | 624                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10222115  | Ca7                                     | 10222115                      | TTATATATATATATATATAT/TTATAT<br>ATATATATATATATATAT                                 | TTTCTTCGATCCCCACT<br>TTTT | TTGTTTTCGTTGACATG<br>TGATT   | 59.9                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10240117  | Ca7                                     | 10240117                      | ATTTTTTT/ATTTTTTTTT                                                               | CCTCAGGATGCGACCA<br>TCTA  | CCAGCTTGAACAATGT<br>TTCTT    | 61.2                             | 687                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10240420  | Ca7                                     | 10240420                      | CTTTTTTTTT/CTTTTTTTTT                                                             | CGTGTTCCTTATATTTT<br>GCCG | AATCTCAAAATGCCCA<br>CTT      | 59.5                             | 629                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10268860  | Ca7                                     | 10268860                      | TTATATATATATATATATATATATATA<br>TATATATATATATA/TTATATATATAT<br>ATATATATATATATATATA | CCACTCCTTTCATCCCT<br>TGA  | AAATGATGCGGCGTT<br>TTAC      | 60.0                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10374231  | Ca7                                     | 10374231                      | TTATATATATATATATATATATATATA<br>T/TTATATATATATATATATATATATA<br>TATATATAT           | AATCGGCATTTTGAAC<br>TGG   | AAACGGCGACTTACCA<br>AAGA     | 59.9                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10442254  | Ca7                                     | 10442254                      | AATATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATATA<br>TATATATATAT         | ATTGGTGGGTCGGGTA<br>CATA  | ATTCATCCAACAATGCC<br>ACA     | 59.9                             | 377                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                      | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                    |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_10790569  | Ca7                                     | 10790569                      | ATT/ATTTT                                                                          | CCAGAAATTTTGTGG<br>GGAA   | TTCCGGAATTTTAGG<br>AAAAA | 59.8                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10791606  | Ca7                                     | 10791606                      | TGGGG/TGGGGG                                                                       | GGTGCCTACCGAAAT<br>CTT    | GTTTTATGGGGTAGC<br>CGGT  | 59.9                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10806849  | Ca7                                     | 10806849                      | ATTTTTTTTT/ATTTTTTTTTT                                                             | GTTTCGCCGTTCAATCA<br>TTTT | CGATGAAGGCAGACCA<br>ATTT | 59.9                             | 824                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10821468  | Ca7                                     | 10821468                      | AAATAATAATAATAATAATAATA<br>ATAATAATAAT/AAATAATAATAATA<br>TAATAATAATAATAATAATAATAAT | ACGTGACGTGGATGGG<br>TTAT  | TTTCGTCGTCTCAAATC<br>GAA | 60.1                             | 816                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10825347  | Ca7                                     | 10825347                      | ATTTTTTTTT/ATTTTTTTT                                                               | CACTCAACGGGAACAG<br>GTTT  | TTGGATCCGACAGTGA<br>TGAA | 60.0                             | 843                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10863846  | Ca7                                     | 10863846                      | TGGGGGGGG/TGGGGGGG                                                                 | GGACAGGGAAGAGGA<br>AAAGG  | ACAACCTACAACAGTC<br>CCCG | 60.0                             | 466                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10911713  | Ca7                                     | 10911713                      | TAAAAAAAAA/TAAAAAAAAA                                                              | ATGAGTACCGGACAGC<br>GAGT  | CACCACTTGTTCACAT<br>GCC  | 59.8                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_10942267  | Ca7                                     | 10942267                      | TAAAAAAAAA/TAAAAAAAAA                                                              | GCATGTATGGATTGAA<br>CGCA  | CATCCCCACCAAT<br>TAAG    | 60.5                             | 898                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_11032853  | Ca7                                     | 11032853                      | TATAATAATAATAATAATAATAA<br>TAATAATAAT/TATAATAATAATAA<br>ATAATAATAATAAT             | GAAATTCAGTTGAGGG<br>ACCG  | CTTCTCGAGGAGCGA<br>CCT   | 59.5                             | 294                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_11034499  | Ca7                                     | 11034499                      | AATATATATATATATATATAT/AA<br>ATATATATATATATATATATAT                                 | TGTCATGTCAACCCA<br>TGCT   | TCAAAGGCCACCTCT<br>TCAT  | 60.0                             | 270                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')   | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|---------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                               |                           |                                 |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_11040579  | Ca7                                     | 11040579                      | GAGATAGA/GAGA                                                                 | AAGCTGTTGTGAATTG<br>GGCT  | CAACAAATGCATGTCC<br>CAAG        | 59.7                             | 335                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_11073789  | Ca7                                     | 11073789                      | CTTTTTTTTT/CTTTTTTTTT                                                         | TTGCAGCATCAACTAG<br>GCAC  | CCTCTCCCAAATCGCT<br>ACAA        | 60.0                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_11074091  | Ca7                                     | 11074091                      | TAAAAAAAAA/TAAAAAAAAA                                                         | TACCGATTGCCATCCT<br>TAGC  | ATTACCTTTCATATTTCT<br>GTTTTCTAA | 60.1                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_11083612  | Ca7                                     | 11083612                      | TAAAAAAAAA/TAAAAAAAAA                                                         | ACTGGTTTGTCACTCA<br>CCTGA | TTTTTAGGCAGGTGGA<br>CATATT      | 58.0                             | 702                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_11332314  | Ca7                                     | 11332314                      | AATATATATATATATATA/AATATATA<br>TATATATATATATA                                 | AACCCAAGTTCCAAAT<br>GACG  | ACCCAAGAGAGGTGCG<br>ACTA        | 59.8                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_11382209  | Ca7                                     | 11382209                      | ATTTTTTTTT/ATTTTTTTTT                                                         | TGTGCTACTTGCCATG<br>CTCT  | CGACCGACTCACTTTT<br>CCAT        | 59.6                             | 826                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_11430729  | Ca7                                     | 11430729                      | CCTACNN/C                                                                     | AAGGTGGTGGTGGAGT<br>TGAG  | TCCTGTGAATGTCCAC<br>CAAA        | 60.0                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_11513709  | Ca7                                     | 11513709                      | CATATATATATATATATATATA/CA<br>TATATATATATATATATATATA                           | GTGTGACGTCGGTGAA<br>TACG  | ACTCAACGAGCCTGCA<br>ATTT        | 60.0                             | 709                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_11572510  | Ca7                                     | 11572510                      | TTATATATATATATATATATATA<br>TATATATATATATATA/TTATATAT<br>ATATATATATATATATATATA | GAAAGGTGAAAGGCGA<br>AATG  | ATCAGCGGACAGGGAT<br>TACA        | 59.7                             | 191                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_11647837  | Ca7                                     | 11647837                      | GATTTTATTTT/GATTTTATTTTAATT<br>TTATTTT                                        | GCACCAACAAGAAGG<br>GAAA   | GGAGATTCGTGCGCAT<br>ATTT        | 60.1                             | 166                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                       | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                     |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_11960847  | Ca7                                     | 11960847                      | ATAT/ATATGTATATGTATGGATGTA<br>T                                                                                     | TGATGGCACATCATTG<br>TCCT | AACCCCATCCCCAAAT<br>AAG  | 59.9                             | 221                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_11977859  | Ca7                                     | 11977859                      | GTTATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATT/GTTAT<br>TATTATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATT | AGGGTGTGGTTATTGA<br>TGCC | TAACGGAATTGGTGGC<br>CTTA | 59.7                             | 808                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_12003043  | Ca7                                     | 12003043                      | TT/TTTTAT                                                                                                           | GATGGCAAAGACACAC<br>ATGG | CGGTTGTGAGCATTGG<br>ACTA | 60.0                             | 884                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_12010139  | Ca7                                     | 12010139                      | TAAAAAAA/TAAAAAAA                                                                                                   | AACACGGGAAAAACAC<br>GAAG | TTTGTGAGGGCTTTATT<br>CGG | 60.0                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_12062688  | Ca7                                     | 12062688                      | GTTTTTTT/GTTTTTTT                                                                                                   | CCTTTTACAGCGCTTTT<br>TCC | TGTCATGCACTATGC<br>GAAA  | 59.0                             | 213                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_12082631  | Ca7                                     | 12082631                      | TA/TAATATAATAATAATAA                                                                                                | CGGATTGCATTGCTT<br>TTCT  | TCAAGGGATTGTCCCC<br>AATA | 60.2                             | 250                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_12183467  | Ca7                                     | 12183467                      | CTGTAGCGT/CT                                                                                                        | CAGCGGTTGAAAACCT<br>TTGT | CCACATTGAGAGGGAA<br>GGAA | 60.1                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_12204671  | Ca7                                     | 12204671                      | ATTTTTTTTTT/ATTTTTTTTTT                                                                                             | GCTTGTTGGATAGCG<br>AGAG  | CACCTCAGCTACCGTT<br>CACA | 60.0                             | 730                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_12261342  | Ca7                                     | 12261342                      | AA/ATCTA                                                                                                            | CTCAATTTCTGTTTGG<br>GGGA | AATATGTTTGCCATGTC<br>GGC | 59.9                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_12261371  | Ca7                                     | 12261371                      | ATA/ATATCTA                                                                                                         | CTCAATTTCTGTTTGG<br>GGGA | AATATGTTTGCCATGTC<br>GGC | 59.9                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_12691360  | Ca7                                     | 12691360                      | CAAAAATCATT/CAAAAATCATT/TT<br>ATTAAAAAATCATT/TT               | GTCAAGGGCCTATGGT<br>CAGA    | TTTGGTCATGGGATGT<br>GCTA     | 60.1                             | 909                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_12733352  | Ca7                                     | 12733352                      | TT/TTATTAT                                                    | ATAAGATTGGGGTGG<br>GGAG     | GGTTGCGTCTAGCGAA<br>AGTT     | 60.0                             | 374                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_12856742  | Ca7                                     | 12856742                      | CAAA/CAA                                                      | CAATCACCAACATCAT<br>GACAA   | TGCCATAATTCCTCTT<br>CCG      | 59.3                             | 565                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_12923739  | Ca7                                     | 12923739                      | TGGAC/T                                                       | GAAGTGTAGCCTTTCA<br>GGCG    | CCTGGACTCGACAAA<br>GGAA      | 60.0                             | 556                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_1295880   | Ca7                                     | 1295880                       | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATATATA<br>TAT | TTTGATTTATCGATGA<br>GGCA    | TGAATTTAATTGGGGC<br>GGTA     | 59.2                             | 538                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_13090405  | Ca7                                     | 13090405                      | ATTTTTTTT/ATTTTTTTTTTT                                        | GGACAAAACGAGGCAT<br>TTGT    | TTTCATCACCCTGCCAT<br>CTAA    | 60.0                             | 156                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_13183128  | Ca7                                     | 13183128                      | TGACCCAG/TG                                                   | AGTATTTGAATCCGAC<br>GAAATAA | GGGGTCTCCTCACTGTT<br>TCAA    | 58.2                             | 100                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_1326824   | Ca7                                     | 1326824                       | T/TA                                                          | TCCAAAAATGCACTCAA<br>ATCA   | ATGAGTGGGAGAACAT<br>TGCC     | 59.1                             | 715                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_13300743  | Ca7                                     | 13300743                      | AAA/AAATTGCAATTAA                                             | TGCAGCAAACATAAGC<br>ATGA    | AGTAACCCGAACTCGG<br>TCCT     | 59.0                             | 494                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_1339137   | Ca7                                     | 1339137                       | ATTTTTTTTT/ATTTTTTTTTTT                                       | CTTCACAACCAGAGCA<br>CCAA    | TGCATTAAATTTTACGG<br>AGAAACA | 59.9                             | 638                                           | INTERGENIC                                           | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                           |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_13397822  | Ca7                                     | 13397822                      | ATTTTTTTT/ATTTTTTTT                                                       | GGCTTACACCAATGCT<br>TAAATG | TTCGAAAATACACAATC<br>CAAAAA | 59.9                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_13526291  | Ca7                                     | 13526291                      | TATAAATAAATAAATAAATAA<br>TAAATAAATAAATAAATAA<br>TAAATAAATAAATAAATAA<br>AA | AAATTGGTCATCGGTG<br>CTTC   | TTCCACACCACACTTGA<br>TCC    | 59.9                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_13559247  | Ca7                                     | 13559247                      | TACA/TA                                                                   | TTCAACTTTCTCCAATC<br>CACA  | TGAAAAGACGGAGGGT<br>TGTT    | 58.2                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_13588964  | Ca7                                     | 13588964                      | AATATATATATATAT/ATATATAT<br>ATATATATAT                                    | AAATCGATGAATGGGT<br>GGAG   | AGAAACGTGCGGTGTC<br>TCTT    | 59.8                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_13609089  | Ca7                                     | 13609089                      | AAATAATAATAATAATAATA<br>AT/AAATAATAATAATAATA<br>TAATAAT                   | CCATTTACGCGGAAC<br>TAAT    | AGTAGCGTTGTCGGA<br>GCAT     | 60.0                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_1368308   | Ca7                                     | 1368308                       | TAAAAAAAA/TAAAAAAAA                                                       | GGGTTTTGTTTTGGG<br>GTTT    | AGGGACACATTTGGC<br>ATGT     | 59.9                             | 854                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_13745061  | Ca7                                     | 13745061                      | CC/CCCCGCCGGGAC                                                           | CGGCAATGTGGTTTGT<br>TATG   | GTGTAAATGGCGTCTG<br>GGTT    | 59.8                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_13866056  | Ca7                                     | 13866056                      | ATTTTTTTTT/ATTTTTTTTT                                                     | TTGCAGACTGGGACTT<br>CCTT   | ATTGTGTGGGAGCCTC<br>GTAT    | 59.8                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_13891702  | Ca7                                     | 13891702                      | CTATATATATATATAT/CTATAT<br>ATATATATATAT                                   | TGCCTTTTACTCTGGT<br>GGG    | GAGTGGGATTTGGAG<br>GTGA     | 60.1                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_13912935  | Ca7                                     | 13912935                      | TTATATATATATATATAT/TTAT<br>ATATATATATATATATAT                             | ACAATCCTCAAATGCG<br>GAGA   | TACTCCAGGCCATTGA<br>CTCC    | 60.6                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_14071479  | Ca7                                     | 14071479                      | TTATTA/TTATTAATATTA                                           | CAATGCGTTTTCCCA<br>CTTT   | CCGTTTTAGCGAACGA<br>CGTA   | 60.0                             | 384                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_14071498  | Ca7                                     | 14071498                      | T/TAATA                                                       | CAATGCGTTTTCCCA<br>CTTT   | CCGTTTTAGCGAACGA<br>CGTA   | 60.0                             | 384                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_14075293  | Ca7                                     | 14075293                      | CATATATATATATATAT/CATATATAT<br>ATATAT                         | TTTGTTTAGCCACAAC<br>TTTGA | CGTGCTCGGGATTAT<br>TTGT    | 57.6                             | 862                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_14083390  | Ca7                                     | 14083390                      | AGACTTTTT/A                                                   | TCCCTACAAACACCG<br>CCTC   | TTTTACAGCGCTTTTGG<br>ACA   | 60.0                             | 291                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_1418041   | Ca7                                     | 1418041                       | AG/A                                                          | CGTTGTGGTGGGTGTA<br>GTTG  | ACACCATGCGTCAGTT<br>GAAA   | 59.9                             | 188                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_1418185   | Ca7                                     | 1418185                       | CAAAAAAAAA/CAAAAAA                                            | TTTCAACTGACGCATG<br>GTGT  | CCACGTGTCAGCCAAA<br>TAGA   | 60.2                             | 324                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_1418248   | Ca7                                     | 1418248                       | CA/CCATTAA                                                    | TTTCAACTGACGCATG<br>GTGT  | CCACGTGTCAGCCAAA<br>TAGA   | 60.2                             | 324                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_1424328   | Ca7                                     | 1424328                       | GAAAAAAAAA/GAAAAAAAAA                                         | TTCCAGCTCCAATTTTC<br>ACC  | ACAGAGAGAGGCTGGA<br>TGGA   | 60.1                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_14244076  | Ca7                                     | 14244076                      | GAAAAAAAAA/GAAAAAAAAA                                         | GCAATTTTGGTCCCTC<br>CTTT  | TTAAAAATTAACCA<br>CCATATTT | 60.3                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_14404415  | Ca7                                     | 14404415                      | CGAGAG/CGAGAGAG                                               | TCTCCCTAGAAGCTGC<br>AACC  | GCCAGAATCATCCCA<br>CCTA    | 59.6                             | 129                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                     | Forward primers (5'-3')   | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------|---------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                   |                           |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_14456818  | Ca7                                     | 14456818                      | CTTA/CTTAATTTA                                                                                    | GACGAACCAAGGGATG<br>GTAA  | TTTCTTCTTCGATT<br>GGTCC        | 59.8                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_14483644  | Ca7                                     | 14483644                      | ATAT/ATATTTAT                                                                                     | TTAATAGGGCCGACGA<br>ATTTT | TAAAGGACCAAGTCGG<br>GAAA       | 59.8                             | 615                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_14657537  | Ca7                                     | 14657537                      | TTTTACT/TTTTACTTTTACT                                                                             | AGAGCATCTCCAAGGG<br>TGAA  | AGCCAAAATGAGTTTG<br>TCGG       | 59.8                             | 607                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_14664323  | Ca7                                     | 14664323                      | CTTTTTTTTTT/CTTTTTTTTTT                                                                           | AATTGAAATGTTGAGG<br>CTGTG | GGTCCTAACAACGCCA<br>GGTA       | 57.7                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_14669638  | Ca7                                     | 14669638                      | AA/AAAGAGACACCTCTGA                                                                               | CATCGAGCGTTGTCAA<br>GGTA  | AATCTTTCTTCCAACAC<br>GGC       | 59.9                             | 114                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_14831868  | Ca7                                     | 14831868                      | AATATATATATATATATATATATAT<br>ATATATA/AATATATATATATATATAT<br>ATATATATATATATATATATA                 | GGCCTATGGCCTGACC<br>TACT  | TGCAACAACCTTCCCAT<br>AAA       | 60.5                             | 796                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_15217322  | Ca7                                     | 15217322                      | AATATATATATATATATAT/AATATAT<br>ATATATATATATATAT                                                   | ACCAATGTCCCTTGCA<br>TGAT  | TCGCAATTACTCTTGC<br>GATG       | 60.2                             | 381                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_15305196  | Ca7                                     | 15305196                      | AG/A                                                                                              | CTGCCCCCACTATTTCT<br>CAA  | ATACAGATCCGTGGAG<br>GCAC       | 60.1                             | 756                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_1531607   | Ca7                                     | 1531607                       | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAA/AAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAA | TCGCAAGATCCAATGT<br>GATG  | CCACAATGATCGCCAC<br>TTTT       | 60.6                             | 402                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_15328060  | Ca7                                     | 15328060                      | CTGATTTG/CTG                                                                                      | TGAACTGAGAGAGGGG<br>AGGA  | CCTAACCCCTTAATAAAA<br>TGAAAGCC | 59.9                             | 137                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                        | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                      |                             |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_15467222  | Ca7                                     | 15467222                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT         | TGGGAAACGGTGCTAA<br>ACTT    | TCCATTACGGCAAATT<br>CAA      | 59.6                             | 716                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_15507878  | Ca7                                     | 15507878                      | TATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAAT/TATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAAT | AACACACTCCCTCCCT<br>CCAT    | CCACCAGCCTTCCCTA<br>ATTT     | 60.8                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_15562093  | Ca7                                     | 15562093                      | GAAAATAA/GAA                                                                                                         | AATACACCACCTTCCA<br>CCCA    | TTTTTAAGGGATCCGA<br>CGTG     | 60.1                             | 161                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_15644224  | Ca7                                     | 15644224                      | ATAT/ATATTTAT                                                                                                        | CCGATTTCCCAAAGGT<br>TTTT    | TTCTGCAGCACCTTCCA<br>CCTA    | 60.2                             | 367                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_15653714  | Ca7                                     | 15653714                      | CTTTTTT/CTTTTTTT                                                                                                     | TTTCTTGCAAGGGTAA<br>TTTGC   | GCTTGTGTGGCCGACT<br>TAAT     | 59.2                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_15667150  | Ca7                                     | 15667150                      | CTTTTTTTTT/CTTTTTTTTTTT                                                                                              | TTTCAAGCTCCATTTTC<br>TTCG   | CGGAAACATTTGTAAAT<br>CAATCA  | 59.5                             | 177                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_15688080  | Ca7                                     | 15688080                      | ATTTTTTTTT/ATTTTTTTTTTT                                                                                              | CCATTTGCCTGATCGT<br>TCTT    | TTTAACCTTGCTTTTG<br>AGTGTGTT | 60.1                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_15688440  | Ca7                                     | 15688440                      | AATATATATATATATATATATAT<br>AT/AATATATATATATATATATATA<br>TATATATATAT                                                  | TCATGGAGAACATTCTT<br>CGTTTT | TTTCCGTCTTGATGCAA<br>TGT     | 60.0                             | 865                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_15693431  | Ca7                                     | 15693431                      | CTTTTTTT/CTTTTTTT                                                                                                    | TGAATTAGTCGGACAA<br>AACTGAA | CGTAAACCGAATTGC<br>TCAAA     | 58.8                             | 907                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_15735780  | Ca7                                     | 15735780                      | CTATATATATATATATAT/CTATAT<br>ATATATATATATATAT                                                                        | CATCAACACAAGGTGCG<br>CATC   | CTTCTCCATTTTGTGA<br>TGTT     | 60.1                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                           |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_15774270  | Ca7                                     | 15774270                      | TCC/TC                                                                    | AAGTGTGACCATGAC<br>TCTCA    | GCGCATTTCTTCCAAA<br>TGT     | 59.8                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_158561    | Ca7                                     | 158561                        | TCACACA/TCACA                                                             | ACTAGACATGACAACG<br>GGGC    | GCTCTAATTAGGTGCG<br>GCTG    | 60.0                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_15932194  | Ca7                                     | 15932194                      | ATATTATTATTATTATTATTATTA<br>TTATTATT/ATATTATTATTATTATTA<br>TTATTATTATTATT | AAGGCACATCATCGAA<br>AACC    | AAATTACAAACATAGGC<br>AAGCCA | 59.9                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_16001405  | Ca7                                     | 16001405                      | AATTATTATTATTATTATTATTAT<br>/AATTATTATTATTATTATTATTATTA<br>TTAT           | AAAACACAACGTGCAA<br>ACGA    | GGGTCACCAAGCACAG<br>TTTT    | 60.2                             | 679                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_16051093  | Ca7                                     | 16051093                      | TAA/TAAA                                                                  | TGGTTCGTCGGATATG<br>TGAA    | TTGAGTTCACGTACGC<br>GTTT    | 59.9                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_1608740   | Ca7                                     | 1608740                       | ATTTTTTTTT/ATTTTTTTTT                                                     | TTCACGTTGCCAACTA<br>CTCG    | CATTGCGTTTCATTTTG<br>TTG    | 59.9                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_16126431  | Ca7                                     | 16126431                      | TAAAAAAAAA/TAAAAAAAAA                                                     | TCACTATTTTCATGCAAC<br>CGC   | TTTGAAGATTTGCGTTA<br>CGA    | 59.7                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_16127650  | Ca7                                     | 16127650                      | AATGATTCT/AATGATTCTCCCATGA<br>TTCT                                        | TCACCGAAATCAAGCA<br>TTCA    | TATGGATTCCGGGTTG<br>TTGT    | 60.2                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_16251371  | Ca7                                     | 16251371                      | TAAAAAAA/TAAAAAAA                                                         | GGAGTCGATTATGCGT<br>AGGG    | CGCACTGGAAGATACG<br>TAGGA   | 59.6                             | 264                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_16298175  | Ca7                                     | 16298175                      | ATTTTTTTTTTTTT/ATTTTTTTTTTT<br>TTTTT                                      | TGCGCTTCTGTATTTA<br>GAGTTTT | CCTTCACCAGATGGAA<br>GAACA   | 57.5                             | 366                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                          | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                        |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_16320388  | Ca7                                     | 16320388                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTA/TTTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTA | TTTGC GTTACGAATTTG<br>ATGA | TTGGTCCTAAACAAGAT<br>GCAAA | 59.2                             | 607                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_16349610  | Ca7                                     | 16349610                      | CTTTTTTTTTT/CTTTTTTTTTT                                                                                                | GCA GTGCTGAATTTTG<br>GTGA  | TTGGTTTCATGACTTGC<br>ATCT  | 59.8                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_164757    | Ca7                                     | 164757                        | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATAT                                                                  | CGTTGCCACAATGTTA<br>TTGG   | CATGAGTTTTTGGTCT<br>GCCA   | 59.8                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_1649022   | Ca7                                     | 1649022                       | ATTTTT/ATTTT                                                                                                           | CCTTAGTGATTGGAG<br>GGCA    | CGAGAAGGTCGTGAGG<br>TAGC   | 60.1                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_16560646  | Ca7                                     | 16560646                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                                                                          | ATTTTCGCATGAAGGG<br>AGTG   | CGCAAAGGAGAAACGA<br>GAAT   | 60.1                             | 724                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_16610320  | Ca7                                     | 16610320                      | TAAAAAAA/TAAAAAAA                                                                                                      | CCACATCTCGTCTCCC<br>TCAT   | TTGCAGGTCATGTGGC<br>TAAC   | 60.1                             | 247                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_16687553  | Ca7                                     | 16687553                      | ATTGATTG/ATTGATTGATTG                                                                                                  | CGTCTTGGGACCAACT<br>CAAT   | TCGATTCACTGCA<br>CTGA      | 60.0                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_1686051   | Ca7                                     | 1686051                       | ATTTTT/ATTTTTT                                                                                                         | TCAAACTTCACATTTG<br>TGCG   | CCTTTTATTTTGTGG<br>GGGA    | 59.8                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_16899888  | Ca7                                     | 16899888                      | AATATATATATATATATA/AATATA<br>TATATATATATATATA                                                                          | TCATCAAATTCGTAACG<br>CAAA  | TCCTCTAATTATCCTT<br>CGTCCA | 59.2                             | 620                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_16941588  | Ca7                                     | 16941588                      | TAAA/TAAAA                                                                                                             | TGCCGTAGTATTCACC<br>ACCA   | TGCCATGAAATTCTGC<br>CATA   | 60.0                             | 852                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_16970696  | Ca7                                     | 16970696                      | AT/A                                                          | CAAAGGAACATTGTGA<br>TCGAA | CAAAGCCAAAACCAAC<br>ATCA    | 58.6                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_17073516  | Ca7                                     | 17073516                      | CATAT/CAT                                                     | TCCTTAGCCAAAGAGC<br>CAAA  | GTGTGGGAACCTTGTT<br>GCTT    | 60.0                             | 726                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_17133790  | Ca7                                     | 17133790                      | ATTTTTTT/ATTTTTT                                              | GACACTACCCGGCATC<br>AAGT  | CCAACCCAAATAAATGA<br>AAATCA | 60.0                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_17155284  | Ca7                                     | 17155284                      | CATATATATATA/CATATATATA                                       | AGTCCATACTTGGCAG<br>GGTG  | ACTACATGTTTGCAATG<br>GCG    | 60.0                             | 957                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_17172621  | Ca7                                     | 17172621                      | AATCATAT/AATCATATCATAT                                        | GGCTAAACCTTGCTT<br>TGCC   | AGACTCTGCTTGACCG<br>GAAA    | 58.8                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_17352977  | Ca7                                     | 17352977                      | AATATATATATA/AATATATATATATA                                   | ATTGCGGTGCAACACA<br>CATA  | TCTCTCCGTTTCCACC<br>ATC     | 60.0                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_17357820  | Ca7                                     | 17357820                      | TTTTATTTATTTATTTATTTATTTAT/T<br>TTTATTTATTTATTTATTTAT         | TGGATCTTATGTCAAAC<br>GCCT | TGAAATGCAAATAGAG<br>CCCC    | 59.6                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_17374590  | Ca7                                     | 17374590                      | CTTTTTTTTTTT/CTTTTTTTTTT                                      | GCATCTGTAAACAAG<br>ACCCG  | ACATCGATAAGAGGCA<br>GCGT    | 59.6                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_174141    | Ca7                                     | 174141                        | CATATATATATATATATATAT/CATAT<br>ATATATATATATATATAT             | CATGTTTGCCATGGGA<br>TCTA  | TCTTTATTCGGTTTGCG<br>CTG    | 59.4                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_174353    | Ca7                                     | 174353                        | TAAAAAAAAA/TAAAAAAAAA                                         | ATTGCGCTTGATAGAC<br>CGAC  | CTTTATTCGGTTTGCG<br>CTGA    | 60.2                             | 333                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_17552678  | Ca7                                     | 17552678                      | GTTTTTTT/GTTTTTTTTT                                           | GCCACCAAGTTTATG<br>TCGG  | TTGTTCCATGTCCCTTT<br>TGC   | 60.4                             | 135                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_17576147  | Ca7                                     | 17576147                      | AAAAATAAAATAAAAT/AAAAATAAAA<br>T                              | CATCAAATCATGCAT<br>GTCCA | CCTTCGCATTGGAAC<br>T       | 60.3                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_17685877  | Ca7                                     | 17685877                      | TAAAA/TAAAAA                                                  | CTCATCCCCCTTCATCT<br>TCA | TGTTGAAGCAAAGTA<br>AAACG   | 60.0                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_1776003   | Ca7                                     | 1776003                       | AAC TT/AAC TTACTT                                             | ATGTCTAGCATGGTTT<br>CGCC | TGTTTCATTATTGGAT<br>TGTGC  | 60.1                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_17841305  | Ca7                                     | 17841305                      | TG/T                                                          | TTTATGTCCATGTGCG<br>TGCT | CCACGGTTAAATTTGAT<br>GTTGA | 60.1                             | 346                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_17961701  | Ca7                                     | 17961701                      | GAAAAAAAA/GAAAAAAAA                                           | AAGACCCACAAATTG<br>GAAA  | GAAAGCGCTTCCGTTT<br>ACAG   | 59.3                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_18007228  | Ca7                                     | 18007228                      | TTAATAATAATAATAATAA/TTAA<br>TAATAATAATAATAATAA                | GGCGACACTTCAATGG<br>ACTT | TGCATTGCCATTTCCA<br>GTTA   | 60.1                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_18007668  | Ca7                                     | 18007668                      | CTTATTATTATTATTAT/CTTATT<br>ATTATTATTAT                       | CTCGTGTCTCGGTG<br>GTTT   | AAGTCCATTGAAGTG<br>CGCC    | 60.1                             | 264                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_180427    | Ca7                                     | 180427                        | C/CAGAGGCA                                                    | TCAACAGCAGCTTTGC<br>ATTC | TTTCGCAGCTGGTATG<br>TGAG   | 60.1                             | 280                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_18045160  | Ca7                                     | 18045160                      | ATTTTTT/ATTTTTTTT                                             | AGGTTTTCAACCTAGC<br>GGGT | GAGGAGTCGGAATGG<br>TACA    | 60.0                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |





| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                 |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_18756922  | Ca7                                     | 18756922                      | CTTTTTTTTT/CTTTTTTTTT                                                                           | CAAAAACAAAAGCTTG<br>CGAA   | TGAGACGTCTACCTTG<br>GGGT    | 59.1                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_18769932  | Ca7                                     | 18769932                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTAT/TTTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTAT | AACAAAATCGGGAATA<br>GGGTT  | TGAAATTTGTGCAACTC<br>GGA    | 58.7                             | 773                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_18770611  | Ca7                                     | 18770611                      | GTTTTTTTTT/GTTTTTTTTT                                                                           | TCCGAGTTGCACAAAT<br>TTCA   | TTCAATTTTGAAAAAC<br>GTTC    | 60.2                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_18774607  | Ca7                                     | 18774607                      | CTTTTTTTTT/CTTTTTTTTT                                                                           | CATGTTTCATTTCTGCA<br>CGG   | CGACATATTTAGTCCCT<br>CTTTGG | 60.1                             | 429                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_18780433  | Ca7                                     | 18780433                      | TTATATATATATATATAT/TTATATAT<br>ATATATAT                                                         | TTTTTGTCGTTTGACT<br>GATATT | CCTCTTGCTTTTACGG<br>CTG     | 58.7                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_18793363  | Ca7                                     | 18793363                      | TTATATATATATATATATATATATA<br>TAT/TTATATATATATATATATATA<br>TATAT                                 | GCCAACCCACAAATCT<br>GTCT   | TGCTTCTCGCTGTTTC<br>ATTG    | 60.0                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_18917406  | Ca7                                     | 18917406                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTAT/TTTATTATTATTATT<br>ATTATTATTATTATTATTATTATT             | CAAACCCAAAAATAAGA<br>TGGA  | AAAACCCACCGAATCA<br>CTCA    | 59.3                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_18928675  | Ca7                                     | 18928675                      | TAAAAAAAAAAAAA/TAAAAAAAAAAAA<br>A                                                               | AGCTCACAGAAAAACA<br>CGGG   | TGTCCCGTGCATTTT<br>TAAT     | 60.3                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_18984652  | Ca7                                     | 18984652                      | C/CTT                                                                                           | AGTGGTTGCGCGTTAT<br>CTTT   | AAAGAGGGAACCACT<br>TTGA     | 59.8                             | 173                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_19008569  | Ca7                                     | 19008569                      | ATTTT/ATTTTCTTTT                                                                                | TTCTGGATCGGATCTT<br>GGAC   | TGAAAGTTTCATCTCAA<br>TCATCA | 60.0                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_1902358   | Ca7                                     | 1902358                       | GTTTTAATAATA/G                                                | CAAGTTTATCTCTTCAA<br>TCGCGT | TCGCATATTGCTCTCC<br>CTCT    | 59.8                             | 318                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_19077612  | Ca7                                     | 19077612                      | C/CTTTCCTAATGTCTTAGT                                          | ACTCGAGCCTTGGAAG<br>ATCA    | GTTGGGAGACTTGTGC<br>CCTA    | 60.0                             | 861                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_19095896  | Ca7                                     | 19095896                      | GTTTTTTTT/GTTTTTTTT                                           | GTTTTGCTTCCACTTC<br>CAA     | CTCCTTGACAGATATAG<br>CGCC   | 60.1                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_19128824  | Ca7                                     | 19128824                      | AG/A                                                          | TAAGACTCCGTCCAAC<br>TCGG    | CCCAAACAACCCCTAA<br>AACA    | 60.2                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_19175066  | Ca7                                     | 19175066                      | ACC/ACCC                                                      | ATCAGCATGGTTAGCC<br>CAAG    | TGCGTTTGTGTCATTG<br>GATT    | 60.1                             | 571                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_19263812  | Ca7                                     | 19263812                      | TTTGTTGTTGTTGTTGTT/TTTGTTG<br>TTGTTGTTGTTGTTGTT               | CCTTCTATCCAGCCAT<br>CCAA    | TTCCCCCTCCTTTTATT<br>TAATTG | 60.0                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_19359942  | Ca7                                     | 19359942                      | TA/TATGCCATTGA                                                | ACGAGTGCGGGTATCA<br>ATGT    | GAGAAATGGAGGCAAT<br>GGAA    | 60.4                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_19444691  | Ca7                                     | 19444691                      | TA/T                                                          | AAGCGGTGTCGACTTT<br>TGTT    | ATAAACGTGTGCCGGA<br>AAAT    | 59.8                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_19554104  | Ca7                                     | 19554104                      | GTTTTTTTTTTTT/GTTTTTTTTTTTT<br>TT                             | TGAACCCCATGAAAGA<br>GGAA    | TTTGGAGGGTGAAGT<br>TCTG     | 60.4                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_19562455  | Ca7                                     | 19562455                      | TAAAAAAAA/TAAAAAAAAA                                          | CCTTTCGACTTGGTTT<br>GGAT    | TTATTCGACTCCACAC<br>GCAC    | 59.0                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                          | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                        |                            |                          |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_19581964  | Ca7                                     | 19581964                      | G/GCCTAGGGAAAGAAAAA                                                                                    | ACGTGCATACGATGCA<br>GAAA   | AAGTCGCCATTTGGAA<br>CTTG | 60.3                             | 341                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_19589014  | Ca7                                     | 19589014                      | AATTTATCTATTTATCTATTTAT/AAT<br>TTATCTATTTATCTATTTATCTATTTA<br>T                                        | GGTCGTCCAAATAGTA<br>CCCG   | CCGATTTCCCAAAGGT<br>TTTT | 59.3                             | 358                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_19589201  | Ca7                                     | 19589201                      | TTATATATATATATATATATATAT/TT<br>ATATATATATATATATATATATATAT                                              | GGTCGTCCAAATAGTA<br>CCCG   | AGGAAGCCCAAGTTCC<br>AAAT | 59.3                             | 828                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_19608417  | Ca7                                     | 19608417                      | TTATATATATATATATATATATATAT/<br>TATATATATATATATATATATATAT<br>ATA                                        | TCATATAGCGAGCCCA<br>ATCC   | AAGACCTTGCCTCTTT<br>GGCT | 60.0                             | 524                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_1961188   | Ca7                                     | 1961188                       | CATATATATATATATATAT/CATATAT<br>ATATATATATATAT                                                          | TTAAGATGCCGTGTCA<br>TGGA   | AATACAAAGCAAATGC<br>CCG  | 60.1                             | 593                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_19707176  | Ca7                                     | 19707176                      | TAAAAAAAAA/TAAAAAAAAA                                                                                  | GCCGAGGGGAGAGA<br>TATAG    | CCGTGCCATTTTCACA<br>CTAA | 60.0                             | 523                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_19718791  | Ca7                                     | 19718791                      | GTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAA/GTAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAA | TTAGGGAGCTTACATC<br>GCGT   | TAGCTGTGAGTTGACG<br>ACGG | 59.9                             | 488                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_19731364  | Ca7                                     | 19731364                      | ATTTTTTTTT/ATTTTTTTTT                                                                                  | CACTTGCACGCAAAAC<br>TGAT   | AATGGAACTCGGTTGC<br>TTTG | 59.9                             | 250                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_19786359  | Ca7                                     | 19786359                      | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATAT<br>ATATATATA                                    | AAATTAAAGTTTCAAAC<br>CACGG | TCAGCTCCACTCACAC<br>CATC | 57.3                             | 679                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_19786465  | Ca7                                     | 19786465                      | TACA/TA                                                                                                | AAATTAAAGTTTCAAAC<br>CACGG | TCAGCTCCACTCACAC<br>CATC | 57.3                             | 679                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                              |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_19857139  | Ca7                                     | 19857139                      | AAATAATAATAATAATAATAATA<br>ATAATAATAA/AAATAATAATAAAT<br>AATAATAATAATAATAATAA | CCATATGTCATAGTGC<br>GGTCA | AGAGGCAACAAGAAC<br>CGAA    | 59.4                             | 314                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_19857337  | Ca7                                     | 19857337                      | GAAAAAAAA/GAAAAAAAA                                                          | TTCGGTTCCTGTTTGC<br>CTCT  | ACGAATTCATGTCCCC<br>TTTG   | 59.9                             | 394                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_19860378  | Ca7                                     | 19860378                      | GT/G                                                                         | CCTCAATATGTTGGGA<br>CATGC | TGATTCTCAGGGAGGG<br>TGTC   | 60.2                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_19993135  | Ca7                                     | 19993135                      | ATTTTTTTTT/ATTTTTTTTTT                                                       | TTAGGGTTGGACAGTG<br>GGTC  | GGAGACAATAGCCAAG<br>TGGG   | 59.8                             | 366                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20032652  | Ca7                                     | 20032652                      | TC/T                                                                         | AGTGCCCATCCAACT<br>GAAC   | TGAAGGAATGCAAGGA<br>AACC   | 60.0                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20032669  | Ca7                                     | 20032669                      | TAAAAAAA/TAAAAATAAAATAAAAA<br>AA                                             | AGTGCCCATCCAACT<br>GAAC   | TGAAGGAATGCAAGGA<br>AACC   | 60.0                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20058919  | Ca7                                     | 20058919                      | AATATATATATATATATATATATAT<br>ATATA/AATATATATATATATATAT<br>ATATATATATATA      | CTCATTTGGTACGACT<br>TGTGG | TAATACGGGATGACCC<br>AACC   | 58.1                             | 840                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20059991  | Ca7                                     | 20059991                      | TTGT/TTGTGT                                                                  | TGATTGCATCAAACC<br>AATAA  | TCATCATTTGAGTCATC<br>TTGCC | 59.0                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20154075  | Ca7                                     | 20154075                      | GTTTTTTT/GTTTTTTT                                                            | GAGGACTGGACGTAAC<br>CCAA  | TGGCGATTTCACAAGGA<br>AGGA  | 60.0                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20164032  | Ca7                                     | 20164032                      | AATATATATATATATATATATATAT<br>ATATATATAT/AATATATATATATAT<br>TATATATATATATATAT | CCTCGTCTCCAAATTC<br>CAA   | GAAGCCACCCTGTAA<br>ATGA    | 60.0                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_20332113  | Ca7                                     | 20332113                      | ATTCTTCTTCTTCTTCTT/ATTCT<br>TCTTCTTCTTCTTCTTCTTCTT            | TGCAGATTTTCCCGA<br>T TAG     | ATCACATTTACGAGGC<br>ACCC     | 60.0                             | 355                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20356212  | Ca7                                     | 20356212                      | GATCCGAAGGAAT/GAT                                             | AAGGCTAAACGGGGAT<br>CAAG     | CTCCATAAGCCTTTTGC<br>TCG     | 60.4                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20485643  | Ca7                                     | 20485643                      | ATTTTTTTTTT/ATTTTTTTTTT                                       | GGCTAAATTACATTTGT<br>GGTCCC  | TTGTTGATATTGTGTCG<br>TAGAGCA | 60.8                             | 621                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20501733  | Ca7                                     | 20501733                      | TGTA/TGTAGTA                                                  | TAATGCACCTTCCGTG<br>TCAA     | TTATAGGAAAAAGAAC<br>GAAGGAAA | 60.1                             | 636                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20502470  | Ca7                                     | 20502470                      | CAAAAA/CAAAAAA                                                | TTCCGATTTACTTCCTC<br>TAAATGA | GCTTCCTCCTATTCATG<br>CGT     | 59.6                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20505830  | Ca7                                     | 20505830                      | TAAAAAA/TAAAAAA                                               | GGCATGGAAAATTCTG<br>AAAAA    | AAGAAGCGACGAAGAG<br>AATTTG   | 59.0                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20505889  | Ca7                                     | 20505889                      | ATA/ATAGAAATTA                                                | GGCATGGAAAATTCTG<br>AAAAA    | TTCATTCTCGATTGAG<br>GGC      | 59.0                             | 803                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20505916  | Ca7                                     | 20505916                      | GGA/G                                                         | GGCATGGAAAATTCTG<br>AAAAA    | TTCATTCTCGATTGAG<br>GGC      | 59.0                             | 803                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20509106  | Ca7                                     | 20509106                      | ATAACTAA/ATAA                                                 | TTTCCGAGCAAACAAA<br>ACCT     | TCGCAATTGGTGATGA<br>GTTC     | 59.7                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20510218  | Ca7                                     | 20510218                      | GTAAT/GTAATAAT                                                | TTGAACAATGCAAGAG<br>CCAC     | CTGCTCATGTTTCCCG<br>TTTT     | 59.8                             | 933                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_20510427  | Ca7                                     | 20510427                      | TTT/TTTATTAGTGTTAAAATT                                        | TGCATTGCTCCCTAGACACA      | GGCACTGCTTTATGCACTCA          | 60.4                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20510596  | Ca7                                     | 20510596                      | TAAAAATAAA/TAAAAATAAAAAATA<br>AAAAAAATAAA                     | TCGTCGGCTAAATCCA<br>ACTC  | GGCACTGCTTTATGCACTCA          | 60.2                             | 366                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20519746  | Ca7                                     | 20519746                      | CTTTTTTT/CTTTTTTTT                                            | TGGGGATGTGGGAAAA<br>ATAA  | AGTGGCATTCTTTGTGAATGA         | 60.0                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20537234  | Ca7                                     | 20537234                      | CAAAAA/CAAAAAA                                                | TCGCACAGGATGAGAA<br>CTTG  | TCAGCCTCTCCATCAAA<br>CCT      | 60.0                             | 179                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20559674  | Ca7                                     | 20559674                      | ATGT/ATGTGT                                                   | TTTTGCGTTTTGCTTT<br>GTG   | TTCTGCAAATTTCAAATGC           | 59.9                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20566181  | Ca7                                     | 20566181                      | CATATATA/CATATA                                               | ATTGTTCCAGCTTTGCACT       | CATTCAAATGTTTGCAACAACC        | 59.7                             | 188                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20566222  | Ca7                                     | 20566222                      | T/TC                                                          | ATTGTTCCAGCTTTGCACT       | CATTCAAATGTTTGCAACAACC        | 59.7                             | 188                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20566359  | Ca7                                     | 20566359                      | T/TA                                                          | GGTGACTGGTGGGATT<br>GTTC  | TGAAAGTTCTCTTTAAT<br>CTGTCACG | 60.2                             | 370                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20566739  | Ca7                                     | 20566739                      | ATTT/ATT                                                      | TGTAATATGTTTAGGAGTTTCAACG | CACCTTCCTTGTTGCCGAT           | 59.9                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20566755  | Ca7                                     | 20566755                      | AT/A                                                          | TGTAATATGTTTAGGAGTTTCAACG | CACCTTCCTTGTTGCCGAT           | 59.9                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_20567011  | Ca7                                     | 20567011                      | TAAAAAAA/TAAAAA                                               | TGGAATTCATGTGCTT<br>TGGA  | CACCTTCCTTGTTCC<br>GAT    | 59.0                             | 281                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20574766  | Ca7                                     | 20574766                      | GTTT/GTTTT                                                    | GGGAGATCGGAATGCA<br>TAGA  | ATGCGTGACGGTGCA<br>AATA   | 60.0                             | 276                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20617780  | Ca7                                     | 20617780                      | C/CAAT                                                        | GGCGAGGGATGGAATT<br>TTAG  | GAATTGGGACTTCTGC<br>CGTA  | 60.8                             | 777                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20623367  | Ca7                                     | 20623367                      | ATGTCTAAGGTGTC/ATGTC                                          | CTTTGAAAAATGGCCAC<br>ATGA | ATTAGATGACCGTCG<br>CACC   | 59.5                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20623409  | Ca7                                     | 20623409                      | TAACAA/TAA                                                    | AGGTGTCGAAGGATCA<br>CCAC  | CTCGAGGAGACGAGAA<br>ATGC  | 60.0                             | 212                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20624207  | Ca7                                     | 20624207                      | TATTTAATTTAATTTAAT/TATTTAAT<br>TTAATTTAATTTAAT                | ATTCCCCGTGCACAAA<br>AATA  | AATCCCCGTTAACCCCG<br>TAAC | 60.2                             | 390                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20626314  | Ca7                                     | 20626314                      | AAAA/AAAATAAA                                                 | TCAGTTATCGTCGTTG<br>GTCG  | TTCATCGAACCGACAT<br>CATC  | 59.7                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20626429  | Ca7                                     | 20626429                      | CTAATA/CTAATAATA                                              | TCAGTTATCGTCGTTG<br>GTCG  | CGTGCAACATTTTCTT<br>CCA   | 59.7                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_20630370  | Ca7                                     | 20630370                      | TAAAAAAA/TAAAAA                                               | ATCAGGCTGGTTTGAT<br>TTGG  | CCAAATGTGTGGTGT<br>TCCA   | 59.9                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_2066755   | Ca7                                     | 2066755                       | CAAAAAAAAA/CAAAAAAAAAA                                        | TCGTTGGAGAGTTGGT<br>GATG  | TGGGATGGTAAGCATT<br>TGAA  | 59.7                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                             |                              |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_20969765  | Ca7                                     | 20969765                      | CTT/CT                                                                      | TGAGTAATTGCCGCTC<br>AGTG     | TTGTCCACCATTATCGA<br>CCTC    | 60.0                             | 103                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21099731  | Ca7                                     | 21099731                      | T/TGCGCAA                                                                   | GAGAAATCAAAATTGC<br>CCCA     | AGTGCCCTCCTGTTCTT<br>GAGA    | 59.9                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21151037  | Ca7                                     | 21151037                      | AAATAATAATAATAATAATAATA<br>ATAATAATAA/AAATAATAATAATAAT<br>AATAATAATAATAATAA | CCCGGAGATGCGAGTA<br>CTAA     | TTGGCACATCTACTCAA<br>CCG     | 60.2                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21171384  | Ca7                                     | 21171384                      | ATTTTTTTTT/ATTTTTTTTT                                                       | GTTTCGCCGTTTTATGT<br>CGTT    | TGTGGCTGTAAACCTG<br>CAAA     | 60.0                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21207750  | Ca7                                     | 21207750                      | GCATCCCCA/GCATCCCCATCCCCA                                                   | TTTTATCCACCAAAAAT<br>TCAAAAA | GAATGAGCAAGAAAGA<br>CGGC     | 58.9                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21264825  | Ca7                                     | 21264825                      | TTATATATATATATATATATATATA/<br>TATATATATATATATATATATATATA<br>ATATA           | GTCATTTGGAATGGCG<br>ACTT     | TTGTCCCAATGTTACAG<br>CCA     | 59.9                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_2128379   | Ca7                                     | 2128379                       | TTCTCTCTCTCT/TTCTCTCTCT                                                     | TGCTTCATGCGTTTCA<br>AGAC     | CTCGTGACAAAACTT<br>TTGA      | 60.0                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21372221  | Ca7                                     | 21372221                      | GCC/GC                                                                      | ACTTCTTTTCATGTTTGG<br>CCG    | GCAACACGCACGAGTT<br>ACAC     | 60.1                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21373697  | Ca7                                     | 21373697                      | AATATATATATATATATATA/ATA<br>TATATATATATATATA                                | TTTAAATTTGCATGTTA<br>GTCGTCA | CCCGTATATGGAACAA<br>TGCG     | 58.8                             | 620                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21434053  | Ca7                                     | 21434053                      | ATTTTTTTTT/ATTTTTTTTT                                                       | TTTTTGTTGGCTAAGT<br>GGAG     | GAAGCACAAGAAATAA<br>AAGCAACA | 57.9                             | 939                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_21448520  | Ca7                                     | 21448520                      | T/TATAATTATTA                                                 | CATGCAGTGCAATGTC<br>CTTT  | TGGTGCAGTGGCAATA<br>AAAA    | 59.7                             | 358                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21598915  | Ca7                                     | 21598915                      | TTATATATATATATATAT/TTATATAT<br>ATATATAT                       | TTTCATGGTTCGCATC<br>ACAT  | AACCCCATGTGTGAAA<br>TGCT    | 59.9                             | 242                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21670841  | Ca7                                     | 21670841                      | A/AAGAT                                                       | TGACAAATCTTTGCAAC<br>CCA  | ATTGCTCATTTCATGCC<br>CTC    | 60.1                             | 217                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21675094  | Ca7                                     | 21675094                      | AAA/AAACAA                                                    | TTCCCTCTGGATCAC<br>AACC   | CAACCTCTTCACGCAT<br>CAAA    | 59.9                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21678026  | Ca7                                     | 21678026                      | TTAAAATTTTAATATAAAAATAAAATTT<br>TA/TTAAAAATTTTA               | GAGCTTTGTTGGAACA<br>TGGA  | ATAACCGTGCCAATAG<br>GTGG    | 58.7                             | 850                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21685577  | Ca7                                     | 21685577                      | TT/TTAT                                                       | TTTATAAATTGGCCCCA<br>TCG  | TAGGGGGACCAAGAAA<br>CTGG    | 59.6                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21728387  | Ca7                                     | 21728387                      | CAAAA/CAAA                                                    | ATCTCTGCGCAATATC<br>GCTT  | AGCCGACTTTTCCTAC<br>CACA    | 60.0                             | 674                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21729097  | Ca7                                     | 21729097                      | TAAAAA/TAAAA                                                  | TGCTCAAAAGGGGAAG<br>AAAA  | GCCACGTGTTGAAAG<br>AAGT     | 59.8                             | 240                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21729303  | Ca7                                     | 21729303                      | T/TC                                                          | TTGCTCAAAAGGGGAA<br>GAAA  | TTGTTATTTTCTTTATG<br>CCGTTG | 59.8                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21731192  | Ca7                                     | 21731192                      | ATTTTTTTTT/ATTTTTTTT                                          | TGATGGATACCCTTTT<br>GAACG | ACCGCTCCAGCTGAGA<br>ATAA    | 59.8                             | 838                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                       | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                     |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_21772693  | Ca7                                     | 21772693                      | AATATATATATATATATATATA/AA<br>TATATATATATATATATATATA                                                 | CAACATGTCCTCATG<br>TCCA      | TGATGGCTTGTGTCAT<br>TGGT    | 57.9                             | 720                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21786856  | Ca7                                     | 21786856                      | CAAA/CAAAA                                                                                          | TGAAAAACGTGTTGCA<br>GCTAA    | TAGAAGGCTGCACAAC<br>TCCA    | 59.5                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_21801971  | Ca7                                     | 21801971                      | GTTTTATTTTATTTTATTTTATTTAT<br>TTTATTTTATTTTATTTTA/GTTTTAT<br>TTTATTTTATTTTATTTTATTTTATTT<br>TATTTTA | GCTTCATTTGGAGCTT<br>TTGC     | TTGGGGATTTCATTT<br>GAGA     | 60.0                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22015790  | Ca7                                     | 22015790                      | T/TTCGG                                                                                             | ACCTCCGTCATCATTTT<br>TCG     | TTCCCCGAACACAGAA<br>ACTC    | 59.9                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22036269  | Ca7                                     | 22036269                      | GCTC/G                                                                                              | GCTCAGCCTTGAAATC<br>GAAC     | TTCATCATCATCTTCAA<br>ACAAAA | 60.0                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22036958  | Ca7                                     | 22036958                      | GAAAAAAAA/GAAAAAAAAA                                                                                | TGAAACATCAAATTGG<br>GAAAAA   | TTGATGGCAATGCTATT<br>GGA    | 59.3                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22038011  | Ca7                                     | 22038011                      | C/CT                                                                                                | CTCCAAATTTCCAGCC<br>AAAA     | ACACGGACGGGTCTTG<br>TATC    | 60.0                             | 822                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22039243  | Ca7                                     | 22039243                      | ACC/AC                                                                                              | CGTTATTGCAACCACA<br>ACCA     | CAATTCAACTCCGACG<br>TGTC    | 60.4                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22043317  | Ca7                                     | 22043317                      | T/TG                                                                                                | TGGTTCAAATGCTGTA<br>ATCTTCTC | ATTGCTCAATACACG<br>GGTC     | 59.7                             | 884                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22045478  | Ca7                                     | 22045478                      | ATTTTTTTT/ATTTTTTT                                                                                  | TGTGGTGTTCCTCAAA<br>GACA     | CAAAGCGAAGTGCAAA<br>ATGA    | 60.0                             | 246                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                           | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                         |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_22046891  | Ca7                                     | 22046891                      | CATAATAATAATAATAATAATAA<br>TAATAATAATAATAAT/CATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAAT | ATAATTGCTTTGCG<br>GTTG    | TTCTGTGAGCAAGGCT<br>GATG | 60.0                             | 319                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22046957  | Ca7                                     | 22046957                      | CTATATATATATATATATATATAT/<br>CTATATATATATATATATATATAT                                                   | ATAATTGCTTTGCG<br>GTTG    | TTCTGTGAGCAAGGCT<br>GATG | 60.0                             | 319                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22046996  | Ca7                                     | 22046996                      | TGCGCGC/TGCGC                                                                                           | ATAATTGCTTTGCG<br>GTTG    | ACCTGGTCGTAGATGC<br>CACT | 60.0                             | 414                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22091542  | Ca7                                     | 22091542                      | GAAAAAAAAA/GAAAAAAAAA                                                                                   | CCCCAACCTCCATTC<br>TATT   | AATTGCAAGATGAGGG<br>CAAC | 60.0                             | 347                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22101651  | Ca7                                     | 22101651                      | CTTTATT/CT                                                                                              | AACCCAAGTTCCAAAT<br>GACG  | GAAGCCCAAGTTCCAA<br>ATGA | 59.8                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22126044  | Ca7                                     | 22126044                      | TAAAAAAAAA/TAAAAAAAAA                                                                                   | TGAAGCAACAAAGCTG<br>ATGAA | TTGTTGCAACCACTTCC<br>AAA | 59.6                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22315085  | Ca7                                     | 22315085                      | ATTTTTTTTT/ATTTTTTTTT                                                                                   | TTTAAGCCCATTTTCCA<br>CCA  | AGGTGCAAGTGTTTC<br>CTCC  | 60.3                             | 836                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22325946  | Ca7                                     | 22325946                      | CACTCCGGACTGCGCGACTCCGGA<br>CTGC/CACTCCGGACTGC                                                          | CTTCAACATGCGGGTC<br>ATC   | AAGATGCACGTGGGGT<br>AGAC | 60.1                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22523165  | Ca7                                     | 22523165                      | CCGG/CCGGACGG                                                                                           | ACCTTGTGGATGGCAG<br>TTTC  | TGGCATTGATGATGGC<br>TTTA | 60.0                             | 328                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22523183  | Ca7                                     | 22523183                      | GGCG/GG                                                                                                 | ACCTTGTGGATGGCAG<br>TTTC  | TGGCATTGATGATGGC<br>TTTA | 60.0                             | 328                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                 |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_22561436  | Ca7                                     | 22561436                      | CAAAAAAAAA/CAAAAAAAAA                                                                           | AGGTTGTTGCATGGAG<br>AAGG    | AAAAGTCATACCCCGT<br>GATCC | 60.1                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22569920  | Ca7                                     | 22569920                      | ATATATT/A                                                                                       | TCTCTCGAAGTGTTTG<br>GGCT    | TGGACTGGCATGATTG<br>GATA  | 60.0                             | 811                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22587401  | Ca7                                     | 22587401                      | TATATATATATATATATATATATAT<br>AT/TATATATATATATATATATATA<br>TATATATAT                             | AAGGAACAAAACGTCA<br>TTTTCAA | AGTCAGACGCTACTCG<br>GCAT  | 59.9                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22960245  | Ca7                                     | 22960245                      | AATATATATATATATATATATATAT<br>ATATATATATATAT/AATATATATATA<br>TATATATATATATATATATATATAT<br>ATATAT | TTGGTATTGAACTCGG<br>AGGC    | CTTTCAGTTCGGTTAC<br>GGT   | 60.1                             | 700                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_22969908  | Ca7                                     | 22969908                      | CTT/CTTT                                                                                        | AATGTGCTGATCTGTG<br>AGCG    | CCTTGGAGTATTCTCG<br>GCAG  | 60.0                             | 894                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_23037556  | Ca7                                     | 23037556                      | ATTTTTTTTT/ATTTTT                                                                               | TTGAGTTTCAAACCTGC<br>CAAG   | GGCTTGGGGCTCCTTA<br>CTAC  | 58.1                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_23075370  | Ca7                                     | 23075370                      | AAATAATAATAATAATAATAATA<br>ATA/AAATAATAATAATAATAATA<br>ATAATAATAATAATA                          | AACGGATGACCCTCTC<br>CTCT    | TTTTGGTTGGGATTTTT<br>GGA  | 60.1                             | 812                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_23184353  | Ca7                                     | 23184353                      | CTATATATATATATATAT/CTATATAT<br>ATATATATATAT                                                     | AGTGGTTGATTGTGGT<br>TCGG    | TTTTTCGGGACACTCCT<br>TTG  | 60.8                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_23195329  | Ca7                                     | 23195329                      | GATATATATATATATATATATA/GA<br>TATATATATATATATATATATATAT<br>A                                     | GCATGGCTTGATCTGA<br>TTTG    | TAAATCGCGGTATGA<br>GGAC   | 59.2                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_23264424  | Ca7                                     | 23264424                      | AATATATATATATATATATAT/AAT<br>ATATATATATATATATAT                                                 | GCGACCCACTTGAAAC<br>AAAT    | CCACCGATGCCTAACT<br>CATT  | 60.0                             | 169                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                               | Forward primers (5'-3')       | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------|-------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                             |                               |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_2327043   | Ca7                                     | 2327043                       | CACACCCAGACACCCAG/CACAC<br>CCCAG                                                                            | CTAAACCGGCAACCAG<br>AGAA      | TGTGTGGTGATGTGC<br>GATG       | 60.2                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_23425466  | Ca7                                     | 23425466                      | AATATATATATATATATATATAT<br>ATATATATATATATATAT/AATATATA<br>TATATATATATATATATATATAT<br>ATATATATATATATATATATAT | GACCGAGTTGAGAAAA<br>GATATGAGA | CGTAATTTTTCACGTTT<br>CCTC     | 60.1                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_2349174   | Ca7                                     | 2349174                       | ATTTTTTTTTT/ATTTTTTTTTT                                                                                     | TGCCAAGTGGAATCAC<br>TTTTT     | TCTTCGGATATGCAAC<br>GTGA      | 59.6                             | 727                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_23780060  | Ca7                                     | 23780060                      | TTATATATATATATAT/TTATATATAT<br>ATAT                                                                         | CGCTCGTCTATGCGAT<br>TGTA      | TAAATCTCCGCTCGC<br>AACT       | 60.0                             | 946                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_23797195  | Ca7                                     | 23797195                      | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATAT<br>ATATATATA                                         | AAGAAATCGCGAGTCA<br>CAGG      | TTAATAGAACGCGCCA<br>AAGG      | 60.4                             | 652                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_23803981  | Ca7                                     | 23803981                      | GTTTT/GTTT                                                                                                  | GCACCGTGAGTAAAT<br>CGGT       | ATGTTTTGGATTTTGGC<br>TCG      | 60.0                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_2380600   | Ca7                                     | 2380600                       | ATTTAATTTGTTTAA/ATTTAATTTGT<br>TTAATTTGTTTAA                                                                | CCACCATTTTGTGAC<br>GTG        | TGGAAAAACCACAAATA<br>TTACATTG | 59.8                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_23868384  | Ca7                                     | 23868384                      | GAAAAAAAA/GAAAAAAAAA                                                                                        | ATCAAGCCACTGGAGA<br>CACC      | TTTTGAATGGAAGACG<br>TCCC      | 60.1                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_23882859  | Ca7                                     | 23882859                      | AATATATATATATATATA/AATATA<br>TATATATATATATATA                                                               | TATTTTGATTTTGGCT<br>CGG       | ATGGGTTTCGCGTAGA<br>CAAC      | 59.9                             | 400                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_23903739  | Ca7                                     | 23903739                      | TAAATAA/TAAATAAAATAA                                                                                        | TGAGCATGGAATTTGG<br>TTGT      | TGAATTCATGGCTAAG<br>AAGCCT    | 59.0                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                         | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                       |                             |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_23907440  | Ca7                                     | 23907440                      | AATATATATAT/AATATATATATAT                                                             | TTGGAGAATTCAAAAAT<br>AAGGCA | CGTGACAAAGCACGAA<br>AGAA | 60.0                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24027767  | Ca7                                     | 24027767                      | GATAATAATAATAATAATAATAA/<br>GATAATAATAATAATAATAATAA<br>TAA                            | ACAATGGATGCTCACG<br>ACAC    | GTTTCCCATCCTCCCTT<br>TGT | 59.6                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24037474  | Ca7                                     | 24037474                      | ATT/ATTT                                                                              | ATGTTGAAGTCGGGAA<br>AACG    | TCTTCTGTGGCCGAC<br>TCTT  | 60.0                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24211988  | Ca7                                     | 24211988                      | CATTATTATTATTATTATTATT/C<br>ATTATTATTATTATTATTATTATT                                  | ACTGGGGATGCAATTT<br>TCTG    | AATGGGTCAAAGAGG<br>AGGAA | 59.9                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24267624  | Ca7                                     | 24267624                      | CTTTTTTTTT/CTTTTTTTTTT                                                                | TTCTCCTGAAGCTGT<br>CGGT     | AACCAATCCACATAAC<br>CCA  | 60.0                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24274526  | Ca7                                     | 24274526                      | GAAAAAAAAA/GAAAAAAAAA                                                                 | AAGAGAGAGGGATGCA<br>TGAGA   | ATCATCCACCCTAGGA<br>ACCC | 59.0                             | 869                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24282647  | Ca7                                     | 24282647                      | TAAAAAAAA/TAAAAAAAA                                                                   | GGAACGAGGGACATAT<br>CAAGA   | CGGTTTAGGCCCTAC<br>ATTT  | 59.0                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_2430437   | Ca7                                     | 2430437                       | AATTATTATTATTATTATTATTAT<br>TATTATTATTATTA/AATTATTATTAT<br>TATTATTATTATTATTATTATTATTA | GCGGTTTCAATTTTGT<br>GAAG    | GAAGATCGAATCCAC<br>GATG  | 60.6                             | 571                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24347972  | Ca7                                     | 24347972                      | TAAAA/TAAAAA                                                                          | CTCTCATCTGAGGGCA<br>AAGC    | CGATTGAATTAAGCCC<br>AGGA | 60.1                             | 356                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24348355  | Ca7                                     | 24348355                      | TAA/TAAA                                                                              | TCCTGGGCTTAATTCA<br>ATCG    | CGTTCCTGAGGGAATT<br>GTGT | 60.0                             | 378                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                 |                            |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_24348515  | Ca7                                     | 24348515                      | CAA/CAAA                                                                                        | TCCTGGGCTTAATTCA<br>ATCG   | CGTTCCTGAGGGAATT<br>GTGT      | 60.0                             | 378                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24354887  | Ca7                                     | 24354887                      | AATATATATAT/AATATATATATAT                                                                       | CAATTCCCACAGGTAC<br>GCTT   | GGAAGACCCCTTGCAAA<br>ATCA     | 60.0                             | 283                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_2438236   | Ca7                                     | 2438236                       | TTATATATATATATATATATAT/TTAT<br>ATATATATATATATATATAT                                             | CATGTTTGATACCATAA<br>TGCGC | TGGGGATTGTTTATCTA<br>GAAGTGTC | 60.1                             | 341                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24421160  | Ca7                                     | 24421160                      | AATATATATATATATATATATA/AAATA<br>TATATATATATATA                                                  | AGGAAGCCCAAGTTCC<br>AAAT   | ACAGCCAACAACCACA<br>TCAA      | 59.9                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24436102  | Ca7                                     | 24436102                      | GTTATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTAT/GTTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTAT | TGCGACGCTTGATCGT<br>TAAT   | AGTTTCGAAGCAATCC<br>GAGA      | 61.7                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24450388  | Ca7                                     | 24450388                      | TTATATATATATATATATAT/TTATAT<br>ATATATATATATATAT                                                 | TTGTTAGTTTGACGAG<br>GGCA   | TGGGTGCTATTTGCAA<br>TCAA      | 59.3                             | 380                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24477362  | Ca7                                     | 24477362                      | ATATATATATATATGT/AT                                                                             | CAATTGAGTTGCGACG<br>AGAG   | TGAAGTTGGGAAATCC<br>TTGC      | 59.6                             | 434                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24485265  | Ca7                                     | 24485265                      | C/CAACTTT                                                                                       | GTCCACCCCTAGGAGC<br>TTTC   | CGGACCAAAAATTAAA<br>GCGA      | 60.1                             | 986                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24485905  | Ca7                                     | 24485905                      | GAAAAA/GAAAA                                                                                    | ATTCAATATTTCCCCCA<br>GCC   | TCACCCCAATTCCATTC<br>ATT      | 60.0                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24486242  | Ca7                                     | 24486242                      | CTTTTTTTTT/CTTTTTTTT                                                                            | ATGAATGGAATTGGGG<br>TGAA   | GGGCATGGCAACCTAA<br>AGTA      | 60.0                             | 341                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                           | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                         |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_24502290  | Ca7                                     | 24502290                      | T/TAAGCA                                                                                | AATTTGGCAGAACAGG<br>GATG    | AGAAAAGCAGGGGAAG<br>CAAT | 59.9                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24535021  | Ca7                                     | 24535021                      | GAATAATAATAATAATAATAATA<br>ATAATAATAATA/GAATAATAATAATA<br>ATAATAATAATAATAATAATAATA<br>A | CCGAGTCGGATCTATC<br>AAAA    | GCGATAGAAATGGGAC<br>CTGA | 57.8                             | 852                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24651390  | Ca7                                     | 24651390                      | TAAAAAAAAA/TAAAAAAAAA                                                                   | CAACCGTTTTGATGTTT<br>TATTCA | GCTGATGGTTCTTTTG<br>GGAA | 58.9                             | 847                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_24861630  | Ca7                                     | 24861630                      | GACTT/GACTTACTT                                                                         | TTCCATTCTCCACAA<br>AGC      | TCATTCCAGAAGGAGA<br>TGGG | 60.1                             | 548                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_25060530  | Ca7                                     | 25060530                      | GTTTTTTTT/GTTTTTTTTT                                                                    | TTGTCGATTTGGCACT<br>TCAG    | TGAATGTGGATCCCCT<br>CAAT | 59.8                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_2512120   | Ca7                                     | 2512120                       | T/TAA                                                                                   | TCCCTAAAAATCAAAAC<br>AGGAA  | ATCGACAAGATCACAA<br>GGGC | 57.8                             | 770                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_25131144  | Ca7                                     | 25131144                      | ATATTATTATTATTATTATTATTA<br>TTA/ATATTATTATTATTATTATT<br>ATTA                            | TTGTTAAAAACGTGTG<br>CCGA    | CGAAGACGATCATCCT<br>TGCT | 60.1                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_25170286  | Ca7                                     | 25170286                      | TAAAAAA/TAAAAAA                                                                         | GTTTGTGGGAGCAGAG<br>CTTC    | CCCTTTCAACGCATCC<br>TTTA | 60.0                             | 629                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_25219421  | Ca7                                     | 25219421                      | CAAA/CAA                                                                                | TGGGATATGGAAGGT<br>TGAG     | CAGATTCTACGGGAA<br>ACGA  | 59.7                             | 202                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_2525335   | Ca7                                     | 2525335                       | CAATACAATTGATTAATA/CAATACA<br>ATTGATTAATACAATTGATTAATA                                  | TGGTGGAAAAATAGCA<br>TTTGG   | CCTCTCCGAATGACT<br>CAAG  | 59.8                             | 868                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                       |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_25342809  | Ca7                                     | 25342809                      | TAAAAAAAA/TAAAAAAAA                                                   | CATTCAACAGCCACAT<br>GACC  | CGGTACCGCATTGAG<br>TATT    | 60.0                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_25411773  | Ca7                                     | 25411773                      | CTATATATATATATATATATATAT<br>ATA/CTATATATATATATATATATA<br>TATATATATATA | GAGGATGCAGTTCCAG<br>AAGG  | GCTTGCTAATCGTTTAT<br>CACCA | 59.8                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_25436582  | Ca7                                     | 25436582                      | GAAAAAAAA/GAAAAAAAA                                                   | ATTTTGTGAGAGCCAAG<br>CCAA | GAACGTGTTTCGGTAAG<br>GGTG  | 59.8                             | 786                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_25540307  | Ca7                                     | 25540307                      | CTTTT/CTTT                                                            | CCTCAGATGAGAGCCA<br>GGAC  | GAGCGCTATTACAGTT<br>CGGC   | 59.9                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_25556203  | Ca7                                     | 25556203                      | TAAA/TAA                                                              | TGCATCAAACTCCAAT<br>CCA   | ATTGAATGGAAGATGG<br>TGGG   | 60.0                             | 236                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_25626892  | Ca7                                     | 25626892                      | CGG/CGGG                                                              | TTGGCCAAGTCCCTGT<br>TTAC  | CCCGTGATAGGCAGTA<br>CGTT   | 60.0                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_25717539  | Ca7                                     | 25717539                      | TCAACCTATCAGGCCTACAACCTAT<br>CAGGCCTA/TCAACCTATCAGGCCT<br>A           | GCCTGAGCCTGACCTA<br>CAAC  | TAGGGGCCTATGACCT<br>GATG   | 59.9                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_25916920  | Ca7                                     | 25916920                      | TAAAAAAAAA/TAAAAAAAAA                                                 | GGAGGCATTGTTTCCT<br>CAAA  | TACCGATTAGTACCCT<br>GGCG   | 60.1                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_26035041  | Ca7                                     | 26035041                      | TAAAAAAAAA/TAAAAAAAAA                                                 | TAAAGAGATTCGCAGC<br>GGTT  | CATGTTTTCGAAGCTCA<br>CCA   | 60.0                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_26075420  | Ca7                                     | 26075420                      | TTATATATATAT/TTATATATATATAT                                           | TATTTTGATTTTGGCT<br>CGG   | TTTGGATCAAGGAGAA<br>ACGG   | 59.9                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_26086416  | Ca7                                     | 26086416                      | GTATATATATATATATATATATAT/ATATATATATATATATATATATAT             | TGAAAAGACGAGCAAC<br>AAGG | CTGCCAAAAGCCCTCA<br>TAAA   | 59.0                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_26095745  | Ca7                                     | 26095745                      | GAAAAAAAA/GAAAAAAAAA                                          | GTGGCGTCTCACTGTT<br>GAAA | TGCTTTACGGAAGAAA<br>CAATCA | 59.9                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_26158210  | Ca7                                     | 26158210                      | GTATATATATATATATATATATATATAT/ATATATATATATATATATATATAT         | TTGTTGACACCGAGTT<br>AGCG | TTTCGCAAAACTCAA<br>AGGA    | 59.9                             | 174                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_26160184  | Ca7                                     | 26160184                      | AG/A                                                          | GTGGCTACCTTCTTGG<br>GTGA | TTTCATCGCCGAAACC<br>TATC   | 60.1                             | 141                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_26221720  | Ca7                                     | 26221720                      | AATATATATATATATATATAT/AAATATATATATATAT                        | CTTGGGAATTGGAGAG<br>CAAG | GGGTTTCTTTCCTTGAA<br>GCC   | 59.8                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_26228410  | Ca7                                     | 26228410                      | GAAAAAAAA/GAAAAAAAAA                                          | ATGGTGCAAAATGGTG<br>ACAA | GAAAGTCGGTGCATGG<br>AAGT   | 59.8                             | 304                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_26233274  | Ca7                                     | 26233274                      | TAAAAAA/TAAAAAA                                               | TACGCCATCCAAAAT<br>GTGA  | CCCTCATCCGAAAAGA<br>TGAA   | 59.9                             | 945                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_26235537  | Ca7                                     | 26235537                      | TTATATATATATA/TTATATATATATA<br>TATA                           | TGCGACCTCAGTTTCT<br>CAAA | GGGGTCATAGCATCCC<br>CTAT   | 59.6                             | 157                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_26277638  | Ca7                                     | 26277638                      | AT/A                                                          | GCCCTCAGATGAGAGT<br>CAGG | GGAAGGCTTGTCGACT<br>TGAG   | 59.9                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_26331505  | Ca7                                     | 26331505                      | AATATATATAT/AATATATATATATATATATATATAT                         | TCTTTAGTAGCCCGCC<br>AAGA | CGTTTTGGGTCGTTGT<br>TACC   | 60.0                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                              | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                            |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_27043217  | Ca7                                     | 27043217                      | T/TC                                                                                       | TGCGCATTGAGACTCA<br>AAAA   | TCATATGCCAGATTG<br>ATCG   | 60.5                             | 774                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_27108973  | Ca7                                     | 27108973                      | TTATATATATATATATATAT/TTATA<br>TATATATATATATATATATA                                         | GAAACAATCGATTTTGA<br>TCCC  | CATTGGTTTTGTGAGA<br>GGGAA | 58.4                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_27341260  | Ca7                                     | 27341260                      | A/AG                                                                                       | CACGATCCACACCAAA<br>ACAC   | TCTCCCTCCTTCTCCCA<br>TTT  | 59.9                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_27346895  | Ca7                                     | 27346895                      | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATATAT                                      | TGCTTGATTGCTTGAG<br>TTCC   | CGCGCAGATTGTCAAA<br>TAGA  | 59.0                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_27365034  | Ca7                                     | 27365034                      | CTTT/CTTTT                                                                                 | TATGGTGCTGTGAAAA<br>GGCA   | GCAAGAGATGGAAAA<br>GGGA   | 60.3                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_27396861  | Ca7                                     | 27396861                      | TATAATAATAATAACTAATAATAA<br>TAATAATAATAA/TATAATAATAAT<br>AATAACTAATAATAATAATAATAA<br>TAATA | AACAATTGATTAGTGG<br>CGCA   | TGCTCTTTAGCGTCG<br>GTTT   | 59.2                             | 427                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_27521328  | Ca7                                     | 27521328                      | CAAA/CAA                                                                                   | GCCAAATTCCTCTTTT<br>TCC    | CCTTCCACACAACCA<br>CAGA   | 60.0                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_27745203  | Ca7                                     | 27745203                      | TTATATATATATATATATATATATA<br>TATAT/TTATATATATATATATATA<br>TATATATATATAT                    | TCAAAATGCCCTACAC<br>TCAAAA | GTCACCTCCTGGACCT<br>ACGG  | 59.6                             | 894                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_27761690  | Ca7                                     | 27761690                      | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATAT                                      | AAATTCGAGCACTTA<br>CGCT    | GTTTGTGAGTAAGCTC<br>GCCC  | 60.0                             | 873                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_27818786  | Ca7                                     | 27818786                      | GAAAAAAAAA/GAAAAAAAAA                                                                      | CAAAAGGGCAACATGC<br>CTAT   | GCAAGATCGCATTCTT<br>GTCA  | 60.0                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_27833544  | Ca7                                     | 27833544                      | C/CCGATCCCTT                                                  | ATGACGGTGATTTCGG<br>TTTC  | GTTTGCTTTCCTTTTGG<br>TGC  | 59.8                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_27834486  | Ca7                                     | 27834486                      | TAAAAAAAA/TAAAAAAAAA                                          | ATTAACGCGAAAAGG<br>CGCT   | TCCAACGATCGATGTC<br>TACG  | 60.1                             | 330                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_27875250  | Ca7                                     | 27875250                      | GAAAAAAAA/GAAAAAAAAA                                          | GGTTGATTATCGTCCG<br>CTGT  | CCTATTCTCTGCTTTG<br>GCG   | 60.0                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_27875295  | Ca7                                     | 27875295                      | TTCT/TTCTCT                                                   | GGTTGATTATCGTCCG<br>CTGT  | CCTATTCTCTGCTTTG<br>GCG   | 60.0                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_2789203   | Ca7                                     | 2789203                       | TTATATATATATATATATATA/TTA<br>TATATATATATATATATATA             | GAATTAGCCGCTATG<br>TTCA   | CCATGCTTCAAAGCT<br>GACA   | 57.9                             | 842                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_27979863  | Ca7                                     | 27979863                      | TGGG/TGGGG                                                    | ACCCAATTTGTCGTGG<br>TGAT  | TGATCCCTCACTTAAT<br>GCC   | 60.1                             | 251                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_2808679   | Ca7                                     | 2808679                       | GAAAAAAAAA/GAAAAAAAAA                                         | ACTTCCCTGTGGAACG<br>ACAC  | ATATGCACGGAACGAA<br>AACC  | 60.0                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_28089294  | Ca7                                     | 28089294                      | GAAAAA/GAAAAA                                                 | CGTAAAGTCCACTTCC<br>GTTTC | CAACAGATGTTGTGCG<br>TGTC  | 58.8                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_28129563  | Ca7                                     | 28129563                      | CAAAAAAAAAA/CAAAAAAAAAA<br>AAAA                               | TCTTCACCAAAACAAAC<br>CCA  | GCATCGTAAAGTTGCA<br>CATCA | 59.0                             | 835                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_28189950  | Ca7                                     | 28189950                      | CTTT/CTTTT                                                    | CTCAACATGCATGCAA<br>AACC  | TCCCAACCAATAAAC<br>CAA    | 60.1                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                | Forward primers (5'-3')        | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------|--------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                              |                                |                             |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_28190197  | Ca7                                     | 28190197                      | AGTTTATTTGG/AGTTTATTTGGTT<br>ATTTGG                                                          | TTGGTTTATTTGGGT<br>GGGA        | ACCAGGAAAAGAAGAA<br>GGGC    | 60.0                             | 519                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_28317021  | Ca7                                     | 28317021                      | ATTTTTTTTTTTT/ATTTTTTTTTTT                                                                   | GATCCCATGTATGGTG<br>AGGG       | CTGTCTGTTGCAGCTG<br>GTGT    | 60.0                             | 481                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_28351627  | Ca7                                     | 28351627                      | T/TTA                                                                                        | TGTTGGGTGAGTTTTC<br>CACA       | GTGAAACCATCGTTCA<br>CACG    | 60.0                             | 472                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_28515180  | Ca7                                     | 28515180                      | AATATATATATAT/AAATATATAT<br>ATATAT                                                           | ACGTGAGCGTGATTTA<br>CTGC       | TTCATCAACGAAAAATA<br>CATTGC | 59.0                             | 281                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_28529637  | Ca7                                     | 28529637                      | ATTTTTTT/ATTTTTTTT                                                                           | CAGACCAGACCGTGCT<br>TTTT       | ATGTGGCCTGTCATAG<br>GCTT    | 60.3                             | 498                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_28550219  | Ca7                                     | 28550219                      | TTCTCTCTCTCTCTCT/TTCTCTC<br>TCTCTCTCTCTCT                                                    | GTTAGACGGGTTTCCC<br>CATT       | GTACAGATCACCCACC<br>CACC    | 60.1                             | 624                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_28562862  | Ca7                                     | 28562862                      | GCAAGTACAAGTACAAGTACAAGTA<br>CAAGT/GCAAGTACAAGTACAAGTA<br>CAAGTACAAGTACAAGTACAAGT            | AAGCAACACAGCACAA<br>CCAA       | TTGAGCACCACATTCA<br>GAGC    | 60.3                             | 658                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_28587444  | Ca7                                     | 28587444                      | ATTTT/ATTTT                                                                                  | TCGTGTATGTGCGCAT<br>GAGT       | TTTTCTGAATGGGGAG<br>TTGC    | 61.3                             | 626                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_28627288  | Ca7                                     | 28627288                      | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATT/ATATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATT | TTTTTCATTAGTTTCT<br>GATTTAATGG | GAGGTCAGTACGCTAG<br>GGGG    | 58.3                             | 875                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_28702659  | Ca7                                     | 28702659                      | ATCCTCC/ATCC                                                                                 | TCCATTAACCTCTTGA<br>GGAAA      | TCAGGATGAAGAAGGG<br>GAGA    | 59.9                             | 531                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                            | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                          |                               |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_28706974  | Ca7                                     | 28706974                      | AA/AAAGGTACAA                                                                                            | TCACCCATCTTACACTC<br>TTGTCA   | TTGGTTTTTGATGGTG<br>GGAT  | 59.6                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_28707261  | Ca7                                     | 28707261                      | ATTT/AT                                                                                                  | TGATGGTGGATATGCG<br>AAAA      | TTGGTTTTTGATGGTG<br>GGAT  | 59.9                             | 314                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_28707412  | Ca7                                     | 28707412                      | GAAATAACAATAAAAAACAATAACAA<br>TAAAA/GAAATAACAATAAAAAACAAA<br>TAACAATAAAAAACAATAACAATAAA<br>A             | ATCCCACCATCAAAAA<br>CCAA      | GATATGTTCCGAGTGC<br>CGTT  | 60.0                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_28881820  | Ca7                                     | 28881820                      | CAAAA/CAAAA                                                                                              | TGGATTTCTGAAGCACA<br>CTTG     | AAAGAGTCTGCCCTGG<br>GAAT  | 59.8                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_28947190  | Ca7                                     | 28947190                      | ATTTTTTTTT/ATTTTTTTTT                                                                                    | TGTATGGGTGGTGGAT<br>GTTG      | CAACCGATCATGAAATA<br>AGCA | 60.1                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_28998182  | Ca7                                     | 28998182                      | TAAAAAAAA/TAAAAAAAA                                                                                      | ACATGGCTCCTCCAAG<br>AATG      | CATCACGATCTTTGTCC<br>ACG  | 60.1                             | 806                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29170377  | Ca7                                     | 29170377                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                                                                | CCAAACCTTCCTATTT<br>CCC       | AAGAAAGATTCCGGTA<br>CGCA  | 59.6                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29245826  | Ca7                                     | 29245826                      | AATATATATATATATATATA/AATA<br>TATATATATATATATATATATA                                                      | ATTTCCAGCATGCCAA<br>TTTC      | GCAACATTGGGTGTTG<br>TTTG  | 59.9                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29311995  | Ca7                                     | 29311995                      | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATT/ATATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATT | TCATCGAAAACTTCAAA<br>AACTATGA | GATGCAGGTCATGAAA<br>CCAA  | 59.2                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29312201  | Ca7                                     | 29312201                      | CGT/CGTGT                                                                                                | TTGGTTTCATGACCTG<br>CATC      | GGCCTTCCTAAATCTTT<br>CCG  | 59.5                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                            | Forward primers (5'-3')        | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------|--------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                          |                                |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_29345782  | Ca7                                     | 29345782                      | AATATATATATATATATATA/AATATA<br>TATATATATATATATATATA                                                      | TGGATGACAAGTGT<br>TTGGC        | AAAATTGCATCTTCCT<br>TTTGA   | 59.5                             | 946                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29416457  | Ca7                                     | 29416457                      | ACC/AC                                                                                                   | AAAATCATTACTCACCA<br>TAAGTGGAA | TGCTCTCCTCCTTCAAC<br>AACT   | 59.3                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29416537  | Ca7                                     | 29416537                      | ATATAAATTATAAATTATAAATTATA/<br>TATAAATTATAAATTATAAATTATAA<br>ATTAT                                       | AAAATCATTACTCACCA<br>TAAGTGGAA | TGCTCTCCTCCTTCAAC<br>AACT   | 59.3                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29416730  | Ca7                                     | 29416730                      | AAGAAGTTGTTGAAGGAG/AAG                                                                                   | ATTGTAGAAGGAAGAG<br>GAGAAGCA   | AAAAAGCTGATGTGT<br>CCTGTTGA | 59.9                             | 100                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29417874  | Ca7                                     | 29417874                      | ATTT/ATT                                                                                                 | AGTTGTTGAAGGAGGA<br>GAGCA      | TTGTAGGCTGGACATC<br>ATGC    | 59.1                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29418101  | Ca7                                     | 29418101                      | C/CT                                                                                                     | CATGTACACGTCACAT<br>CGGA       | TTGTAGGCTGGACATC<br>ATGC    | 59.0                             | 329                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29460571  | Ca7                                     | 29460571                      | GAAAAAAAA/GAAAAAAAA                                                                                      | GTGCTAAAGCCTGAAA<br>CCCA       | GATGAATTTGGGGTTT<br>CCCT    | 60.2                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29461689  | Ca7                                     | 29461689                      | T/TA                                                                                                     | CCCAACCTTCGAAGAT<br>CTCA       | GCACCTCTCATCCTAG<br>GCAC    | 60.2                             | 457                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29567635  | Ca7                                     | 29567635                      | CTAATAATAATAATAATAATAAT<br>AATAATAATAATAAT/CTAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAAT | GGCGCCTGAATTGTGA<br>CTAC       | CGCACACAGACACACA<br>ATGA    | 60.7                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29631320  | Ca7                                     | 29631320                      | CTTTT/CTTTT                                                                                              | CACTATTTCCGCATTTT<br>CCAA      | CGTCAGTCATGTGGAT<br>TTTTG   | 60.0                             | 198                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)  | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_29669931  | Ca7                                     | 29669931                      | AAATAATAATAATAATAATAATA<br>ATAAT/AAATAATAATAATAATAA<br>TAATAAT | TGATAGGTGAAGCGT<br>TGAT  | TGTGGCAAAAGAGCAT<br>GAAG | 58.2                             | 652                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29743864  | Ca7                                     | 29743864                      | ATTTTTTTTT/ATTTTTTTTT                                          | GGCCCGACTATTGTGG<br>ACTA | TCAGCCTAACCAATAC<br>GCA  | 60.0                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29776063  | Ca7                                     | 29776063                      | TAAAAAA/TAAAAAA                                                | TGGTTACACTTCGTGG<br>CAAA | CATGGGCACTACATCG<br>TCAC | 60.1                             | 679                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29779156  | Ca7                                     | 29779156                      | AATATATATATATATATATA/AA<br>TATATATATATATATATATA                | TTTTTGCCACCACTT<br>TTT   | TGAGAGGAGAGACGA<br>GCAT  | 58.2                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29853160  | Ca7                                     | 29853160                      | AAATAATAATAATAATAATAA/AA<br>ATAATAATAATAATAATAATAA             | TTACGATGGCGTATGC<br>AAGA | TCTTCATTTGGGTTT<br>GGG   | 60.2                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29935640  | Ca7                                     | 29935640                      | AATATATATATATATA/AATATATA<br>TATATATATATATA                    | CGTGACTGGCTCACAA<br>GCTA | TGGTGGTTGTGTCTC<br>CTCA  | 60.2                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29972245  | Ca7                                     | 29972245                      | TAGAAGAA/TAGAA                                                 | CATTGTCGGTGACATC<br>CAAG | GGTTGTTGCCATCTTT<br>CGT  | 60.0                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_29987440  | Ca7                                     | 29987440                      | AAATAATAATAATAATAATAA/<br>AAATAATAATAATAATAATAA<br>ATAATAATAA  | GAACATGTTGATTGG<br>ATTGC | CTCCTCGTTGTGTGG<br>ATCA  | 60.2                             | 751                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30003777  | Ca7                                     | 30003777                      | TAAAAAA/TAAAAAA                                                | TGGTGTTTATCAACCG<br>TCCA | TTTCTCCTCCTCACTG<br>CTG  | 59.8                             | 358                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30016514  | Ca7                                     | 30016514                      | CATAT/CAT                                                      | ATCAACCGTTCACCT<br>CGAG  | CCAACCGTGAAAACA<br>AAGAA | 60.1                             | 292                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_30016779  | Ca7                                     | 30016779                      | ATTTTCATTT/ATTTTCATTTTTCAT<br>TT                              | ATCAACCGTTCACTT<br>CGAG    | TGCTTGAGCCTAAACC<br>AATAA    | 60.1                             | 739                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30021337  | Ca7                                     | 30021337                      | CAAAAA/CAAAAAAAA                                              | TGTGGTGTTCAAAAG<br>CAAAA   | TTGGAGTTGGAGGGAG<br>TTTG     | 60.2                             | 774                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30031455  | Ca7                                     | 30031455                      | AATCTA/AA                                                     | GCTACAAGGTCTCTCG<br>CACC   | GAAAAATTGATTTAACA<br>CAAGCCC | 60.0                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30053648  | Ca7                                     | 30053648                      | CAAAGT/C                                                      | GGACTGAAAAGAAAA<br>TATGCGA | GTGCTCTCTTTGCCG<br>ATTG      | 59.6                             | 774                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30069284  | Ca7                                     | 30069284                      | AAAAACAATAAAAA/AAAAA                                          | ATTGCCACAGCCTAAA<br>CACC   | TTTCATCGGTAAGCTGT<br>TCG     | 60.0                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30078953  | Ca7                                     | 30078953                      | GAAAA/GAAA                                                    | ATGCCAAAACGTAGCA<br>AAGC   | CGCACCACTTTCCATC<br>ATAA     | 60.3                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30079045  | Ca7                                     | 30079045                      | CAAA/CAA                                                      | ATGCCAAAACGTAGCA<br>AAGC   | CTCCTATCCTGCTATCC<br>GCA     | 60.3                             | 802                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30090813  | Ca7                                     | 30090813                      | CTATACTAT/CTATACTATATACTAT                                    | TGCCCAACAGATCCAT<br>AACA   | GCAGCTAGACCGTGGA<br>ATGT     | 59.9                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30093153  | Ca7                                     | 30093153                      | TCTATATACTAC/T                                                | TACGACCACCGTACTC<br>ACGA   | TCGACAAATTCGATGC<br>ATAA     | 60.2                             | 723                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30095365  | Ca7                                     | 30095365                      | TG/T                                                          | ATGATGACCGACATTT<br>GCAT   | AGGTGACCGTTGCGTA<br>AAAT     | 58.8                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)  | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_3009772   | Ca7                                     | 3009772                       | AATATATATATATATATATATATATA/<br>AATATATATATATATATATATATATA<br>A | TCACCTAACACTGTTG<br>GATCACTT | CAAGAAATCTGACACA<br>TCACGA  | 60.0                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30099359  | Ca7                                     | 30099359                      | GACA/GACATTAACA                                                | TGGGCACATGTCACAA<br>AACT     | TGAGGTATGGGAAGGG<br>TGAG    | 60.0                             | 840                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30105526  | Ca7                                     | 30105526                      | TTATAATATA/TTATAATATATAATAT<br>A                               | CCTCATTCCTTTAAAGG<br>GGGTT   | TTGTTATAGCGATTAA<br>GGTGAAA | 59.7                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30117022  | Ca7                                     | 30117022                      | AC/A                                                           | TTCGCAAAAGCCTCAA<br>GTTT     | GAGAGTCGCTAACCGA<br>AACG    | 60.0                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30146254  | Ca7                                     | 30146254                      | TC/T                                                           | TGATTTTGAATGCCCT<br>CCTC     | AAAGGGCAATTGGAGC<br>ACTA    | 60.0                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30155155  | Ca7                                     | 30155155                      | CTTTTTTTTTT/CTTTTTTTTTTTT                                      | CTGGTGGTTGGTGGGT<br>TAAG     | CATGGTGAACCTCTAG<br>CACTCA  | 60.3                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30156816  | Ca7                                     | 30156816                      | CAAAAA/CAAAAAA                                                 | GGTGCTTAACGTCAAG<br>TGAATG   | TGGGCGTTACAAGAAT<br>GTGA    | 59.7                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30173118  | Ca7                                     | 30173118                      | GTTTTTTTT/GTTTTTTTTTT                                          | TCTCGTGCTTCCACAT<br>TGTC     | TGCAGGAGGTCCAAGT<br>TCAT    | 59.8                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30186601  | Ca7                                     | 30186601                      | TAA/TA                                                         | TCGACAAATCTTGTC<br>TGACTT    | TTATTGGACTAAACCG<br>CCG     | 59.9                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30207135  | Ca7                                     | 30207135                      | TATAAACATAAACATAA/TATAAACAT<br>AA                              | GCAACAATTCTTTTCT<br>TCACAA   | GAACCATTTCTTGTC<br>AAAA     | 58.5                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                             |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_30221695  | Ca7                                     | 30221695                      | T/TGAA                                                                      | CTTGTTGATGCAATGTT<br>GGC   | TTTGCCACACAAAA<br>CAAA     | 60.1                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30225464  | Ca7                                     | 30225464                      | TTTATTATTATTATT/TTTATTATTATT<br>ATTATT                                      | CAGGGTGAGGTGTGT<br>GATTG   | ACAGGCTGACAGCGTA<br>AAGA   | 60.0                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30228795  | Ca7                                     | 30228795                      | TAGAGAGAGA/TAGAGAGAGAGA                                                     | AGACATGTCGCATCAT<br>GGAA   | ATCACGTCGTGGATCA<br>CCTA   | 60.1                             | 915                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30235069  | Ca7                                     | 30235069                      | TTTCTTCTTCTTCT/TTTCTTCTT<br>CTTCT                                           | TGCGTGTCGAGTTGT<br>AAGG    | AACGTGCCAAAAACCA<br>CTTC   | 59.9                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30249477  | Ca7                                     | 30249477                      | TTATATATATATATATAT/TTATATAT<br>ATATATAT                                     | CCCTCCACCTATGAGT<br>GCAT   | AGCTTCGGCTTAATTTG<br>GCT   | 60.0                             | 966                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30345500  | Ca7                                     | 30345500                      | TTATATATATATATATAT/TTATATAT<br>ATATATATATAT                                 | ATGACAACGCAATTCC<br>CATA   | TTTGAATTTTCCGTCC<br>CAC    | 60.1                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3036070   | Ca7                                     | 3036070                       | ATATATATATATATAT/ATATATATAT<br>ATTTATATATATATATAT                           | TCAATGACTCAACCTTA<br>ACCGA | AGGGGAAGGCAAGTGA<br>GATT   | 59.6                             | 434                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30415200  | Ca7                                     | 30415200                      | C/CG                                                                        | CAATTCAAAGAAACC<br>CCAGA   | GTAAATCGCCTTTTCC<br>ACG    | 59.1                             | 750                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30415380  | Ca7                                     | 30415380                      | AATATATATATATATATAT/AAAT<br>ATATATATATATATATATAT                            | GGAGTCATTCTCTCCC<br>ATGAA  | GTCCTCGTCCCTCATG<br>TTGT   | 59.1                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30635121  | Ca7                                     | 30635121                      | TTTATTATTATTATTATTATTATT<br>ATTATTATT/TTTATTATTATTATTAT<br>TATTATTATTATTATT | ACCTCCTAAGATTTC<br>CCCA    | CAAGCCCTCAATTTTCA<br>AAAGA | 59.8                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_30674255  | Ca7                                     | 30674255                      | CTTTTTTTTT/CTTTTTTTTT                                         | CGTTTAAAGTTTATCG<br>CCACA | CACCAACCATATACACC<br>CCTC | 59.2                             | 830                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30737184  | Ca7                                     | 30737184                      | TTATATATATATATATATATATATA<br>TA/TTATATATATATATATATATAT<br>A   | TCCGCTTTTATTTGTGT<br>GTCA | AATCTGAACAAGGGCC<br>AATTA | 59.2                             | 717                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3076524   | Ca7                                     | 3076524                       | ATTTT/ATTT                                                    | GAAATGGATTGTGGAA<br>GGGA  | CCTCTTAGGTGTGCCT<br>CTGC  | 59.7                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30981750  | Ca7                                     | 30981750                      | TG/TGG                                                        | GGTAAGGGCTCCTTCC<br>AAAC  | GGGCTGCACGATTTA<br>CAAAA  | 59.9                             | 967                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30988034  | Ca7                                     | 30988034                      | AATATATATATATATATATATA/AA<br>TATATATATATATATATATATAT<br>ATA   | AATGGGAGGTGATGTG<br>GAAA  | TCCGCGAGAGAGTTAT<br>AGCC  | 60.2                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_30990597  | Ca7                                     | 30990597                      | AA/AAATA                                                      | TGCGACAAGAAATGTC<br>GAAG  | GCACGATCCATTAAGC<br>CATT  | 60.0                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31006901  | Ca7                                     | 31006901                      | T/TA                                                          | CCTACGGACGGGAATG<br>TAGA  | GAAACCAAGGCAATCA<br>GGAA  | 59.9                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31042938  | Ca7                                     | 31042938                      | AATATATATATATATATAT/AAAT<br>ATATATATATAT                      | GGTATGAAGGTGATGG<br>TGCC  | CTTCCCATGTTATCAC<br>GCC   | 60.2                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31112471  | Ca7                                     | 31112471                      | TGG/TG                                                        | GCAAAGGCACTCATT<br>CATT   | GCAAAAACACGAGAAG<br>GAGG  | 60.1                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31206370  | Ca7                                     | 31206370                      | TAGAGAGA/TAGAGA                                               | TGGAGTGATGAAAATG<br>GGGT  | TTTCTCTGGAAATCAA<br>CATGA | 60.2                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_31206812  | Ca7                                     | 31206812                      | ATTTTTTTTT/ATTTTTTTTTTT                                       | TCATCATGTTGATTCC<br>AGGAG | AGCCCCTAACCATCCT<br>CACT  | 59.9                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31209239  | Ca7                                     | 31209239                      | TAAA/TA                                                       | GACCAATGAAGTTGGC<br>GTTT  | TGATGGGTCGTACACA<br>TGCT  | 60.0                             | 729                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3121868   | Ca7                                     | 3121868                       | CATATATATATATATATATA/CATA<br>TATATATATATATATA                 | TTCTGAAAAGAACAAC<br>CGCA  | GCAAGTGTTCGCCAA<br>TTTAA  | 59.4                             | 846                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31232674  | Ca7                                     | 31232674                      | CTTTTTTT/CTTTTTTTTT                                           | GCAAAATAGCTCTTGC<br>GGTC  | CTCTTCTCGTTGAAC<br>GCC    | 60.0                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31240937  | Ca7                                     | 31240937                      | GTTTTTTTTTTT/GTTTTTTTTTT                                      | TGGACAAAGCTCACAA<br>CTGC  | TTGTTTGGCATCAGTAT<br>GCAC | 60.0                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31247213  | Ca7                                     | 31247213                      | AGTTTCAAATGTT/AGTTTCAAATGT<br>TTCAAATGTT                      | CACCTCTCACGTTGCG<br>ATTA  | CCTCACACCCATCCT<br>ATTG   | 59.9                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31247477  | Ca7                                     | 31247477                      | TAAAAAA/TAAAAAA                                               | GAAAGTTTGGGGGTGT<br>GAGA  | CCGGGAGATACGTAGG<br>AACA  | 59.9                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31250362  | Ca7                                     | 31250362                      | ATTTTT/ATTTT                                                  | TTCCAATACCAACCAG<br>CCAT  | CCCACCTTGAAGCCCA<br>ATAA  | 60.2                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31253409  | Ca7                                     | 31253409                      | CTTTTT/CTTTTTT                                                | TTGAACAACTCATCAC<br>GGG   | GCAATACGAGGAATT<br>GTGG   | 59.5                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3128484   | Ca7                                     | 3128484                       | ATTTTTTTTT/ATTTTTTTTTT                                        | ACTGGTAGGCAACGAA<br>CACC  | GCTACCGAAAATTCA<br>GAAAA  | 60.0                             | 315                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                           |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_3128980   | Ca7                                     | 3128980                       | CATAATGAAAGAATAATGAAAGA/CA<br>TAATGAAAGA                                  | TTTTTCTGAAATTTTCG<br>GTAGC | TGTGTGTCATTTGTGA<br>GCCA    | 57.7                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31378000  | Ca7                                     | 31378000                      | AAAAATTAATAATAATAATAATA/AA<br>AAATTAATAATAATAA                            | AGCTTAGGGCTACCTG<br>CACA   | TACGGAACACATCATG<br>GGAA    | 60.0                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31406570  | Ca7                                     | 31406570                      | CAATAATA/CAATA                                                            | GACCATCTTAAATGAC<br>CGCAA  | ATGCGTCGGTGCAATA<br>ATAA    | 60.0                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31491336  | Ca7                                     | 31491336                      | TATCTTTGA/TA                                                              | TCCAACACCATGCCTT<br>ATTTT  | TCGTAAATAGCTGTTGT<br>CCGTC  | 59.3                             | 810                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31496011  | Ca7                                     | 31496011                      | AATATATATATATATATATATATATA<br>ATA/AATATATATATATATATATATA<br>ATATA         | CGTCCTCCTATTTGTTT<br>TGACA | ACCAAAATGCCACACAT<br>TGA    | 59.1                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31537680  | Ca7                                     | 31537680                      | TTATATATATATATATATA/TTATA<br>TATATATATATATATA                             | TTCGAAGGTTGGGTTG<br>AATC   | TCATGTTCATACAAATT<br>TTGGCA | 59.9                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31542273  | Ca7                                     | 31542273                      | TTCTCTCTCTCTCTCTCTCTCTCTCT<br>CTC/TTCTCTCTCTCTCTCTCTCTCT<br>CTCTCTCTCTC   | TGGATTTTGAAGATGT<br>GGCA   | CCAATACAACACGAGT<br>CGCC    | 60.0                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_31745904  | Ca7                                     | 31745904                      | TCCCC/TCCC                                                                | TGCATGGAATGGTGAG<br>TGAT   | ATTGATGGGTTTACTTG<br>GCG    | 59.9                             | 219                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32103149  | Ca7                                     | 32103149                      | CTTAAGGT/CT                                                               | GGGGGTGCACAATACA<br>TTTC   | CTTGACGAAAGCTAGC<br>CACC    | 60.1                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32188225  | Ca7                                     | 32188225                      | GATATATATATATATATATATATA<br>TATATATA/GATATATATATATATA<br>TATATATATATATATA | TCCGGTTGAAACTGGT<br>GAAT   | AATGTGCCAGATAAGG<br>GTGG    | 60.4                             | 253                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3')     | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|-----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                           |                             |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_32358180  | Ca7                                     | 32358180                      | TTGG/TTGGACAGGATGG                                                                        | GTTTGGAGAGCAGCT<br>GGAG     | GCGGGTCTGGTTTTG<br>ATAA        | 60.1                             | 246                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32395782  | Ca7                                     | 32395782                      | CAAAAAAAAA/CAAAAAAAAA                                                                     | CGATTTGAATCCAACA<br>ATAACA  | TTTATTATTAGCGTAAA<br>CTTTTCCAA | 58.9                             | 328                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32424381  | Ca7                                     | 32424381                      | TTATATATATATATATATATATATA<br>TATATATATA/TTATATATATATATAT<br>ATATATATATATATATATATATATA     | TGGGCATGGACATTGT<br>TAGA    | CAATGGGCTAATCAT<br>GGCT        | 59.9                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3243289   | Ca7                                     | 3243289                       | AGTTATTTGATTTGTATTTTGAT<br>TTTGT/AGTTATTTGATTTTGT                                         | TGAGTTTGATATCGT<br>TTTTACAC | CATTTTGTCTAGCCAC<br>GCA        | 57.4                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32442832  | Ca7                                     | 32442832                      | GATATATATATATATATATATATA<br>TATATATATATATATATA/GATATATA<br>TATATATATATATATATATATATAT<br>A | TTTTTCGGCACGTAAT<br>GTC     | TTTTTCAAAACCAAAAT<br>TGAA      | 58.7                             | 901                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3247094   | Ca7                                     | 3247094                       | TAAAAAAAA/TAAAAAAAA                                                                       | GATGAGGGAGAACGTG<br>GAAA    | ACCCAAATCAAGTGGG<br>ATCA       | 60.1                             | 597                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32479028  | Ca7                                     | 32479028                      | AATATATATATATATATATATAT/A<br>ATATATATATATATATATATATAT                                     | AGGGAGTTTAGTGGTG<br>GGCT    | CGGATGCATGAAAGTG<br>AAAA       | 60.0                             | 636                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32515668  | Ca7                                     | 32515668                      | GAAAAAAAAAAAAA/GAAAAAAAAAA<br>AA                                                          | CATCCGTGGTCCCTTA<br>ACTT    | ATCCGCAAGGAAAATT<br>AGCA       | 58.9                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3256595   | Ca7                                     | 3256595                       | CTCGTTCGT/CTCGT                                                                           | AAAGAAAACGTCGCCT<br>GAGA    | CACGGAATTGGCTTGG<br>TAAT       | 60.0                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32572777  | Ca7                                     | 32572777                      | TA/TTAA                                                                                   | TTTTGAATGGAAGACG<br>TCCC    | TGAGTCGGATGTAGTG<br>CAGC       | 59.9                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                       | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                     |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_32583860  | Ca7                                     | 32583860                      | TAAAAAAATAATTATAAAAAAA/TA<br>AAAAAA                                                                 | TTGATTTTGTATTGCG<br>GTGTT   | TCCGATTTCAAATGAT<br>GGTT   | 59.4                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32589973  | Ca7                                     | 32589973                      | TATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAA/TA<br>TAATAATAATAATAATAATAA<br>ATAATAATAATAATAATAA | CAAAGTGAGAATTGTG<br>AGCATGA | TATCGGATGTTCTGA<br>AGGG    | 60.3                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32596845  | Ca7                                     | 32596845                      | T/TCTTTTTCC                                                                                         | CGTTGGACCAATCTCT<br>AATTCA  | GAAAGGAAGGGAAAGA<br>GGGA   | 60.4                             | 319                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32613866  | Ca7                                     | 32613866                      | AT/ATT                                                                                              | AAAAGGTGGTTAGCTC<br>TTTGACA | GGGGCGAAAGATTTT<br>ATTT    | 59.4                             | 377                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32614218  | Ca7                                     | 32614218                      | AAAAAATTATAAA/AAAA                                                                                  | AAATAAAATCTTTCGCC<br>CCC    | GGAGGGATTGCAGTGA<br>CAGT   | 59.3                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32649545  | Ca7                                     | 32649545                      | T/TC                                                                                                | TTGCAGGATGCACAGA<br>AAAG    | AGGTGCATCCCCTGTA<br>ACTG   | 60.0                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32650059  | Ca7                                     | 32650059                      | TAATAATGTAAAAA/T                                                                                    | ATGGGACTGTGGGAGA<br>GAGA    | GAAAAAGGCTTCAAAC<br>ATCAAA | 59.6                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32653182  | Ca7                                     | 32653182                      | G/GA                                                                                                | TTTTCAAATTCGGTT<br>TGC      | CCAATTCCTGTGGAAA<br>TGCT   | 59.9                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32654894  | Ca7                                     | 32654894                      | AAATAATAATAATAAT/AAATAAT<br>AATAATAATAATAATAAT                                                      | AACGAAGTGAGACGTG<br>AGCA    | TGATGGCTATGGTGGA<br>ACAA   | 59.6                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32655163  | Ca7                                     | 32655163                      | TTAATA/TTA                                                                                          | AACGAAGTGAGACGTG<br>AGCA    | TGATGGCTATGGTGGA<br>ACAA   | 59.6                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_32655249  | Ca7                                     | 32655249                      | TATTAATTAA/TATTAA                                             | TGTTGTTCCAAATTTTA<br>CCTGAA | TACAGACCGGGCTCAA<br>AATC  | 58.6                             | 935                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32675968  | Ca7                                     | 32675968                      | T/TTA                                                         | GACGACCCGACCTCC<br>TAAA     | CAACAATTGACATGGT<br>CGC   | 60.1                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3276292   | Ca7                                     | 3276292                       | AAATAATAATAATAATAATAATA<br>AT/AAATAATAATAATAATAATAA<br>T      | TCTTTTATCACTCCCGT<br>GTGC   | TTGGCTTGATTAAATGT<br>TGGG | 60.1                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32873082  | Ca7                                     | 32873082                      | ATT/ATTTTT                                                    | TGAATATGCAGTGCTC<br>CAGG    | GAATTTGCAATTTGATT<br>TCCG | 59.8                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3288787   | Ca7                                     | 3288787                       | AATATATATATATAT/AATATATATAT<br>ATATAT                         | CGTGCCACCTTAAAG<br>TCAT     | AATGATGCATGTTGTTG<br>GTG  | 60.0                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3292429   | Ca7                                     | 3292429                       | ATTTTT/ATTTTTTT                                               | AAGATAGGCACCAATC<br>CAAAA   | CAGAGAACAACGAGGA<br>TCGC  | 58.6                             | 908                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32969816  | Ca7                                     | 32969816                      | GAGATGTAGA/GAGATGTAGATGTA<br>GA                               | TTCCAAATAATAAACCG<br>GTGG   | TGTGACCGTGGGTAGA<br>ACAA  | 58.7                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_32986552  | Ca7                                     | 32986552                      | TTATATATATATATATAT/TTATAT<br>ATATATATATATATAT                 | GTTGAATTGCCCTTCC<br>AAAA    | AAAGAAGCCAACATGC<br>ATCA  | 59.9                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33049395  | Ca7                                     | 33049395                      | AG/A                                                          | TTTGAACATCCTCGCTA<br>TTCAC  | CGCTTGAGACATTGAG<br>CAAG  | 59.2                             | 822                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33051432  | Ca7                                     | 33051432                      | TAAAAA/TAAAAAAA                                               | TCAAAATTTTAAACAA<br>AACCCA  | CCTTGCCTCATGTTATG<br>TGC  | 57.7                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33056585  | Ca7                                     | 33056585                      | G/GA                                                          | CAGTTTGGCGATTGA<br>GGTT    | TATGGGTCCGGCTATT<br>ACCA   | 60.1                             | 492                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33056642  | Ca7                                     | 33056642                      | T/TC                                                          | CAGTTTGGCGATTGA<br>GGTT    | TATGGGTCCGGCTATT<br>ACCA   | 60.1                             | 492                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33062204  | Ca7                                     | 33062204                      | AT/ATT                                                        | CGATCAATGACTGTCC<br>AACG   | GGGCCCTCTACTTGAA<br>CTAAAA | 60.1                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33127717  | Ca7                                     | 33127717                      | TAAAAA/TAAAAA                                                 | GACACATGAGCAATTG<br>ATTCG  | GGGTTACCCCGCCTTA<br>TCTA   | 59.1                             | 911                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33129086  | Ca7                                     | 33129086                      | CTTTT/CTT                                                     | TAAGGTTCTCTTCGGC<br>TGCT   | ACTTGAGTCTGGCGCC<br>TTAG   | 59.2                             | 916                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33161089  | Ca7                                     | 33161089                      | TAAAAAAAAAAAAA/TAAAAAAAAA                                     | TAAGGCACCACGTGAA<br>TTTG   | TCCACCTCCTTAAAGC<br>CTCA   | 59.6                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33161942  | Ca7                                     | 33161942                      | AAATATTATAATATTATAA/AAATATT<br>ATAA                           | TGAGGCTTTAAGGAGG<br>TGGA   | TTTTGCTAAATCGTGGA<br>ATCAA | 59.8                             | 430                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33169523  | Ca7                                     | 33169523                      | TT/TTCACT                                                     | TTGGGCTAAGCAATGT<br>TTGA   | GCCGATCCAACACATT<br>ATGA   | 59.3                             | 730                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33171683  | Ca7                                     | 33171683                      | TA/TAA                                                        | CTTGTTCGCAAGAGTT<br>GGCA   | TGAGTGTAGTGTGCC<br>TATCG   | 60.0                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33175105  | Ca7                                     | 33175105                      | CTT/CT                                                        | TGAAGAAATCAATCAT<br>GCAAGT | AACTTGCGTTAGAGTC<br>GGGA   | 57.4                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_3317609   | Ca7                                     | 3317609                       | GTTT/GTTTT                                                    | CCACGGTTCTGAAGT<br>TGTT      | TGGGAAGTTGGTCTGT<br>GTGA     | 60.0                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33188888  | Ca7                                     | 33188888                      | CAAAAAAAAA/CAAAAAAAAAA                                        | CTCGGAAGTCTCACCA<br>TTCG     | TCATCCATGGAGTTTA<br>GCACC    | 60.8                             | 687                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33189130  | Ca7                                     | 33189130                      | TG/TGCAG                                                      | AGACATTTTGTTCAATG<br>GATCTG  | AGGAGAAATGCGAGGA<br>AACA     | 58.1                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33193623  | Ca7                                     | 33193623                      | ATTT/ATT                                                      | GCATTGGAGATCACAT<br>GACG     | TCTTGGGTTTTGTATA<br>TAGGTCAA | 60.1                             | 234                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33194117  | Ca7                                     | 33194117                      | TAAAAAAAA/TAAAAAAAA                                           | TTGACCTATATACAAA<br>CCCAAAGA | CCCACGTGCTTTTCAA<br>GGT      | 58.2                             | 796                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33194389  | Ca7                                     | 33194389                      | GTT/GT                                                        | ACACAAGATGCTTCTT<br>CGCA     | ATTGCCCCAAGAGAA<br>GTTT      | 59.6                             | 131                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33194624  | Ca7                                     | 33194624                      | ATT/ATTT                                                      | ACCTTGAAAAGACACG<br>TGGG     | GGATTTAATCGAAATAC<br>TGCAACA | 60.0                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33195041  | Ca7                                     | 33195041                      | TTATATATATATATATA/TTATATATA<br>TATATA                         | GCAGTATTTGATTAA<br>TCCTCAA   | TTTGTGATTAGCGCGT<br>GAAA     | 59.9                             | 272                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33207535  | Ca7                                     | 33207535                      | CAA/CAATTCGAGAAAA                                             | TTGGTTAGGTTTGAG<br>ACCG      | CAGAATTCGATTGAGG<br>GACAA    | 60.0                             | 402                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33211070  | Ca7                                     | 33211070                      | TAA/TAAA                                                      | ACCTGCCATCTTTTGA<br>GCAT     | AATTTCCGTCGGGTCT<br>TTTT     | 59.7                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33212250  | Ca7                                     | 33212250                      | AA/AAGA                                                       | TGCATTTCATGCTTA<br>CACT  | CCTTTTTCGGAGTTTT<br>GAA  | 57.9                             | 798                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33212534  | Ca7                                     | 33212534                      | AG/A                                                          | CAGCTGAATTTGAAAA<br>GGGC | CCTTTTTCGGAGTTTT<br>GAA  | 59.8                             | 257                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33236353  | Ca7                                     | 33236353                      | TAAAAA/TAAAAA                                                 | GCGGTTGTTTGGATCA<br>ATTT | TAAATCAACCGCATTTT<br>ACG | 59.8                             | 290                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33237386  | Ca7                                     | 33237386                      | AA/AACA                                                       | ACGTTGCCTCTTCGC<br>TGTC  | TTGGGTGATAAGGCCA<br>AAAC | 60.5                             | 433                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33237542  | Ca7                                     | 33237542                      | CAT/CATGTTTAT                                                 | ACGTTGCCTCTTCGC<br>TGTC  | TTGGGTGATAAGGCCA<br>AAAC | 60.5                             | 433                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33239110  | Ca7                                     | 33239110                      | GTTTTT/GTTTTTT                                                | TTCCCATGCCAATTGTA<br>GGT | TGCACAAGAAATCGAA<br>TGGA | 60.2                             | 592                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33246780  | Ca7                                     | 33246780                      | ATGATGTTTG/ATGATGTTTGATGTT<br>TG                              | GCATAATGTCTTGGGC<br>AGGT | TTATGACATTTTCCCC<br>ACA  | 60.0                             | 471                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33247703  | Ca7                                     | 33247703                      | ATCTCT/ATCTCTCT                                               | TGTAACGCGTAGGGTA<br>AGGG | TAAGCATCCGCTTCTTC<br>AGG | 60.0                             | 136                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33265044  | Ca7                                     | 33265044                      | GATA/GATATA                                                   | AAGGTTGCGTATTTT<br>GTCG  | ATAACAATGGGTTTGG<br>CAGG | 60.0                             | 496                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33266991  | Ca7                                     | 33266991                      | T/TTA                                                         | CTCACTCTCCTCCGCA<br>AATC | CTGCCGAATTAGAATG<br>CACA | 60.0                             | 683                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                                |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33274696  | Ca7                                     | 33274696                      | TTAGCTGGTCCTAGC/TTAGC                                         | ATAGCATTGGCACAAA<br>AGGG   | CATGATTGTGAATATGT<br>TTTGAAGA  | 60.0                             | 736                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33287681  | Ca7                                     | 33287681                      | AAAAA/AAAAAGAAAGAAAA                                          | ACGGTAGAAATCCCCT<br>TTGG   | TTGCATCCTTTTTATTG<br>GTGG      | 60.2                             | 204                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33294521  | Ca7                                     | 33294521                      | GAAAAAAAAA/GAAAAAAAAA                                         | AAAAACTTGGACACAC<br>GTCA   | TTCAATTCATCTCCCA<br>ACC        | 58.2                             | 480                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33296076  | Ca7                                     | 33296076                      | T/TA                                                          | TGACGACGGTTGTTCC<br>TTTT   | TTCCACTGAAGTCAAT<br>GAAAGAA    | 60.5                             | 391                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33308518  | Ca7                                     | 33308518                      | GTTTTTT/GTTTTT                                                | TTTTGGAATTGTTTTGG<br>TCATC | TGCATTTTTCTTCATCT<br>TAATTTGTT | 58.8                             | 653                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33324825  | Ca7                                     | 33324825                      | ATT/ATTT                                                      | TGGAACACAACTTTGG<br>ACACA  | TTCTTTACGGATAATGA<br>TGGA      | 60.0                             | 560                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33327221  | Ca7                                     | 33327221                      | TAAA/TAAAA                                                    | TGCACATAACTTGTGC<br>GACC   | TTCCATTTCCCTTAGT<br>GCG        | 60.7                             | 658                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33327595  | Ca7                                     | 33327595                      | T/TG                                                          | GCATTGATCCGCCTAA<br>AGAA   | TGGGCTGTCTATCCCA<br>ATTC       | 60.2                             | 882                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33329178  | Ca7                                     | 33329178                      | GTTTTTT/GTTTTTTT                                              | TCACCTTCTGACCTTG<br>AATGAA | TGGTGGGCTATGAACA<br>AACA       | 59.7                             | 619                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33370763  | Ca7                                     | 33370763                      | CTTTT/CTTT                                                    | GCCAAAATTGGTTCTT<br>CCAA   | GGAGCCATGGAAGTT<br>TGAG        | 59.9                             | 411                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33384005  | Ca7                                     | 33384005                      | GAAAAAAAAA/GAAAAAAAAA                                         | TCAAAATTTTCAAACAA<br>AATCCA | CCATGATCAAGACACG<br>ACTCA   | 58.6                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33385317  | Ca7                                     | 33385317                      | AT/A                                                          | TTCATCGTTTTCCGAA<br>CTC     | CCTCTTTGTCTTCTTGT<br>GGCA   | 60.1                             | 723                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33431270  | Ca7                                     | 33431270                      | TAAAAA/TAAAA                                                  | AAAAACTTGAAATTGCC<br>CCC    | TGAGGTGAACACACCA<br>CACC    | 60.2                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33443533  | Ca7                                     | 33443533                      | AT/ATGAGCTATT                                                 | TAAACCCCTTTCGAG<br>TTTG     | GACATTTGCTGGGTAC<br>CAAAA   | 60.1                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33472559  | Ca7                                     | 33472559                      | ATTTTT/ATTTT                                                  | GCTGCAAAGGATTGAG<br>GATT    | TGTCTCGTCATCGTTTT<br>CCA    | 59.3                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33475251  | Ca7                                     | 33475251                      | TATAAATAA/TATAA                                               | TCACAATCTGGTGGCG<br>ATTA    | GATTGGGGAGATTAC<br>CCGT     | 60.1                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33478615  | Ca7                                     | 33478615                      | ATTTTTT/ATTTTT                                                | AATAGCTCCGCATGTC<br>GTTT    | GCACCATAACTTTCATG<br>ATTCAA | 59.7                             | 748                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33479483  | Ca7                                     | 33479483                      | TGGGG/TGGG                                                    | GGTATCGCCATACACC<br>CACT    | GCACAAAATGACCAGA<br>TGGA    | 59.7                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33479514  | Ca7                                     | 33479514                      | CAAAAA/CAAAAA                                                 | GGTATCGCCATACACC<br>CACT    | GCACAAAATGACCAGA<br>TGGA    | 59.7                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33490057  | Ca7                                     | 33490057                      | ATTTTTT/ATTTTTT                                               | CCAACATGCAAATGCA<br>ACTC    | AGGTGGGATGAGATT<br>CGTG     | 60.1                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33490130  | Ca7                                     | 33490130                      | AAA/AAATAA                                                    | CCAACATGCAAATGCA<br>ACTC     | AGGTGGGATGAGATT<br>CGTG     | 60.1                             | 388                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33490449  | Ca7                                     | 33490449                      | GAT/GATCAT                                                    | CACGAAATCTCATCCC<br>ACCT     | TTTCGGGCCAAGACAA<br>TTAG    | 59.9                             | 427                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33490514  | Ca7                                     | 33490514                      | A/AC                                                          | CACGAAATCTCATCCC<br>ACCT     | TTTCGGGCCAAGACAA<br>TTAG    | 59.9                             | 427                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33520215  | Ca7                                     | 33520215                      | TAAAAAAA/TAAAAAAA                                             | TGCTCAAGTCCACGTT<br>CAAA     | AAAGGACCAACACGGA<br>AAAA    | 60.4                             | 525                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33521411  | Ca7                                     | 33521411                      | ATT/ATTT                                                      | TGTTGAACATTGTAACA<br>GCCG    | GACGAAAAATGATTAG<br>ACGTTCA | 59.6                             | 364                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33527812  | Ca7                                     | 33527812                      | ATTTTTTT/ATTTTTTTT                                            | ATCAATCGTCGAAATT<br>GCC      | GATTGCGATCTCCACC<br>AAAT    | 59.9                             | 795                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33528549  | Ca7                                     | 33528549                      | TGTAAG/TG                                                     | GAATATTTGGTGGAGA<br>TCGCA    | AATGGAGCGGAATTT<br>CCTT     | 59.9                             | 482                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33531738  | Ca7                                     | 33531738                      | TTATATATAT/TTATATATATAT                                       | CATGCACTTGAGCACA<br>CAAA     | GGCGTAAGTAATCAGG<br>CCAA    | 59.5                             | 486                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33535580  | Ca7                                     | 33535580                      | AT/A                                                          | TGCAATGAAAACACTG<br>GGAG     | AAAGTTCTCATTACGCA<br>TTACGG | 59.7                             | 246                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_33535956  | Ca7                                     | 33535956                      | TCC/TC                                                        | CCGTAAATGCTGAATGA<br>GAACTTT | GCTTCCCTGTAAAAAG<br>GTTGG   | 59.7                             | 489                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33539096  | Ca7                                     | 33539096                      | AA/AATA                                                       | GGTAAATATGTGCATG<br>GCCC   | GGATTAGCACCGTCCA<br>ATTT   | 60.0                             | 722                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33539636  | Ca7                                     | 33539636                      | GTTTT/GTTT                                                    | AAATTGGACGGTGCTA<br>ATCC   | CACGAAAGGTTTCATC<br>ACAAA  | 58.9                             | 243                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33539716  | Ca7                                     | 33539716                      | TATTAATTA/TATTA                                               | AAATTGGACGGTGCTA<br>ATCC   | TTGCCATGCCTTTAGC<br>AAAT   | 58.9                             | 754                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33556326  | Ca7                                     | 33556326                      | A/AT                                                          | CCCGTGTTCTTACCTT<br>CTGG   | CTGTAGTACCCACCAT<br>GCCC   | 59.6                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33556600  | Ca7                                     | 33556600                      | ATTTTTTTT/ATTTTTTT                                            | GGGCATGGTGGGTACT<br>ACAG   | CACATTGGCGCTTGAA<br>AAAT   | 60.3                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33557490  | Ca7                                     | 33557490                      | AATAT/AAT                                                     | AAATTTTCAAGCGCCA<br>ATG    | AACCACCACAACAAGC<br>ATGA   | 60.1                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33558467  | Ca7                                     | 33558467                      | A/AGCTT                                                       | TGAAGGACAACTCAGT<br>GTCACC | TGCATTTTTCCTTCTTC<br>CACTT | 60.2                             | 897                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33586035  | Ca7                                     | 33586035                      | GA/GACGAGCTTA                                                 | GACAAAAAGATGCAGA<br>GGGC   | AGAAGAGGGAGTGGG<br>GGTTA   | 59.8                             | 198                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33586281  | Ca7                                     | 33586281                      | TCCC/TCCAAATGCCCCC                                            | GCAGAGGGCATTGGA<br>TTTA    | CCGCAAGAAAACATGG<br>ATCT   | 60.0                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33586427  | Ca7                                     | 33586427                      | CACAG/CACAGACAG                                               | GCAGAGGGCATTGGA<br>TTTA    | CCGCAAGAAAACATGG<br>ATCT   | 60.0                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33587703  | Ca7                                     | 33587703                      | CTTTTTTT/CTTTTTTT                                             | GTGTTTGGTTTGGGG<br>AATG        | TGATGCCAGGTAGAGT<br>GTGG       | 60.1                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33597364  | Ca7                                     | 33597364                      | CTAATTAATT/CTAATT                                             | GATGTTAACGCACCTC<br>CACC       | CACACTTCGATCTCCG<br>ATCA       | 60.4                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33597431  | Ca7                                     | 33597431                      | GAAAAAAAAA/GAAAAAAAAA                                         | GATGTTAACGCACCTC<br>CACC       | CACACTTCGATCTCCG<br>ATCA       | 60.4                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33597487  | Ca7                                     | 33597487                      | ATTTTTTT/ATTTTTTT                                             | GATGTTAACGCACCTC<br>CACC       | CACACTTCGATCTCCG<br>ATCA       | 60.4                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33597756  | Ca7                                     | 33597756                      | T/TA                                                          | TGATCGGAGATCGAAG<br>TG TG      | CTGGTGCCACGTAAAC<br>GACT       | 59.8                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33603742  | Ca7                                     | 33603742                      | TTATGT/TT                                                     | CAAGAAGGAGGAGGA<br>GGAGG       | TCAAGGTCCTTTCAA<br>CTTCA       | 60.3                             | 423                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33606263  | Ca7                                     | 33606263                      | TT/TTCT                                                       | TTCGAAGACAGGTGTT<br>GACG       | AAGTGTTTCATTTGTTT<br>GTGATTTTT | 59.9                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33606488  | Ca7                                     | 33606488                      | CAAAAAAAAAAAAA/CAAAAAAAAA<br>A                                | TTCGAAGACAGGTGTT<br>GACG       | AATTTCTTGCAATTCGC<br>TGG       | 59.9                             | 885                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33606729  | Ca7                                     | 33606729                      | A/AC                                                          | TGCAATTAGTCACTACA<br>AAACACAAA | AATTTCTTGCAATTCGC<br>TGG       | 60.0                             | 238                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33608322  | Ca7                                     | 33608322                      | CT/C                                                          | TCATTTGAGTGGGAT<br>GGTT        | TCTTTTAGCTGGTCGC<br>ATCC       | 60.3                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33612055  | Ca7                                     | 33612055                      | TTT/TTTATT                                                    | TCTTTTAGCTGGTCGC<br>ATCC  | GATGTGTGTGAGGGTT<br>GTGG  | 60.4                             | 747                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33622229  | Ca7                                     | 33622229                      | ATTTTTTT/ATTTTTTT                                             | GCGCACCTCATCGATA<br>TACA  | AATTGATTTTGGTTGCA<br>GCAT | 59.7                             | 959                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33630534  | Ca7                                     | 33630534                      | TACAC/TAC                                                     | CAAGGAAGCACTTGCA<br>GTCA  | GAAAATGGGAGTGGTC<br>TGGA  | 60.2                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33630653  | Ca7                                     | 33630653                      | AG/A                                                          | CAAGGAAGCACTTGCA<br>GTCA  | CGGTTCCCATAGATCA<br>GCAT  | 60.2                             | 832                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33633702  | Ca7                                     | 33633702                      | A/AC                                                          | TTCGCTTTGGTCTTCTT<br>CATC | AAATTGAATGAAGGGG<br>AAGGA | 59.4                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33637510  | Ca7                                     | 33637510                      | TAA/TA                                                        | TCAGCCCAAACTTAAG<br>TGCC  | TGACCAAGTCCAACCG<br>TGTA  | 60.2                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33638744  | Ca7                                     | 33638744                      | A/AC                                                          | TCGCAAGAGTTTGGAC<br>CTTT  | GCACATGGTTTCGAAT<br>GTTG  | 59.9                             | 882                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33644686  | Ca7                                     | 33644686                      | TTTA/TTTATTA                                                  | TTTTCTCAATCAAGAGG<br>CCA  | CAATATGACATGACGG<br>CTGG  | 58.4                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33645082  | Ca7                                     | 33645082                      | CTT/CTTT                                                      | TTGACATTGCGCTTCT<br>CAAG  | CAATATGACATGACGG<br>CTGG  | 60.1                             | 202                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33645463  | Ca7                                     | 33645463                      | TT/TTAAT                                                      | CCAGCCGTCATGTGCT<br>ATTG  | TGATTTTCCTTCGCGA<br>TCT   | 59.9                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33648106  | Ca7                                     | 33648106                      | GTAAT/GTAATTAAT                                               | CAACTAAACAGGGG<br>ACCA        | TTCATCCTAATGCTTAT<br>TTGGGA | 59.8                             | 701                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33648564  | Ca7                                     | 33648564                      | A/AT                                                          | TCCCAAATAAGCATT<br>GGATGAA    | GGGGGATATATTGAAT<br>GAAGAAA | 59.8                             | 317                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33649269  | Ca7                                     | 33649269                      | ATTGTT/ATT                                                    | AAAACACAGCTTTAATG<br>GTAGAAGA | GGATGCTACGACGCTT<br>ATTTTT  | 57.8                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33649463  | Ca7                                     | 33649463                      | GAAAAAAA/GAAAAAA                                              | TTGTGATTTTCGAAGCT<br>GAA      | TGAATGCACCTTTTACA<br>GCG    | 57.1                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33649648  | Ca7                                     | 33649648                      | GTTTTTTTTTT/GTTTTTTTTT                                        | TTGTGATTTTCGAAGCT<br>GAA      | TGAATGCACCTTTTACA<br>GCG    | 57.1                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33653424  | Ca7                                     | 33653424                      | GAAAAAAA/GAAAAAAA                                             | TGCCACATCACCTAA<br>ATCA       | TTGGAGTTGTGCCAAT<br>GTGT    | 59.9                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33656060  | Ca7                                     | 33656060                      | GTTTTTTTT/GTTTTTTTTT                                          | CGTATTCGGTGGCGAT<br>TCTA      | TTGATTGTGTCTAAGG<br>GTGGG   | 61.0                             | 585                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33660304  | Ca7                                     | 33660304                      | GAAAA/GAAAAA                                                  | TCGGCAGTACCAATTT<br>CACA      | TACAACGGTTTGATCG<br>GTGA    | 60.1                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33661689  | Ca7                                     | 33661689                      | AT/A                                                          | ACGCCACGTATTGTGT<br>CAAA      | ATGTTTCAGCCCCCA<br>ACTA     | 60.0                             | 729                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33662023  | Ca7                                     | 33662023                      | A/AGTTT                                                       | ATAGTTGGGGCTGAA<br>AACA       | CCCATTGTGTTGAGTG<br>CCTT    | 59.4                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33670193  | Ca7                                     | 33670193                      | AT/ATCTTGT                                                    | CAAGTCCAACCCAAAC<br>CAAC   | TGGGTCAAACTGAA<br>TTTTGTAAT | 60.2                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33671236  | Ca7                                     | 33671236                      | TAAAAAAAAA/TAAAAAAAAA                                         | CCATTGGACCCACTCA<br>TCTT   | GTGTTTCATCCCACGC<br>TAGT    | 59.8                             | 308                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33671286  | Ca7                                     | 33671286                      | CTTTTT/CTTTTT                                                 | CCATTGGACCCACTCA<br>TCTT   | GTGTTTCATCCCACGC<br>TAGT    | 59.8                             | 308                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33671331  | Ca7                                     | 33671331                      | ATTTTTTTTT/ATTTTTTTTT                                         | CCATTGGACCCACTCA<br>TCTT   | GTGTTTCATCCCACGC<br>TAGT    | 59.8                             | 308                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33677139  | Ca7                                     | 33677139                      | CCACAC/CCAC                                                   | TCATCTTATGGGGTTC<br>AGCC   | TTGGCATAGGGAAAC<br>ATGG     | 59.9                             | 299                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33683063  | Ca7                                     | 33683063                      | ATCATATT/AT                                                   | CGACTTCCTGAAGGAA<br>CGAA   | CGTTGGCAAAGTTTGT<br>TGAA    | 60.4                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33683185  | Ca7                                     | 33683185                      | GCAAGTCA/GCA                                                  | GGGCATTTCAGGAATA<br>TTGTTT | GATTGAGCCGAAAGTG<br>AAGC    | 59.2                             | 919                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33683250  | Ca7                                     | 33683250                      | CAA/CA                                                        | AAAAACGCAAGTCATC<br>ATCCT  | GATTGAGCCGAAAGTG<br>AAGC    | 58.7                             | 427                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33683634  | Ca7                                     | 33683634                      | C/CCTT                                                        | GCTTCACTTTCGGCTC<br>AATC   | CACAATCAAGGCCATC<br>AAAA    | 60.0                             | 214                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33684248  | Ca7                                     | 33684248                      | CCAC/CC                                                       | TTTTGATGGCCTTGATT<br>GTG   | GAAGGCCACACCAAAC<br>TGAT    | 59.5                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33712768  | Ca7                                     | 33712768                      | AA/AATATATA                                                   | TCCAAAGTGGTTAATG<br>TGATGG | TTCCACAAGTTCTACGT<br>GCG   | 59.7                             | 548                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33713773  | Ca7                                     | 33713773                      | TC/TCC                                                        | CTATGGGCCGACCTTG<br>ATTA   | TTTCTTTAGCATTGAG<br>CAACA  | 59.9                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33714022  | Ca7                                     | 33714022                      | TAAAAAAA/TAAAAAAA                                             | CTATGGGCCGACCTTG<br>ATTA   | CCAATTGGTCCCTCAG<br>AAAA   | 59.9                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33714061  | Ca7                                     | 33714061                      | ATTT/ATT                                                      | CTATGGGCCGACCTTG<br>ATTA   | CCAATTGGTCCCTCAG<br>AAAA   | 59.9                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33719498  | Ca7                                     | 33719498                      | CTT/CTTT                                                      | CGAGCTCGTATACACA<br>GGACAC | CATGTGCTTCTGTTGT<br>GGGT   | 59.8                             | 879                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33724600  | Ca7                                     | 33724600                      | G/GGAA                                                        | TCTCAGCAAATAACT<br>GCCG    | TTTTTCTCATTGGGAGC<br>TGG   | 59.2                             | 297                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33725103  | Ca7                                     | 33725103                      | CAAA/CAA                                                      | TTAATCCCAGCTCCC<br>AATG    | GTGATTTTTGCCTCCTT<br>CCA   | 59.9                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33726209  | Ca7                                     | 33726209                      | TAAAAATAAAAAATAAAAAAT/TAAAA<br>ATAAAAAATAAAAAATAAAAAAT        | TTTCCGAAGCGATAAA<br>TTGG   | AATAGGATCATCGTCA<br>CGGC   | 60.0                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33726416  | Ca7                                     | 33726416                      | T/TC                                                          | TAAATTGCCGTGACG<br>ATGA    | TCGATTGAGATTGAAG<br>GCTTTT | 60.1                             | 366                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33731980  | Ca7                                     | 33731980                      | AG/AGGTCG                                                     | ATCACCGATCAAAAGC<br>AAGG   | ATCCCTTTTTCCCGATC<br>AAC   | 60.1                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33732435  | Ca7                                     | 33732435                      | ATTTTTTTTT/ATTTTTTTTTT                                        | GTTGATCGGGAAAAAG<br>GGAT   | GGAAGCGATAAGCACC<br>AAAG     | 60.1                             | 190                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33732724  | Ca7                                     | 33732724                      | TTATAT/TTATATAT                                               | GTTGATCGGGAAAAAG<br>GGAT   | CTCATATCCATCACACG<br>AGCA    | 60.1                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33732749  | Ca7                                     | 33732749                      | CAAAAA/CAAAAAA                                                | GTTGATCGGGAAAAAG<br>GGAT   | CTCATATCCATCACACG<br>AGCA    | 60.1                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33733056  | Ca7                                     | 33733056                      | GTTTTTTTT/GTTTTTTTTT                                          | TGCTCGTGTGATGGAT<br>ATGAG  | TTGACGATTATTGGCG<br>ATGA     | 59.7                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33736659  | Ca7                                     | 33736659                      | TATTATTATAATTATTATA/TATTATT<br>ATA                            | ACGGCGTTTACCATCA<br>AGAA   | AAGTGAAAACCTAAC<br>GCGA      | 60.5                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33749071  | Ca7                                     | 33749071                      | ATTTTTTTTT/ATTTTTTTT                                          | ATTCCGACTCTGTCCC<br>ATTG   | CCAAGGATGAATGGTT<br>TGGT     | 59.9                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33767556  | Ca7                                     | 33767556                      | ATTTTTTTTT/ATTTTTTTTTT                                        | GACTCCCTTGTTGCA<br>TGAT    | GGGGTGAAGTAGCCTA<br>ATTGA    | 59.9                             | 269                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33768087  | Ca7                                     | 33768087                      | TAAAAAA/TAAAAAAA                                              | TCAAATTAGGCTAGTTC<br>ACCCC | AAAGGATGCACCAATG<br>AAGC     | 59.5                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33768316  | Ca7                                     | 33768316                      | CTA/CTATA                                                     | GCTTCATTGGTGCATC<br>CTTT   | TCAGGCTAAAAGTGAA<br>AACTCG   | 60.1                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33768477  | Ca7                                     | 33768477                      | T/TATGATAAG                                                   | GCTTCATTGGTGCATC<br>CTTT   | AAAAAGACAAAACCTACC<br>CTTGTA | 60.1                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33768562  | Ca7                                     | 33768562                      | ATCTTCTT/ATCTT                                                | GCTTCATTGGTGCATC<br>CTTT  | AAAAAGACAAAACCTACC<br>CTTGTA | 60.1                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33768691  | Ca7                                     | 33768691                      | TAAA/TAAAA                                                    | TCATGTGGGGAAGAAA<br>TTCA  | AAAAAGACAAAACCTACC<br>CTTGTA | 58.9                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33770829  | Ca7                                     | 33770829                      | TC/T                                                          | TTGCATTTAGGGCATG<br>AAAA  | TTTTTCTCCGACTTGGT<br>CCTT    | 59.1                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33772575  | Ca7                                     | 33772575                      | ATTTTTTTT/ATTTTTTTT                                           | TGGATTTTGTGGAT<br>GCAG    | TTCCCACTTTTCAAAA<br>TATCCA   | 59.5                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33772634  | Ca7                                     | 33772634                      | AAGA/AA                                                       | TGGATTTTGTGGAT<br>GCAG    | TTCCCACTTTTCAAAA<br>TATCCA   | 59.5                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33775282  | Ca7                                     | 33775282                      | GTT/GTTT                                                      | ACCCCAAAATCTTTGA<br>CACG  | TCGTGCATCCTCACTC<br>TCAC     | 59.8                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33780221  | Ca7                                     | 33780221                      | CTT/CT                                                        | CAGCCTGACGCCTTTC<br>TAGT  | CGCAAGAATGATGTGA<br>GCAT     | 59.6                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33781250  | Ca7                                     | 33781250                      | AA/AATA                                                       | TTGAGGTGACTAAAGC<br>TCCGA | TCGAACCACACAGAAT<br>TCCA     | 60.0                             | 379                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33795926  | Ca7                                     | 33795926                      | CATTAATTAATTAATTAATTA<br>TTAATT/CATTAATTAATTAATTA<br>AATTAATT | GTGGGCATAGCTTCG<br>TTTA   | TTCCCCGGGTAAACACA<br>ATAA    | 60.1                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33797573  | Ca7                                     | 33797573                      | TTTT/TTTTGTTT                                                 | TGATGTGTGTGCAATT<br>CTGC  | TCTCGAATATCCAACGTG<br>CGA    | 59.3                             | 223                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33798743  | Ca7                                     | 33798743                      | TTA/T                                                         | AGCATTGCATCTGACT<br>GTGC     | CACTCGTGTGATCCT<br>CACA      | 60.0                             | 948                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33798765  | Ca7                                     | 33798765                      | TA/TAATAACACA                                                 | AGCATTGCATCTGACT<br>GTGC     | CACTCGTGTGATCCT<br>CACA      | 60.0                             | 948                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33805672  | Ca7                                     | 33805672                      | TAAATGAAAAATGAAAA/TAAATG<br>AAAAATGAAAAATGAAAA                | TCACCGCAACTGACAA<br>AGTC     | GCGTTATTAGACGAAT<br>GACTTGAA | 59.9                             | 406                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33806992  | Ca7                                     | 33806992                      | CTTTTTTTTT/CTTTTTTTTT                                         | TCCAATCCAAGAGCTA<br>AACCA    | TTCGATAGTCGCACAA<br>CCAC     | 59.7                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33813677  | Ca7                                     | 33813677                      | CAAA/CAA                                                      | CAGCTGGATATTGGAT<br>GGAGA    | GAAGGGCTAGTGCCAA<br>GTGA     | 60.0                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33823403  | Ca7                                     | 33823403                      | ATTTTTTTTT/ATTTTTTTTTTT                                       | GCGAATCAGAAGCCAT<br>TGAA     | CGAAACGCGACTAGTA<br>ACCA     | 60.0                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33827430  | Ca7                                     | 33827430                      | GTTTT/GTTTT                                                   | CGAGTGATGACTTTTC<br>CCGT     | TCAACTTTGTTACTTGC<br>AGTTGTG | 60.1                             | 212                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33830170  | Ca7                                     | 33830170                      | CTT/CT                                                        | TTTGATGGGTTTTGTTT<br>GAAAAAT | CCACAATGGCGGAACT<br>TTAT     | 59.6                             | 667                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33830731  | Ca7                                     | 33830731                      | T/TC                                                          | GGGGAGAAACGAATAA<br>TCCC     | GGTAACTTCCATTGCC<br>GAAA     | 59.6                             | 259                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33839740  | Ca7                                     | 33839740                      | TA/TAA                                                        | GCTGGCAGAGTAAATA<br>GCCG     | TGGAAGAACATAAGG<br>TCAGGAA   | 60.0                             | 243                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33851299  | Ca7                                     | 33851299                      | GA/G                                                          | CCCACTTTGCAATTTAG<br>GACA | CGGAATTTCTCGGACA<br>TCAT    | 60.0                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33852197  | Ca7                                     | 33852197                      | CTATATATATAT/CTATATATATATAT                                   | TGCATCAACTTTTTGG<br>GTGA  | TTGGCCATATTTGAACC<br>ACTC   | 60.1                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33853228  | Ca7                                     | 33853228                      | CTTT/CTTTTTTT                                                 | GGAAAGAAGTCCAAGA<br>GGGC  | AGAGTGTTCGCGGT<br>TGTT      | 60.2                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33855439  | Ca7                                     | 33855439                      | CAA/CA                                                        | TCCAGAAGATGGTGAG<br>AGTGG | ACTTGATTGCACATGG<br>ATCG    | 60.2                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33857243  | Ca7                                     | 33857243                      | GAAAAA/GAAAAA                                                 | TTGGAAGCCAGAGCAA<br>AAGT  | GCCTCGTTTCATTTAAT<br>CTGC   | 60.0                             | 691                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33857564  | Ca7                                     | 33857564                      | TTA/TTAAAATTTATAATAGATA                                       | GGCATGACATTCAAGA<br>GCATT | GCCTCGTTTCATTTAAT<br>CTGC   | 60.1                             | 333                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33859459  | Ca7                                     | 33859459                      | AAG/A                                                         | AAAATGCGAAGATGTT<br>TACGG | CTTACCCTCTCGTAG<br>CACC     | 59.1                             | 768                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33873981  | Ca7                                     | 33873981                      | ACTCT/ACT                                                     | TTTTTGCGAAATCAGAA<br>CGG  | TCGAGAGATACTAGGA<br>TGTGCGT | 61.1                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33886522  | Ca7                                     | 33886522                      | TATCA/TATCATCA                                                | TTGAGGCAATTTCTTC<br>CTTGA | CTTGAGCATGCTTGT<br>TGAA     | 59.8                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33894708  | Ca7                                     | 33894708                      | ATTTTTT/ATTTTT                                                | TCACTATGACAACGGG<br>GTGA  | CCCGTGAAATGCTTG<br>GAGT     | 60.0                             | 286                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33895177  | Ca7                                     | 33895177                      | CTTTTT/CTTTT                                                  | ACTCCAAGACATTCA<br>CGGG   | GCATGCAATTCACGCA<br>TTAT     | 60.0                             | 340                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_33895271  | Ca7                                     | 33895271                      | TGG/TG                                                        | ACTCCAAGACATTCA<br>CGGG   | AAAATCATATTCTCTAA<br>CCGCCTC | 60.0                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34108455  | Ca7                                     | 34108455                      | TAAAAAAAA/TAAAAAAAA                                           | TTGTTGCGTCCATATT<br>TCG   | TCTTTTGGCCCTCTT<br>GTA       | 59.6                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34109983  | Ca7                                     | 34109983                      | GAAA/GAAAA                                                    | TCGGGACCCACTTATT<br>TGAC  | AAAATTGTGTGGTGGT<br>GGGT     | 59.8                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34110831  | Ca7                                     | 34110831                      | AGATGA/AGATGATGA                                              | TGATGTCGCATATGCC<br>TTTT  | TGGTGGTCATGTTGT<br>TGCT      | 59.1                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34116846  | Ca7                                     | 34116846                      | ATTTTTTT/ATTTTTTTTT                                           | GATTTGACGTCCTGTC<br>TCGG  | AGAATTGGCAGATTCTG<br>ATGG    | 60.7                             | 571                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34117745  | Ca7                                     | 34117745                      | TGGC/TGGCGGC                                                  | CGAATCTGCCAATTCT<br>GGAT  | AGTTGCAGTGCCTGTG<br>TTTG     | 60.0                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34171978  | Ca7                                     | 34171978                      | TTTTTTTT/TTTTTTTTTTTT                                         | CCAATCCAATCACCCA<br>ATTCT | AGCACCGTTACTTGGT<br>CCAC     | 60.0                             | 764                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34184526  | Ca7                                     | 34184526                      | T/TA                                                          | TTCACTCCGAAAATTC<br>GTCC  | CGCCACAGTAGTCCAT<br>GAAA     | 60.1                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34184730  | Ca7                                     | 34184730                      | AA/AAACTAAATA                                                 | TGGCGGAGTGATGACA<br>ATTA  | TTTGAAGTGAGAAGAA<br>GAAGACCA | 60.1                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_34185206  | Ca7                                     | 34185206                      | AA/AATA                                                       | TGGTCTTCTTCTTCTCA<br>CTTCAAA  | CCATCAAACGCATCATA<br>TCG   | 59.6                             | 819                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34186198  | Ca7                                     | 34186198                      | ATTCTTCTTCTTCTTCTTC/ATTCTTC<br>TTCTTCTTCTTCTTC                | TATTAGGATCCGTAAC<br>CCGC      | CAGAGCCGGAAAGAGA<br>AATG   | 58.9                             | 369                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34191111  | Ca7                                     | 34191111                      | CATGAATGAAT/CATGAATGAATGAA<br>T                               | CAATGACATGAGTGCA<br>ACACC     | TTTGAGTCCGAATTTTG<br>AACC  | 60.0                             | 120                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34191517  | Ca7                                     | 34191517                      | ATTTTTTTTT/ATTTTTTTT                                          | CAATGACATGAGTGCA<br>ACACC     | GTTTCGATCGCCATTGA<br>AGTT  | 60.0                             | 893                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34191589  | Ca7                                     | 34191589                      | TAAAAAAAA/TAAAAAAAA                                           | TGGTTCAAAATTCGGA<br>CTCAA     | GTTTCGATCGCCATTGA<br>AGTT  | 60.5                             | 795                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34191630  | Ca7                                     | 34191630                      | TAAA/TAAAA                                                    | TGGTTCAAAATTCGGA<br>CTCAA     | GTTTCGATCGCCATTGA<br>AGTT  | 60.5                             | 795                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34203381  | Ca7                                     | 34203381                      | A/AATATATAGGTAG                                               | GTAAAGCTGGCAAGCA<br>CGAT      | CCCAGAACAAAAGTTG<br>GTGAA  | 60.4                             | 725                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34205393  | Ca7                                     | 34205393                      | CTTTTTTTTT/CTTTTTTTT                                          | TTGAAATACACACACAA<br>AATTGACA | TTGACCTTGAAATCAAC<br>TCACC | 59.4                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34205414  | Ca7                                     | 34205414                      | ATTTT/ATTTTT                                                  | TTGAAATACACACACAA<br>AATTGACA | TTGACCTTGAAATCAAC<br>TCACC | 59.4                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34226505  | Ca7                                     | 34226505                      | AAATA/AA                                                      | AACACCAATCGCTCTT<br>CCAC      | GAGGGAACACCAACTC<br>CAAA   | 60.1                             | 889                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_34237601  | Ca7                                     | 34237601                      | TTG/TTGGTTTTGGTTATG                                           | TGGGAGGATGAGATGA<br>GACC   | CAAGGAACCATCCATT<br>GCT     | 60.0                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34237749  | Ca7                                     | 34237749                      | ACT/A                                                         | TGGGAGGATGAGATGA<br>GACC   | CAAGGAACCATCCATT<br>GCT     | 60.0                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34240747  | Ca7                                     | 34240747                      | ATTT/ATTTTT                                                   | ATCCTCCAATGTCATG<br>CCTC   | CAACCAAGTCCACATG<br>ATGC    | 59.9                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34241125  | Ca7                                     | 34241125                      | TC/TCGAGTATCC                                                 | GCATCATGTGGACTTG<br>GTTG   | CAAAGCTACCACACCT<br>TACTTGC | 60.0                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34241176  | Ca7                                     | 34241176                      | TAA/TA                                                        | GCATCATGTGGACTTG<br>GTTG   | CAAAGCTACCACACCT<br>TACTTGC | 60.0                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34241485  | Ca7                                     | 34241485                      | CTTTT/CTT                                                     | TGGTTGTTCCATCACA<br>TGTCT  | CAAAGCTACCACACCT<br>TACTTGC | 58.8                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34241510  | Ca7                                     | 34241510                      | GGTGTG/GGTG                                                   | CGCAATATCTTTTATT<br>GTGTTC | AAGAAACTGCAGGTT<br>GAGATT   | 59.0                             | 795                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34243256  | Ca7                                     | 34243256                      | A/AATG                                                        | TCAATACTCCACCACC<br>ACCA   | TGGGACATCGTTCATA<br>TTCA    | 59.8                             | 709                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34243286  | Ca7                                     | 34243286                      | A/AC                                                          | TGTAAGTGTGGCTTTC<br>TCTCG  | TGGGACATCGTTCATA<br>TTCA    | 58.2                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34247804  | Ca7                                     | 34247804                      | TTA/TTATA                                                     | CAAGACATGTTTCATC<br>CCCT   | TGGAGAAGTTGGCTTT<br>GGTC    | 59.8                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_34249701  | Ca7                                     | 34249701                      | GA/GAA                                                        | CCATTGGTGGTACAAG<br>ACCC     | ATAGCTGACCACCCAA<br>AACG | 60.1                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34277307  | Ca7                                     | 34277307                      | T/TG                                                          | CAATGGCAGAAGAAGC<br>ACAA     | TTTGTGGTGCCAGTGT<br>GAAT | 60.0                             | 335                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34278071  | Ca7                                     | 34278071                      | T/TC                                                          | TCTTCAAGTGGTCGCT<br>TCCT     | CCTTCGCCATTTAATTT<br>TGG | 60.0                             | 915                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34278231  | Ca7                                     | 34278231                      | ATTTTTT/ATTT                                                  | TGGACTGCTCGATTGT<br>CAAA     | CCTTCGCCATTTAATTT<br>TGG | 60.4                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34286325  | Ca7                                     | 34286325                      | A/AAATAT                                                      | ACGTCAGACATTGGAT<br>GTGC     | TTGTTTTCAAGGAGTTG<br>CGA | 59.6                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34286498  | Ca7                                     | 34286498                      | ATT/A                                                         | CCTCTAAAAATGGAAAA<br>TGACCA  | GTCTCTGCCGCTGAAC<br>TCTT | 59.4                             | 793                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34287454  | Ca7                                     | 34287454                      | GAAAAAA/GAAAAAA                                               | TGACTATTTTGCATAAC<br>GAAGAGA | ATAGAGCTCTTGCCGG<br>TTGA | 58.2                             | 242                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34288517  | Ca7                                     | 34288517                      | CAA/CAAA                                                      | GGAGCTATAGGGCATA<br>CCGA     | TGCGCAGCTAAAATAT<br>GAGG | 59.2                             | 853                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34306144  | Ca7                                     | 34306144                      | AG/A                                                          | CGGTTACAAGCACACC<br>ATTG     | GATGGCGATAGCAACC<br>AAAT | 60.0                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34309692  | Ca7                                     | 34309692                      | TA/T                                                          | TGTGAGTCGATGAATC<br>AGCC     | TCGAATTCGTGTCCA<br>CTCA  | 59.8                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')         | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                 |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_34310917  | Ca7                                     | 34310917                      | CTTT/CTTTT                                                    | CCACAAAATTCATGCT<br>GCAA        | GGACCAGAAAAGCAGG<br>AGGT | 60.6                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34311495  | Ca7                                     | 34311495                      | TAAAA/TAAA                                                    | TCCAGCATGCAGCATA<br>GTTT        | TGCAGGACCAGATAGG<br>GAAG | 59.4                             | 214                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34312312  | Ca7                                     | 34312312                      | TTAT/TT                                                       | CTCCTTTCTCACACTCA<br>CTCCA      | TTGGTGGACTTCCAA<br>CTTC  | 59.5                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34312381  | Ca7                                     | 34312381                      | CTTT/CTTTTT                                                   | CTCCTTTCTCACACTCA<br>CTCCA      | TTGGTGGACTTCCAA<br>CTTC  | 59.5                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34312433  | Ca7                                     | 34312433                      | GATAAATA/GATA                                                 | CTCCTTTCTCACACTCA<br>CTCCA      | TTGGTGGACTTCCAA<br>CTTC  | 59.5                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34312582  | Ca7                                     | 34312582                      | TAA/TAAA                                                      | CTCCTTTCTCACACTCA<br>CTCCA      | TTGGTGGACTTCCAA<br>CTTC  | 59.5                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34312678  | Ca7                                     | 34312678                      | ATTTTTTTTT/ATTTTTTTT                                          | CTCCTTTCTCACACTCA<br>CTCCA      | TTGGTGGACTTCCAA<br>CTTC  | 59.5                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34313485  | Ca7                                     | 34313485                      | TACCA/TA                                                      | TCTGGAATTCACAATCA<br>CGG        | AATGTCCCACTCCAA<br>AAAG  | 59.5                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34315074  | Ca7                                     | 34315074                      | GATATATA/GATATATACATATATATA<br>TA                             | TTCTGATAATTGGAATC<br>ACTTCTAACA | TTGCACCCGTAGTATT<br>GTGG | 59.5                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34316435  | Ca7                                     | 34316435                      | ATAATTAAT/ATAATTAATTAAT                                       | CATGGGTCTCACCCCT<br>AGAA        | AAGGTTGCCATTGTATT<br>GGG | 59.9                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_34317406  | Ca7                                     | 34317406                      | ATATA/ATATAGTATA                                              | TGGAATTTGTATGCGA<br>GACG    | GCAGGGTTTTGTTTT<br>GGA     | 59.7                             | 896                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34317462  | Ca7                                     | 34317462                      | TAAAAAAAA/TAAAAAAAAA                                          | TTGTTTTTGGTGAAAAG<br>TGTGTG | GCAGGGTTTTGTTTT<br>GGA     | 60.0                             | 429                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34317535  | Ca7                                     | 34317535                      | AATATATATATATA/AATATATATATA                                   | TTGTTTTTGGTGAAAAG<br>TGTGTG | GCAGGGTTTTGTTTT<br>GGA     | 60.0                             | 429                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34317797  | Ca7                                     | 34317797                      | TAAATAAAATAAAAAA/TAAAA                                        | AATCATCCACCTCACC<br>TCCC    | GCAGGGTTTTGTTTT<br>GGA     | 61.1                             | 258                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34318595  | Ca7                                     | 34318595                      | CATTATTACAGATT/CATTATTACA<br>GATTATTATTACAGATT                | TCAATGACTGTGACAA<br>AATCCA  | GCTAGCAGCCACCTC<br>TTTG    | 59.0                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34320519  | Ca7                                     | 34320519                      | C/CTA                                                         | TTAACAAAACGGCTCC<br>AACC    | ACATGGCTTGGAGTTG<br>GAAT   | 60.0                             | 438                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34321844  | Ca7                                     | 34321844                      | ATTTTTTT/ATTTTTTTTT                                           | TCGGTGCCTTCATATT<br>GACT    | TTTTCTCATGGATCTTT<br>TGGA  | 59.6                             | 812                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34328779  | Ca7                                     | 34328779                      | AT/ATTCAGT                                                    | AGGGAGGCACCTCGGA<br>GTAT    | GTGCAACCGATTGGTA<br>TCCT   | 60.1                             | 793                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34335084  | Ca7                                     | 34335084                      | TTATATA/TTATA                                                 | CCAATAACAATGGGG<br>TTCA     | CCTCTTTGTTGGATGA<br>GGGA   | 60.4                             | 259                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34336023  | Ca7                                     | 34336023                      | AA/AAAAAGA                                                    | TATTTGACCCGTGAGA<br>CGTG    | CAACCACAATTCAATT<br>ATGCAA | 59.6                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_34336261  | Ca7                                     | 34336261                      | TAAA/TAA                                                      | TTTTTGGAGGAAAAGT<br>GTTGC    | TGAAATCAATCTTTGTG<br>TTGCTC | 59.2                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34337201  | Ca7                                     | 34337201                      | TATAATAATAATA/TATAATAATA                                      | GCCGTCCTTAGCCTTC<br>TTTT     | TCTTTTGCAGTTGTGT<br>TTGC    | 59.9                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34337758  | Ca7                                     | 34337758                      | TAAAA/TAAA                                                    | TGCAAAACACAACTGCA<br>AAAAG   | TGCAACATCCATTGAT<br>GACC    | 59.9                             | 755                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34338469  | Ca7                                     | 34338469                      | TAAAAA/TAAAAA                                                 | CCCCAACAAAGGTCAT<br>CAAT     | TGAGCTCCACCTTTTG<br>ATCC    | 59.6                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34342061  | Ca7                                     | 34342061                      | ATTTTT/ATTTTT                                                 | GATAGGTGGACGTTCA<br>AATTTTC  | GCCCATACGGGATTAT<br>TTTTG   | 58.9                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34342253  | Ca7                                     | 34342253                      | TTTTT/TTTTTATTTT                                              | AATGATAGGTGGACGT<br>TCAAA    | GGGTAACCTCGCCACA<br>ACTA    | 57.1                             | 725                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34374813  | Ca7                                     | 34374813                      | CATGTATG/CATG                                                 | CATGGGTTCAACGTCG<br>TTACT    | GGAGTGGAGTGGACGA<br>ACAT    | 59.9                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34375146  | Ca7                                     | 34375146                      | GTCCACTCCACTCCACTC/GTCCAC<br>TCCACTCCACTCCACTC                | GAGGGGTTTGTGGAAT<br>GGTA     | GTAATCACCAACCAATC<br>GGG    | 59.6                             | 271                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34383561  | Ca7                                     | 34383561                      | GTGTT/G                                                       | TTGGATCCTGAGTACC<br>TCGC     | TGGATAGGTTTACCAA<br>ACAAAAA | 60.2                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34384368  | Ca7                                     | 34384368                      | CCACCTTCAAAGT/C                                               | TGTATTCAACGTGTATT<br>TTCCAGA | AAAATGAAAAATCGTCG<br>AACAAA | 58.6                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_34392098  | Ca7                                     | 34392098                      | ATTTTTTT/ATTTTTTTTT                                           | GCGAGCATGAAATAC<br>CAAT    | TCTGCCAAAACGAAG<br>ATCG    | 59.9                             | 819                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34394315  | Ca7                                     | 34394315                      | AG/A                                                          | TATTTGGCTATCTGCG<br>GTCC   | TCGGATGTAAATGCGA<br>TGAA   | 60.1                             | 726                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34400530  | Ca7                                     | 34400530                      | CT/C                                                          | TGCAGATTGAACCGCT<br>AATG   | ACGAACTAATGCCGA<br>ATTG    | 59.8                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34405257  | Ca7                                     | 34405257                      | G/GCTA                                                        | ATGTGGCGCCAATACA<br>CTTA   | GAAAGCATAAACCGGC<br>AAAA   | 59.1                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34405422  | Ca7                                     | 34405422                      | ATTTTTTT/ATTTTTTT                                             | ATGTGGCGCCAATACA<br>CTTA   | TCCTTCAAGGCATTGT<br>GTGT   | 59.1                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34407596  | Ca7                                     | 34407596                      | CTAT/CTATAT                                                   | TGCATGCAGCTTCCTT<br>CTAA   | GCATGCAGCCTTGTTG<br>ATTA   | 59.7                             | 809                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34408093  | Ca7                                     | 34408093                      | TTCTCTCTCT/TTCTCTCTCTCT                                       | TTCCCCGGTGACATAA<br>CAGT   | TTCAGTAAGTGCTGCA<br>TGGC   | 60.2                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34408969  | Ca7                                     | 34408969                      | GAAAAAA/GAAAAAAA                                              | TTTTGCAGGCTTATGC<br>AGTG   | CATCACCTCAATTGTGA<br>TTGC  | 60.0                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34480302  | Ca7                                     | 34480302                      | CTATATATATATATATATATATAT<br>ATATAT/CTATATATATATATATAT<br>AT   | CGAAGAGACATGACTT<br>TGTCCA | TTGAAGATGATGACGA<br>CAATGA | 60.3                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3450236   | Ca7                                     | 3450236                       | AATATATATATATATATA/AATATATA<br>TATATATATATATA                 | GCACAATATAAGTGAG<br>CCCCA  | TCAGAGTTCAGACCCC<br>ATCC   | 60.0                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                       | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                     |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_34509858  | Ca7                                     | 34509858                      | GAGAGGGAGAGAGAGA/GAGAGGG<br>AGAGAGAGAAAGAGGGAGAGAGAG<br>A                                                           | TTTGTGGTTCTTCCTC<br>GACC    | GGGTGGATATCAAATG<br>ACCAA  | 60.1                             | 173                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34583170  | Ca7                                     | 34583170                      | CATATATATATATATATATATATATA<br>TATATATAT/CATATATATATATATAT<br>ATATATATATATAT                                         | TTTCATCCACCAAGAAG<br>CTCA   | GAATCGACCAAGTGCA<br>GACA   | 59.4                             | 253                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34603134  | Ca7                                     | 34603134                      | TTTATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATTATT<br>/TTTATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATT | TACCAGCAATTTGTGC<br>CTTG    | TTGATTTTGAAATTTCC<br>GGG   | 59.7                             | 198                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34663130  | Ca7                                     | 34663130                      | ATTTTTTTTTTT/ATTTTTTTTTTTT                                                                                          | AAATTTTGGTTGCGATT<br>CCA    | ACCCGGGTATAAGGTT<br>CCAC   | 60.3                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34735432  | Ca7                                     | 34735432                      | CAA/CAA                                                                                                             | GGTTTTGCCCTATTT<br>CCAT     | TTGCAAGTTTAGATCG<br>CTTGTC | 60.0                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34833504  | Ca7                                     | 34833504                      | ATTTTTTTTTTT/ATTTTTTTTTTTT                                                                                          | GCAAACGAGCCTTTCA<br>TTGT    | GCTGTTTGTGAGAG<br>CATAGG   | 60.3                             | 340                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_34922873  | Ca7                                     | 34922873                      | AATTATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTA/AATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTA         | GCCACCACCTTCTTGA<br>ACAT    | TTGTCCAAGGTGCAAT<br>TCAA   | 60.0                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35082940  | Ca7                                     | 35082940                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                                                                           | TTGTCTCTACTCATTT<br>GGTTGGA | GCTTATGCTTTAAGCC<br>GCAC   | 60.0                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35109014  | Ca7                                     | 35109014                      | ATTTTTTT/ATTTTTTTTTTT                                                                                               | CCTGGGATGGTGATGA<br>GAGT    | TCCCAACCAGACTGAA<br>CTGG   | 59.9                             | 806                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35119755  | Ca7                                     | 35119755                      | CTT/CTTT                                                                                                            | ATGTCACCACCAGCTG<br>TTCA    | GCTAAATGCCAATGAG<br>GCTT   | 60.2                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_35120111  | Ca7                                     | 35120111                      | T/TG                                                          | GCCTCATTGGCATTTA<br>GCTT   | AAAAAGAAGTCGAGTC<br>ACCG   | 59.3                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35120290  | Ca7                                     | 35120290                      | CTATATAT/CTATAT                                               | GCCTCATTGGCATTTA<br>GCTT   | TGCATCATTCTTACAC<br>GTTGA  | 59.3                             | 814                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35121825  | Ca7                                     | 35121825                      | CATAT/CAT                                                     | AAAAATAATTGGCACAA<br>ACCAA | GGGCAATTTTCTGTCT<br>CCAA   | 58.5                             | 851                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35121887  | Ca7                                     | 35121887                      | GAAAAAAAA/GAAAAAAAA                                           | AAAAATAATTGGCACAA<br>ACCAA | GGGCAATTTTCTGTCT<br>CCAA   | 58.5                             | 851                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35122692  | Ca7                                     | 35122692                      | ATTTTT/ATTTTTTTTT                                             | TTGAGACAGAAAATT<br>GCCC    | ACCTGAATGTGCGAAC<br>AAGA   | 60.1                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35126886  | Ca7                                     | 35126886                      | GTTTTT/GTTTTTTT                                               | GGAGAGCCTCACAAAG<br>AACG   | CGTGATAGACAAGTCG<br>ATTCCA | 60.0                             | 320                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35130007  | Ca7                                     | 35130007                      | AAA/AAATTAA                                                   | TCTCTGCAATTTCCAA<br>GCC    | AAGTTTGGTTGACGGA<br>TTGC   | 60.3                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35131412  | Ca7                                     | 35131412                      | TAAAAAA/TAAAAAAA                                              | TCGTGGTCGCATTGAA<br>CTTA   | GAATCAAAATGGAGCG<br>GAAA   | 60.3                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35135579  | Ca7                                     | 35135579                      | TGG/T                                                         | TGTTGGGTCACGCAAT<br>TTTA   | TGGTGAACACTCCAAC<br>GCTA   | 60.0                             | 409                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35135655  | Ca7                                     | 35135655                      | AATATATA/AATATATATA                                           | TGTTGGGTCACGCAAT<br>TTTA   | TGGTGAACACTCCAAC<br>GCTA   | 60.0                             | 409                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_35138152  | Ca7                                     | 35138152                      | CAGA/CA                                                       | TTCGGATATGAAAAGTT<br>TTTAGCA | TGGGTAGGTACGCCAC<br>TTTC  | 59.2                             | 137                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35138981  | Ca7                                     | 35138981                      | ATTTTTTTTT/ATTTTTTTT                                          | ATGGGTGCGTTTCTTT<br>TCAG     | TCGCTCTCATCAATCAC<br>ATCA | 60.1                             | 171                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35140849  | Ca7                                     | 35140849                      | GAAAAAAA/GAAAAAAA                                             | CACCATGAGATCTTGA<br>GGCA     | GTTCTCCCTCCATCC<br>CTAA   | 59.8                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35141972  | Ca7                                     | 35141972                      | TA/TAA                                                        | TTGTCCACGAGGAGA<br>AAAC      | CGACAAACACAATCACT<br>GGG  | 60.1                             | 824                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35148211  | Ca7                                     | 35148211                      | ATT/AT                                                        | TCAAATTTGCCCTGA<br>CTTT      | AACGGCTAACATTGG<br>CAAC   | 59.5                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35148239  | Ca7                                     | 35148239                      | CAAAAAA/CAAAAAA                                               | TCAAATTTGCCCTGA<br>CTTT      | AACGGCTAACATTGG<br>CAAC   | 59.5                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35148641  | Ca7                                     | 35148641                      | ATCTCT/ATCT                                                   | GTTGCCAAATGTTAGC<br>CGTT     | GTCTTTGTCAGGGGAG<br>TGGA  | 60.0                             | 221                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35150109  | Ca7                                     | 35150109                      | TTTTATTTATTTATTTATTT/TTT<br>TATTTATTTATTTATTTATTT             | GGGGAACTTTTGGGG<br>AGTA      | CACCTTCGCCAATTCA<br>TCT   | 60.2                             | 820                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35155463  | Ca7                                     | 35155463                      | TAAAAAAA/TAAAAAAA                                             | GGAGAATGTTTGGGAC<br>CGTA     | GGGGTGCTACAAAACA<br>GGAA  | 59.8                             | 908                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35156256  | Ca7                                     | 35156256                      | ATTTTT/ATTTTTT                                                | TTCTGTTTTGTAGCAC<br>CCC      | CACCATTGTCCGATTG<br>TCAG  | 60.0                             | 757                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_35166415  | Ca7                                     | 35166415                      | TC/T                                                          | ATCAAGGTGGGATTG<br>TTGA     | TTGTAGTTTTTCACGTG<br>GTGC  | 60.2                             | 781                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35166766  | Ca7                                     | 35166766                      | TAAAAAAA/TAAAAAA                                              | GGCGCTATATGGTATT<br>TTGAGTT | GGTCTTCGCCTTCAC<br>AAAC    | 58.7                             | 948                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35175388  | Ca7                                     | 35175388                      | TAAAAAAA/TAAAAAAA                                             | TACTTTGCGTGTCTC<br>GTCG     | CCCATGAAGGAAAAAT<br>AGCG   | 60.1                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35175572  | Ca7                                     | 35175572                      | AAATA/AA                                                      | GGCCATGGGAATAA<br>ACTG      | CCCATGAAGGAAAAAT<br>AGCG   | 59.4                             | 239                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35175664  | Ca7                                     | 35175664                      | TAAAAAAA/TAAAAAAA                                             | GGCCATGGGAATAA<br>ACTG      | CCCATGAAGGAAAAAT<br>AGCG   | 59.4                             | 239                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35177660  | Ca7                                     | 35177660                      | A/ATAAAATAAAT                                                 | GCCAACCGACTCCATC<br>TTTA    | TTAGCAGTTTTTCAAT<br>TTCCAA | 60.1                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35178628  | Ca7                                     | 35178628                      | TT/TTCT                                                       | TTTTCAAATTTTCCCC<br>TCG     | TCGTTCAATCAATCACG<br>AGAA  | 59.2                             | 241                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35211759  | Ca7                                     | 35211759                      | TAAACAAAA/TAAACAAAA<br>AAA                                    | GATTCGAACAGGACCT<br>CCAA    | GGTCCGTTCTGAGTGG<br>TTGT   | 60.1                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35212272  | Ca7                                     | 35212272                      | GATATATATAT/GATATATAT                                         | ACAACCACTCAGAAGC<br>GACC    | TGCACTTGTGTATGTG<br>AATGTT | 60.0                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35215568  | Ca7                                     | 35215568                      | TAAAAAAA/TAAAAAAA                                             | TGATTTTGGTGGGGCT<br>TTTA    | ATGCTCCACCGTACAC<br>CTTC   | 60.3                             | 712                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_35216311  | Ca7                                     | 35216311                      | CTTTTTTTT/CTTTTTTTT                                           | TGCCTCATTCTTTTGGAA<br>ACC     | GGAAGGAGGGACAAA<br>CACA     | 60.1                             | 839                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35218713  | Ca7                                     | 35218713                      | AAT/AATAT                                                     | TGTTTCGATCCACATT<br>GTAGAATTA | TGATGAGAGAAACCGA<br>ACCC    | 59.8                             | 957                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35219845  | Ca7                                     | 35219845                      | TAAAAAAAAAAAA/TAAAAAAAAAA                                     | TTTCCTTTTGTCTTCA<br>TGG       | CGGATTTACCTCTCCC<br>AACA    | 60.0                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35230825  | Ca7                                     | 35230825                      | ATTTTTTTTT/ATTTTTTTTT                                         | AAGTAGCAAAGCCTCA<br>CCCA      | CGGATAATTTCAAATG<br>GATCACT | 59.9                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35230846  | Ca7                                     | 35230846                      | ATTTT/ATTT                                                    | AAGTAGCAAAGCCTCA<br>CCCA      | CGGATAATTTCAAATG<br>GATCACT | 59.9                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35232044  | Ca7                                     | 35232044                      | AA/AAATTA                                                     | TTTGACCCTCAGCCAT<br>TTTC      | GAAAAATGGGAATGCA<br>ATGG    | 60.1                             | 244                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35232062  | Ca7                                     | 35232062                      | TCTCACTCAC/TCTCACTCACTCAC                                     | TTTGACCCTCAGCCAT<br>TTTC      | GAAAAATGGGAATGCA<br>ATGG    | 60.1                             | 244                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35256420  | Ca7                                     | 35256420                      | ATTTTTTTTTTT/ATTTTTTTTTT                                      | CATTGTGGACTTGTGCG<br>GAGA     | CTCACACGGTGCTTCT<br>CAAA    | 59.7                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35256727  | Ca7                                     | 35256727                      | TC/TCAAC                                                      | GCAAGGGGCAATTTAG<br>TCAA      | CTCACACGGTGCTTCT<br>CAAA    | 60.1                             | 148                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35302573  | Ca7                                     | 35302573                      | GTTTTT/GTTTTTT                                                | TTTGAACAGCAATCCA<br>ACCA      | AGTGAACAACCAACCC<br>ATTTT   | 60.1                             | 299                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_35304579  | Ca7                                     | 35304579                      | CAAAAA/CAAAAA                                                 | TTTGGAATGAAGAGC<br>ACAG     | CTGTATGCCCAAGTGTG<br>TTGG  | 60.0                             | 263                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35313643  | Ca7                                     | 35313643                      | TC/T                                                          | TTCGATAAAGCAAAAG<br>CTCCA   | AACTGAATATGGGCCA<br>GTCG   | 60.0                             | 805                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35318451  | Ca7                                     | 35318451                      | AAAT/A                                                        | CCTCTGAAGCAAGCAA<br>CACA    | TCAATCACGCGAATTG<br>AAAA   | 60.2                             | 203                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35347916  | Ca7                                     | 35347916                      | CGTGATAGATTTAATAGG/CGTGAT<br>AGATTTAATAGGTGATAGATTTAAT<br>AGG | TTTATGGGTTGGATAG<br>GAGG    | CCATGTCAACACAAAG<br>CGAG   | 59.7                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35357002  | Ca7                                     | 35357002                      | CTTTTTTTTT/CTTTTTTTTTTT                                       | TGGATGTCATGTTTCTT<br>AATGGA | CACATACGGGGTTTTA<br>GATTCG | 59.3                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35357103  | Ca7                                     | 35357103                      | ATTAATATATAGT/AT                                              | CCCAATCAGCTTGTCT<br>TGTTTC  | CACATACGGGGTTTTA<br>GATTCG | 59.7                             | 406                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35364062  | Ca7                                     | 35364062                      | ATTTT/ATTT                                                    | AGGCCTGCACATTTTT<br>CAGT    | ATGACCGAGCCTGATA<br>CCTG   | 59.7                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35364737  | Ca7                                     | 35364737                      | AGATTAGGA/AGA                                                 | CGCATTCTCTCGAAA<br>AGTC     | TTGGAGAAAGATCTCC<br>GGTT   | 60.0                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35366726  | Ca7                                     | 35366726                      | GAA/GA                                                        | ATTAGCAAAAACGGCA<br>GCAG    | TGCGACCTTCTGTTGA<br>ATTG   | 60.4                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35366746  | Ca7                                     | 35366746                      | TCC/TCCC                                                      | ATTAGCAAAAACGGCA<br>GCAG    | TGCGACCTTCTGTTGA<br>ATTG   | 60.4                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_35367066  | Ca7                                     | 35367066                      | GAAAAA/GAAAAA                                                 | CAATTCAACAGAAGGT<br>CGCA      | GCACAGTCAACCGTCA<br>CACT | 59.8                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35368672  | Ca7                                     | 35368672                      | TAAAAAAAAA/TAAAAAAAAA                                         | TTAGGAAGTCGTTGGA<br>TGGG      | TCATACCCCCAAGTTT<br>GCT  | 59.9                             | 309                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35382567  | Ca7                                     | 35382567                      | G/GCTAA                                                       | CCGATCCAATTATATC<br>GACAG     | TTATCAAGGCTCCAC<br>CATC  | 57.1                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35385600  | Ca7                                     | 35385600                      | AATATA/AATATATA                                               | ATTGGATTGCTGAGGC<br>AGTT      | TTTGCTGGAGCTTTGA<br>AACA | 59.7                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3540136   | Ca7                                     | 3540136                       | C/CATAT                                                       | TTGTTGGTACGTGCAT<br>AGAGC     | CATTCACTACGTGCAAA<br>CGG | 58.9                             | 762                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3540381   | Ca7                                     | 3540381                       | CAAA/CAA                                                      | TCAACAATGAAGCAAC<br>ACATCA    | CATTGCGCAAGAGAAT<br>ACGA | 60.2                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3540652   | Ca7                                     | 3540652                       | TG/T                                                          | TCGGATAATCCAATC<br>CGTC       | GGTTTGTAATGTTGC<br>GGCT  | 59.9                             | 647                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35428023  | Ca7                                     | 35428023                      | TTTATTATTATTATTATTATTATT<br>/TTTATTATTATTATTATTATTATT         | CAAGAGCAGATCCCG<br>AGAC       | AACCGGACAATAACTG<br>ACGC | 60.0                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3552289   | Ca7                                     | 3552289                       | TAAA/TAAAA                                                    | CCCTGCTTCAATTTAT<br>CTCTCA    | TGTTGTTGGCACAGA<br>TGTT  | 59.7                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3553337   | Ca7                                     | 3553337                       | TAA/TAAA                                                      | CGATGTGACTTTGTTTA<br>TGTTTTTG | TCTCCAGAAAACGCCA<br>GAGT | 59.9                             | 799                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                           | Forward primers (5'-3')     | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                         |                             |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_35564247  | Ca7                                     | 35564247                      | GAAAAAAAA/GAAAAAAAA                                                                                                                                     | TTTTCGGCCCAATATG<br>ATGT    | TGATTGTCAACTCATGC<br>ACAAA     | 60.2                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35605462  | Ca7                                     | 35605462                      | CATATATATATATATATATA/CATA<br>TATATATATATATATATATA                                                                                                       | TCAACCATTCCGAGTG<br>CATA    | CGCCGTAAATGGCTTA<br>AAAA       | 60.1                             | 667                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35605787  | Ca7                                     | 35605787                      | GAAAAAAAAAAAA/GAAAAAAAAAAAA                                                                                                                             | TTTTTAAGCCATTACG<br>GCG     | TTTGTGTGCATTATC<br>GCAA        | 60.1                             | 225                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35634127  | Ca7                                     | 35634127                      | TTATATATATATATATATA/TTATA<br>TATATATATATATATATA                                                                                                         | TTTGAGTTGGAAATAG<br>GCGAA   | TGAGACCCAAATCAAC<br>CACA       | 59.7                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35645934  | Ca7                                     | 35645934                      | CTTTTTTT/CTTTTTTTT                                                                                                                                      | TTGTCTCGTTTGAATT<br>TGTGG   | CATCATTTCAATCCAAC<br>CCC       | 60.0                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35716080  | Ca7                                     | 35716080                      | TTTATTT/TTTATTAGTTATTT                                                                                                                                  | ACTATAGTACCCACCC<br>CGCC    | TGGAGGTCACAGCACG<br>ATAC       | 60.1                             | 356                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35727024  | Ca7                                     | 35727024                      | GAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAAT/GAATAATAGTA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TATAATAATAATAAT | AAATCTGGCTGAATGG<br>ATGAA   | CGTGAAAACATGTTAA<br>AATTGATAGT | 59.5                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35766599  | Ca7                                     | 35766599                      | TAAAAAAAAAAAA/TAAAAAAAAAAAA                                                                                                                             | TGTCGTGTTTGACGTG<br>TTCA    | TGAAGTTGAGTGTTGG<br>CAGG       | 59.8                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35786413  | Ca7                                     | 35786413                      | TTATTAATATTA/TTATTA                                                                                                                                     | GGGAAACCCACCTTTT<br>GATT    | GGAGGGTGTAATTGG<br>AAGA        | 60.0                             | 679                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35787388  | Ca7                                     | 35787388                      | A/AG                                                                                                                                                    | CCTTCCAATGTAGCTG<br>ATGTTTT | TGGACGCAATAGATG<br>CAAA        | 59.6                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                   | Forward primers (5'-3')  | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                 |                          |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_35789236  | Ca7                                     | 35789236                      | CTTATTTATTTATTTATTTATTTATTT<br>ATTTATTTATTTATTTATTTATTTATTT<br>TATTTATTTATTTATTTATTTATTTATTT<br>TATTTATTTATTTATTTATTTATTTATTT<br>TTATTTATTTATTT | GTGAGGTCTAAGGCAG<br>TGCC | AAATTGAGGATCCATG<br>AGAGGA    | 59.9                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35794267  | Ca7                                     | 35794267                      | CTTTT/CTTT                                                                                                                                      | ATGTAGACGATTGCTT<br>CCCG | GCAACAACTTTGCACT<br>CCA       | 60.1                             | 700                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3582811   | Ca7                                     | 3582811                       | GTTT/GTT                                                                                                                                        | AACTGGTGTCTAAGCT<br>CCGA | GAATGGGTGGGTGTG<br>TTCC       | 60.0                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3582866   | Ca7                                     | 3582866                       | TG/T                                                                                                                                            | TGTACAGAACCAACG<br>CAGC  | CCTCAAGTCGCCGTAT<br>CATT      | 59.9                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35845872  | Ca7                                     | 35845872                      | TAAAAAAAAA/TAAAAAAAAA                                                                                                                           | GCCGGTTGTGTATGT<br>TGTG  | TGCTTAATTCACATCC<br>TCTCG     | 59.9                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35861781  | Ca7                                     | 35861781                      | TTATATATATATATATATATAT/TTAT<br>ATATATATATATATAT                                                                                                 | AAATGATGTTTTTGCCC<br>TCG | CTCTAGAGGATTCATC<br>GCGG      | 59.9                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_35861827  | Ca7                                     | 35861827                      | ATTTTTTTTT/ATTTTTTTTTT                                                                                                                          | AAATGATGTTTTTGCCC<br>TCG | CTCTAGAGGATTCATC<br>GCGG      | 59.9                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3588381   | Ca7                                     | 3588381                       | GAAAAAAAAA/GAAAAAAAAA<br>A                                                                                                                      | GACATGCGAGATTCCA<br>AACA | GGGGTTATGGTTGGGT<br>TTTT      | 59.7                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3588470   | Ca7                                     | 3588470                       | T/TC                                                                                                                                            | TGAGGCCTAAATTTAA<br>ACCG | GCCTTCACATTAGCGA<br>CCAT      | 58.3                             | 967                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_36008729  | Ca7                                     | 36008729                      | AAATAATAATAATAATAATAATA<br>ATA/AAATAATAATAATAATAATA                                                                                             | GAATCCAACGCGAAAT<br>AGGA | CAGATTCATGTCAATCA<br>AAAGAAAA | 60.0                             | 808                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_3608175   | Ca7                                     | 3608175                       | CA/CAA                                                        | TTTTCGTGGGATCAAA<br>TTCC | ATTCACGAACCTGCGA<br>TACC  | 59.7                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3608219   | Ca7                                     | 3608219                       | GT/GTCCCAATTT                                                 | TTTTCGTGGGATCAAA<br>TTCC | ATTCACGAACCTGCGA<br>TACC  | 59.7                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3609150   | Ca7                                     | 3609150                       | TAAAAAAAA/TAAAAAAAAA                                          | CTTTCCTTTTCCGACC<br>CAAT | TCATCACATCACATCAC<br>ATGC | 60.3                             | 621                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3610326   | Ca7                                     | 3610326                       | AATATATATATATATAT/AATATAT                                     | ATTTAGCCTAGCTCAC<br>GGGG | TAGGCGTCAACCTCT<br>CGTC   | 60.6                             | 783                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3612730   | Ca7                                     | 3612730                       | G/GTTTAA                                                      | CTATGGCATCGACATT<br>GCAT | ATCGAGAGATCGCGAG<br>AGAG  | 59.5                             | 803                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3612993   | Ca7                                     | 3612993                       | ATATAATT/AT                                                   | AACACTCCGTATGTCC<br>CACC | ATCGAGAGATCGCGAG<br>AGAG  | 59.7                             | 148                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3613058   | Ca7                                     | 3613058                       | CAGAA/CAGAAGAA                                                | AACACTCCGTATGTCC<br>CACC | CAACCCAACCCAAC<br>TACA    | 59.7                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3613671   | Ca7                                     | 3613671                       | ATTTTT/ATTTTT                                                 | GCAAGTGCTCCATTT<br>CATT  | ACTTGGCAATGCAAGA<br>GTCC  | 60.1                             | 297                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3614313   | Ca7                                     | 3614313                       | ACTCT/ACT                                                     | ATCGAGTGATTGGATT<br>TGGG | AACCGGCTCAATTCAT<br>CAAG  | 59.8                             | 973                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_36149566  | Ca7                                     | 36149566                      | TTATATATATATATATATA/TTATA<br>TATATATATATATATATATATA           | CCGTACCGTTTCTGGG<br>ATTA | TGCACGGCAATTACAA<br>CAAT  | 59.8                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_3617634   | Ca7                                     | 3617634                       | TAAA/TAA                                                      | CCGCTACTTTTCGAA<br>CACTTC    | TCAAACCACCCCAAA<br>AATA     | 60.3                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3620872   | Ca7                                     | 3620872                       | TTAA/TTAATTATATA                                              | ATTGTGTGTGGTTGGC<br>AGGT     | GATGCAGCTGTTGCAA<br>GTTC    | 60.3                             | 242                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3621424   | Ca7                                     | 3621424                       | TAGAAGAA/TAGAA                                                | TGCAACAGCTGCATCA<br>AAAT     | TCAAGTTAAGGGACTC<br>GAGAAA  | 60.4                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3621751   | Ca7                                     | 3621751                       | GAAAAAA/GAAAAAAA                                              | GACCAAAAGGAAACAA<br>ATGAAA   | TCGTTGCTTAGTTTCAC<br>TCTCAA | 58.1                             | 930                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3622161   | Ca7                                     | 3622161                       | GTTTTTTTTT/GTTTTTTTTTTTTT                                     | TTTATTGTAGGATTG<br>ATGTTGA   | TGCAATGGTGACTAAA<br>GCAA    | 58.4                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3622629   | Ca7                                     | 3622629                       | ATTTTT/ATTTTTTTT                                              | TGCTTTAGTCACCATT<br>GCACA    | ATGACGTGTTCCACAA<br>CCAA    | 60.3                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3622771   | Ca7                                     | 3622771                       | TAAAAAA/TAAAAAAA                                              | TGCTTTAGTCACCATT<br>GCACA    | ATGACGTGTTCCACAA<br>CCAA    | 60.3                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_36243491  | Ca7                                     | 36243491                      | TAAAAAAA/TAAAAAAA                                             | TGTATCGCGTTAATCT<br>GCGT     | TTTGTTTCATGGATGT<br>GGA     | 59.4                             | 886                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_36283006  | Ca7                                     | 36283006                      | TTATATATATATATAT/TTATATAT<br>ATATATAT                         | TAGTGCTCTGACGTCC<br>CAAA     | TTTTTGACGCATCTTCA<br>ATT    | 59.4                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_36353585  | Ca7                                     | 36353585                      | TTAATTAATAAT/TTAATTAATAAT<br>TAAATAAT                         | CACCGATGTGAAATCT<br>CTATTTTT | GCGTTTCAGCCAACCTT<br>GTGT   | 58.6                             | 996                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_36439529  | Ca7                                     | 36439529                      | ATTTTTTT/ATTTTTTTT                                            | CGCTTTTTCGCTTAA<br>GTGC    | TCATTTGATAATTTCA<br>CACAAA | 60.0                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_36475569  | Ca7                                     | 36475569                      | GA/GAA                                                        | GAAATGTGAGTTTAAT<br>TCCCCA | TGGCCTATGTGCTTCT<br>ATTGG  | 59.3                             | 235                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_36564169  | Ca7                                     | 36564169                      | TGTTG/T                                                       | CAATTGACAAATTGG<br>CTTTCA  | TGGTAGCATCGGTCAA<br>TCAA   | 60.0                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_36565312  | Ca7                                     | 36565312                      | CAAAAAAAAAAAAA/CAAAAAAAAAAA<br>AA                             | GGCCACGTCATTTGTT<br>TCTT   | CGAACATGGTGCATAT<br>TTCC   | 60.0                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_36663708  | Ca7                                     | 36663708                      | TAA/TAAA                                                      | CAAAATTGTCATCCCG<br>GTTT   | TGTGACCCATACGAAT<br>GCAA   | 59.7                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_36665367  | Ca7                                     | 36665367                      | GTATATATATATATATATATAT/GT<br>ATATATATATATATATAT               | AGACCAATTTGAGT<br>TCAACA   | GAATGCTCTCTCCAC<br>ATTCG   | 59.6                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_36667779  | Ca7                                     | 36667779                      | AATATATATATATATATATAT/AA<br>TATATATATATATATATAT               | TGCATCAACAACCTTAC<br>CCAA  | TGTTTACAAGAGGTTT<br>GTGGC  | 59.1                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3668391   | Ca7                                     | 3668391                       | GC/GCC                                                        | GCGGGTTTTTGACAA<br>GTTT    | TTACTTTTGACGGGAAA<br>CGG   | 59.8                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_36683918  | Ca7                                     | 36683918                      | TAA/TA                                                        | TTCGTAATGGACGGGA<br>TGAT   | AAGGCCTTTTACAACG<br>CTCA   | 60.2                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3677148   | Ca7                                     | 3677148                       | TC/T                                                          | TTGAGTGGCATTTTCAG<br>CAAG  | TCTTGGCATGGAAACA<br>CAAA   | 60.0                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_3684686   | Ca7                                     | 3684686                       | T/TA                                                          | ATATCGCGCCAACCTA<br>TCAC   | CGGTTTGATCTTTGA<br>GAGAA  | 60.0                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3684785   | Ca7                                     | 3684785                       | TA/T                                                          | ATATCGCGCCAACCTA<br>TCAC   | TTCAGCCTCCCCCTTC<br>TAGT  | 60.0                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3685066   | Ca7                                     | 3685066                       | ATT/ATTT                                                      | ATATCGCGCCAACCTA<br>TCAC   | TAATCATCCTCGGGTT<br>GAGG  | 60.0                             | 828                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3687092   | Ca7                                     | 3687092                       | TTCT/TT                                                       | AAACAACATATCCATCC<br>AACCA | ATAAGTGGCGTGTGTG<br>GTGA  | 59.1                             | 244                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_36973404  | Ca7                                     | 36973404                      | ATTTTTTTTTTTT/ATTTTTTTTTTT                                    | TAAATATTGGACCGGC<br>CTTG   | TCAGCTGAAATGGGT<br>TAAA   | 59.8                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3708997   | Ca7                                     | 3708997                       | CAATAATAATAATAATAATAA/CA<br>ATAATAATAATAATAATAA               | CGCATGCGAACTTGTA<br>CTGT   | CTCCTCGTTTTTGGCA<br>CATT  | 59.9                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_37205527  | Ca7                                     | 37205527                      | A/AAT                                                         | TTGAAATAATTGCGTTG<br>CCA   | TGTGCCGATGATGATG<br>TTCT  | 60.1                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_37282057  | Ca7                                     | 37282057                      | GAATAAATAAATAAT/GAATAAATA<br>AATAAATAAATAAATAAAT              | GCGAGGGAATTATAGC<br>CACA   | TCGTGTAGCCAATAGC<br>TTTGT | 60.1                             | 374                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_37374332  | Ca7                                     | 37374332                      | GTGGCTAAT/GTGGCTAATTAACCA<br>TGGCTAAT                         | TTGAAACGGTGGTGAA<br>ACAA   | TTGGTTTTCATTTCCC<br>TCG   | 60.0                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_37491114  | Ca7                                     | 37491114                      | TAAAAA/TAAAAA                                                 | CAATCTAGCCATCTTC<br>CGCT   | ATGGATTGGATGTAGC<br>TGCC  | 59.4                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_37543297  | Ca7                                     | 37543297                      | GAAAAAAAA/GAAAAAAAA                                           | TTTTTGGGGATTTCATT<br>GGA    | AAGTGCCCTTACCTCG<br>ATGA   | 60.1                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_37548473  | Ca7                                     | 37548473                      | GTCA/GTCATCA                                                  | CAAACGCCAAACACAA<br>ACAC    | ACAATGTGTTGGACTT<br>GCCA   | 60.1                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_37568106  | Ca7                                     | 37568106                      | CT/C                                                          | TGTGTTGCAAGTGTGC<br>TTGA    | CCAAGTCTCATCTGGA<br>AGCC   | 60.1                             | 259                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_37585595  | Ca7                                     | 37585595                      | TA/T                                                          | AGGTAGGCCTTGCCAT<br>TTTT    | CGCACTTGAAAACTCT<br>AATTGC | 60.0                             | 357                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_37586131  | Ca7                                     | 37586131                      | CATTGAC/CATTGACTATTTGAC                                       | GCAATTAGAGTTTTTCA<br>AGTGCG | ACAATCCTCAGCATTAG<br>GGG   | 60.3                             | 746                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_37593690  | Ca7                                     | 37593690                      | ATTTTTTTTT/ATTTTTTTT                                          | TATGCATGCGGACAAG<br>AGTC    | GTGCTCACAACTTGC<br>CAAA    | 59.8                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_37595726  | Ca7                                     | 37595726                      | ATTTTTTTTT/ATTTTTTTT                                          | CAAAGTATCTACCGGG<br>TTCCA   | CAACTCGGTTACACAC<br>TTCA   | 59.0                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_37618164  | Ca7                                     | 37618164                      | TTTATTATTATTATTATTAT/TTT<br>ATTATTATTATTATTAT                 | CCCAAGCGGTACTGAC<br>ATTT    | GAATAGGTCAGGTCAG<br>GCCA   | 60.0                             | 744                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_37618737  | Ca7                                     | 37618737                      | GAAAAAAAAA/GAAAAAAAAA                                         | TGGCCTGACCTGACCT<br>ATTC    | CACCATCATGAGTCGC<br>AAAG   | 60.1                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_37622218  | Ca7                                     | 37622218                      | TCA/T                                                         | TACCCACGGTAGCTC<br>TTTG     | TTCGATCATCACCTCA<br>ACA    | 60.1                             | 722                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                            | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                          |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_38401031  | Ca7                                     | 38401031                      | AATATATATATATA/AATATATATATA<br>TATA                                                                                      | TTCCCTGGTTGTTGA<br>ATCC     | AGCAACACAAATTCAC<br>TCTG | 59.8                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_38623362  | Ca7                                     | 38623362                      | TATTCATTCAATTCATTCAATTCAT<br>TTTATTCATTCAATTCATTCAATTCAT<br>TCATTCAATTCATTCAATTCATTCAATTCAT<br>ATTCAATTC                 | GGGCTCTCCACCCATT<br>TCTT    | GGATTATTGATTTCCCG<br>GCT | 60.2                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_38626397  | Ca7                                     | 38626397                      | GATAATAATAATAATAATAATAATA<br>TAATAATAATAATAATAATAATAATA<br>AATAATAATAATAATAATAATAATA<br>TAATAATAATAATAATAATAATAATA       | CCAAGCCCAATAAAAC<br>CCTT    | GGACTCACTCCCCAA<br>TTGA  | 60.2                             | 131                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_38669994  | Ca7                                     | 38669994                      | TTTATTATTATTATTATTATTATT<br>ATT/TTTATTATTATTATTATTATT<br>TATT                                                            | CCTGCCGTTTATTTT<br>GTTC     | GCGATCGAATGGCAAT<br>ATCT | 59.5                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_38673360  | Ca7                                     | 38673360                      | GAAAAAAAAA/GAAAAAAAAA<br>A                                                                                               | TGCATGTAAACATCAT<br>TCAAAAA | TTGTGGCTTCAACCA<br>GTGT  | 59.4                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_38681899  | Ca7                                     | 38681899                      | GAAAAAAAAA/GAAAAAAAAA                                                                                                    | GAGCTGTGTCTTGGCA<br>ATCA    | TTACCTTCAAGTGGC<br>CAAG  | 60.0                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_38743655  | Ca7                                     | 38743655                      | CTATTTATTTATTTATTTATTTATTTA<br>TTT/CTATTTATTTATTTATTTATTTA<br>TTTATTTATTTATTT                                            | CTTAGGTTTGCACTCA<br>GCC     | CTCAATCGTGGGTGAC<br>CTTT | 59.9                             | 932                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_38951007  | Ca7                                     | 38951007                      | TTTATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATTATT | AATAGGCTAAGCCGTC<br>CGTT    | CAGACTTCGAAAGGCC<br>TGAG | 60.1                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_38991294  | Ca7                                     | 38991294                      | ACC/AC                                                                                                                   | CCGATGTGTGGCTT<br>CTTA      | CCTCTCTGGTGACG<br>GTGT   | 59.7                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39029142  | Ca7                                     | 39029142                      | ATTTTTTT/ATTTTTTTT                                                                                                       | CTTCCTTCAAAAGACG<br>CCAG    | ACTCCAATTCAACAAAG<br>CCA | 60.0                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                               | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                             |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_39029671  | Ca7                                     | 39029671                      | C/CTAAGTCTA                                                                                 | CAATGGCTTTGTTGAA<br>TTGG | TGCCGCTATGTACTTTT<br>GGC  | 59.0                             | 789                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39032671  | Ca7                                     | 39032671                      | TC/T                                                                                        | ATCAATCCTAAGGAGC<br>GCAA | CTTGGCAAGACGAAAA<br>ATCA  | 59.8                             | 700                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39053146  | Ca7                                     | 39053146                      | ATTATT/ATTATTTTTATT                                                                         | AACCCCAAATCCCTAA<br>CCTG | TTTTTGTCATTGATT<br>GATGTT | 60.0                             | 780                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3905558   | Ca7                                     | 3905558                       | TG/T                                                                                        | ACTCTGTGTTTGAGGT<br>GGGG | TGAGGGATGAAGAGGA<br>CAAAA | 60.0                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39141821  | Ca7                                     | 39141821                      | TAAAAAA/TAAAAAAA                                                                            | GTGAGTTTGAGGGGGA<br>GATG | TGAACCTGCAAAGCCA<br>CTTG  | 59.5                             | 864                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39149719  | Ca7                                     | 39149719                      | AT/ATT                                                                                      | GCACTAAGTCAGGGGC<br>TCAG | TGGAACCCATTACAC<br>AAGA   | 60.0                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39254289  | Ca7                                     | 39254289                      | T/TAAATGAA                                                                                  | AGTTGCGAGCGGAGAT<br>TTTA | TCAAGTAGTGACACGC<br>CAAA  | 60.0                             | 378                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39275720  | Ca7                                     | 39275720                      | AATTATTATTATTATTATTATTAT<br>TATTATTATT/AATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT         | TGGCACTTGTGTCTTT<br>TCCA | TGACATTAGTGCAACA<br>CGAGG | 60.3                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3934957   | Ca7                                     | 3934957                       | AATATATATATATATATATATATAT<br>ATATATATATATATATATATATATAT<br>T                                | TTCCATATTTGGGTGC<br>CATT | TGTGCATCTTTTCCAA<br>TGC   | 60.0                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39495828  | Ca7                                     | 39495828                      | TTATATATATATATATATATATATAT<br>TATATATAT/TTATATATATATATAT<br>TATATATATATATATATATATATAT<br>AT | GGAGGATCCAGTGGAC<br>GTAA | CCTCACCTTCCCTACC<br>ATCA  | 59.9                             | 792                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                             |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_39518115  | Ca7                                     | 39518115                      | TAAACAAAAACAAA/TAAACAAAA<br>CAAAACAAAA                                      | GGTCCCTTGTAGCC<br>AAAT      | TTTACGAGCCCATTTGT<br>TGA    | 60.2                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39523876  | Ca7                                     | 39523876                      | TAAAAAAAAAAAA/TAAAAAAAAA                                                    | CCATCAATTGAATTCTC<br>CTCC   | GTTAAGGGATCGCGGA<br>TGTA    | 58.4                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39525063  | Ca7                                     | 39525063                      | ATTTTTTTTT/ATTTTTTTTT                                                       | AACGACCAACTTGGGA<br>AAAA    | GGAGTGGGTCACCGAG<br>AATA    | 59.4                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39546561  | Ca7                                     | 39546561                      | AATATATATATATA/AATATATATA<br>TATATATA                                       | AAGCTCAACAAATGC<br>ACCT     | TTGAGACTTTTGCCCA<br>CTGA    | 57.5                             | 143                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39547832  | Ca7                                     | 39547832                      | ATT/ATT                                                                     | TGAGTCGCACAAACAC<br>ATCA    | CCTCATGGAAGTCACG<br>GTTT    | 59.9                             | 430                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39611392  | Ca7                                     | 39611392                      | AAATAATAATAATAATAATAATA<br>ATAATAATAA/AAATAATAATAAT<br>AATAATAATAATAATAATAA | CTGTGCGCTTGACTGA<br>TGTT    | CTAAATTCGAAATTCGG<br>CCA    | 60.1                             | 930                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39611474  | Ca7                                     | 39611474                      | TAATAAAATAAAATAAAATAA/TA<br>ATAAAATAAAATAAAATAA<br>AATAAAATAA               | AAAGGATCAATGGGT<br>TGACC    | CTAAATTCGAAATTCGG<br>CCA    | 60.0                             | 424                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_3976290   | Ca7                                     | 3976290                       | ATTTTTTTT/ATTTTTTT                                                          | AAAAAGTTGAGGTGGG<br>TAAAAAT | TTGCAAGCTATTGTTCC<br>ACG    | 57.3                             | 730                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39799960  | Ca7                                     | 39799960                      | ATTTTTTTTTT/ATTTTTTTTT                                                      | TGGTATGAGAATCCAT<br>CGATCA  | TGGAATGCTTACTCCTA<br>TCCATC | 60.3                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39861336  | Ca7                                     | 39861336                      | CG/C                                                                        | AGGGTGACTTTGCTCA<br>TTGG    | TGGTCATGGTGCTTT<br>GGTA     | 60.1                             | 689                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_39983093  | Ca7                                     | 39983093                      | AAATTTATAA/AAATTTATAATTATA<br>A                               | TCAGCCAAAAAGATGA<br>CGTG  | TGTCGATTTTATGATT<br>GATTATGTGG  | 59.8                             | 348                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_39984645  | Ca7                                     | 39984645                      | ATT/AT                                                        | CAACAATTTCTCATGCT<br>CGC  | TGATTAAGAAAATTAAA<br>ATGAGGGAAA | 59.4                             | 352                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_40011182  | Ca7                                     | 40011182                      | TG/T                                                          | GTGAAACACCCACAAA<br>TCCC  | CAATCGAGGTTGGAC<br>AAGG         | 60.1                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_40034151  | Ca7                                     | 40034151                      | ATTTTTTTTT/ATTTTTTTT                                          | AATTGGGGGCAATTT<br>CATT   | GGGATTATGGTCAATC<br>CCATT       | 60.4                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_40043748  | Ca7                                     | 40043748                      | TAAA/TA                                                       | CATTGATTGCAACAG<br>CACC   | ATAAGTCATCCACGCC<br>TTGC        | 60.1                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_40086965  | Ca7                                     | 40086965                      | G/GCATTGCTAC                                                  | GGTGAAAACGGGTGG<br>AAGA   | ATACAATTGTGCCTGCT<br>CCC        | 59.9                             | 880                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_40086992  | Ca7                                     | 40086992                      | G/GA                                                          | GGTGAAAACGGGTGG<br>AAGA   | ATACAATTGTGCCTGCT<br>CCC        | 59.9                             | 880                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_40414910  | Ca7                                     | 40414910                      | C/CCTT                                                        | CGTCAAAATCTCGTAC<br>GTGTG | CCAGAAGCAGAAAAAC<br>CAGG        | 59.3                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_40487128  | Ca7                                     | 40487128                      | TAGAGAGAGAGAGAGAG/TAGAG<br>AGAGAGAGAGAGAGAG                   | AAGCGAAGCGTACCTT<br>TGAA  | TTCCCAGAAAACCAAG<br>CATC        | 60.0                             | 252                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_40768727  | Ca7                                     | 40768727                      | TAAC/TAACAAC                                                  | GGTCTAACGAAGAACA<br>TCCCA | AGGCAATCATTGTGCA<br>AACA        | 59.0                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_40801094  | Ca7                                     | 40801094                      | GGGAATTAAA/G                                                  | AAAGGGAAAGTTGCAC<br>CAAG     | TTTTTGA CTGACACGCT<br>GCT  | 59.2                             | 728                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_40965776  | Ca7                                     | 40965776                      | ATTTTTTTTT/ATTTTTTTT                                          | TGGTATTGAAACACCC<br>CAAA     | AATATGAAGTTGCGGC<br>TGCT   | 58.7                             | 857                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_40985025  | Ca7                                     | 40985025                      | TAAAA/TAAAAA                                                  | GCAACTGCCTTAAAA<br>TGGAA     | GGAACGTGCGTACATT<br>GTTG   | 59.2                             | 303                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_41008241  | Ca7                                     | 41008241                      | CAAAAAAAAAAAAA/CAAAAAAAAAA<br>A                               | GCCAATCAGGACACAT<br>CTCA     | TCAGAACATTCCATCG<br>GTGA   | 59.6                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_41008810  | Ca7                                     | 41008810                      | TTAA/TTAACTAA                                                 | TAGCGCCTACATCGGA<br>GAGT     | GTTCAATTATGCGCAAG<br>CATT  | 60.0                             | 387                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_41009153  | Ca7                                     | 41009153                      | TA/TAGTGTGA                                                   | TAGCGCCTACATCGGA<br>GAGT     | TTATTGAAAACCGAGG<br>TCATGT | 60.0                             | 775                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_41009960  | Ca7                                     | 41009960                      | ATTTTTTTTT/ATTTTTTTTTT                                        | CATGACCTCGGTTTTT<br>AATAA    | CCCTCACATTTTAAAGG<br>CACA  | 57.6                             | 814                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_41010142  | Ca7                                     | 41010142                      | CAA/CAAAA                                                     | TGCAATGAATGAAAGT<br>ATGCTACC | GAAAAAGCGCTGTAAA<br>TGGC   | 60.4                             | 815                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_41170497  | Ca7                                     | 41170497                      | CATATATATATATA/CATATATATATA<br>TATA                           | GGGAGAAATGTAACAC<br>CCCA     | CGGCGAATTTGTTTTCT<br>TTT   | 59.6                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_4118702   | Ca7                                     | 4118702                       | ATTTTTTTTT/ATTTTTTTT                                          | TTGTTATTGCTTGGTGT<br>GGTT    | GCAAAAAGAGACCTGC<br>CAAG   | 58.1                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_4125090   | Ca7                                     | 4125090                       | GTT/GTTT                                                      | TCAATTAGTTAAACGA<br>AATGGGT | ATCCAAACAAGACGCC<br>AAAG | 58.2                             | 831                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_41251256  | Ca7                                     | 41251256                      | AG/A                                                          | CCAATAGTTTAGTGGG<br>CCAAA   | AAGGGTCCTCTTGAAG<br>CGTT | 59.0                             | 213                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_41252327  | Ca7                                     | 41252327                      | TTAT/TT                                                       | TGCAATGCAATGTCCA<br>TTTT    | TTTTCTCATGGTGCA<br>GTG   | 59.9                             | 324                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_41464356  | Ca7                                     | 41464356                      | T/TAACA                                                       | ATTTCGACAGCCAAA<br>TGAG     | GGCTTTAGGTTTAGG<br>GTCG  | 60.1                             | 828                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_41484126  | Ca7                                     | 41484126                      | GTATATATATATATATATAT/GTAT<br>ATATATATATATAT                   | AGATTTCGAGGCAGTT<br>GAGT    | CGAGAGAGTGTACGC<br>ATGT  | 60.0                             | 701                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_41575433  | Ca7                                     | 41575433                      | CAT/CATAATAAT                                                 | AAAGGTTTTGCCGACT<br>CTCA    | TTGGCCTCCTTCCACTT<br>ATG | 59.9                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_41740525  | Ca7                                     | 41740525                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                     | TCGAAATTTTAGGCCA<br>CGAC    | TCACCTTGTTTTGAGA<br>GGC  | 60.1                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_41751259  | Ca7                                     | 41751259                      | TAAAAAAAAAAAAAAAA/TAAAAAAAA<br>AAAA                           | GAGATACCCACTGCCA<br>CGAT    | AGGTGACAAACCGCCA<br>TAAC | 60.0                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_41834121  | Ca7                                     | 41834121                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                     | CGGGAAGAGGACTGAT<br>GAAG    | CCTAATCGATCAACCA<br>GGC  | 59.8                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_42052936  | Ca7                                     | 42052936                      | C/CTATAATCATTAA                                               | CAAAGCGGGCTTAATT<br>TCAC    | CTCAATTGTGCATGAA<br>GCGT | 59.7                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                             | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                           |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_4233974   | Ca7                                     | 4233974                       | CTATATATATATATATATAT/CTAT<br>ATATATATATATATATATATATAT<br>TAT                                              | TTCTGCGTGAGATTG<br>AAAA   | CGCCACTCAAAAACAT<br>GCTA    | 59.4                             | 442                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_4234613   | Ca7                                     | 4234613                       | GTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAA/GTAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA | TAGCATGTTTTGAGT<br>GGCG   | CAATTGCTACTCCTTCC<br>ATCG   | 59.9                             | 755                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_42384922  | Ca7                                     | 42384922                      | C/CAAAATAA                                                                                                | TTTACAGGCAGCGGAA<br>AAGT  | GCTAAGGTGCATGCTT<br>GGTT    | 59.9                             | 340                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_42472631  | Ca7                                     | 42472631                      | CTTTTTTTTT/CTTTTTTTT                                                                                      | TGACATGAAAATTCAAA<br>CCCC | TTTTGATTTGTCTCTT<br>TGATGGA | 59.7                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_42473883  | Ca7                                     | 42473883                      | TAAAAAAAA/TAAAAAAAA                                                                                       | GGATTTCGAATCCTCC<br>CATT  | TTATTTGAATGGGCA<br>ATCC     | 60.0                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_42475836  | Ca7                                     | 42475836                      | TGAAGA/TGA                                                                                                | CGTGTTCGGGTGTGG<br>TACT   | CCACCAGTCCAGATCA<br>ACCT    | 60.9                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_42496965  | Ca7                                     | 42496965                      | TGATTC/TGATTCGATTC                                                                                        | TATCTCGTGCTTGCGA<br>AATG  | AATTACCGCCAATTCAC<br>ACC    | 60.0                             | 668                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_42618849  | Ca7                                     | 42618849                      | TAA/TA                                                                                                    | AAAGGATTTGTGGGTG<br>TCCA  | CGCAGAAGTCAAAATG<br>CAGA    | 60.2                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_42660005  | Ca7                                     | 42660005                      | TAAA/TAA                                                                                                  | AGCCAAGTCCCTGTTA<br>CCCT  | TCGTTTTCGTCGCTTTT<br>TTT    | 60.0                             | 314                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_42738535  | Ca7                                     | 42738535                      | TAAAAAAAA/TAAAAAAAA                                                                                       | TCCCGCTACACTTTGA<br>GGAC  | TCAAAAGCAAGTGTTC<br>CAGG    | 60.3                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                              |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_42832699  | Ca7                                     | 42832699                      | CATTATTATTATTATTATTATTATT<br>TATTGTTATTATTATTATTATTATT<br>TATTATTATTA/CATTATTATTATTAT<br>TATTATTATTATTGTTATTATTATTAT<br>TATTATTATTATTATTATTA | CCCAACATAGCAAGGT<br>TGAAA  | TTGTGTTGGGAAAAAG<br>AAGG | 60.0                             | 816                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_42919520  | Ca7                                     | 42919520                      | AAT/AAAGAATCAT                                                                                                                               | TCAGCACTGCACCAAA<br>ACAT   | AAAAGGCGCATACGCT<br>AAGA | 60.3                             | 621                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_42937139  | Ca7                                     | 42937139                      | TTATATATATATATATATATATATA<br>TATATATATATATATATATAT/TTATA<br>TATATATATATATATATATATATAT<br>ATATATAT                                            | TTGGCATGAGCCATTT<br>ACAG   | TGGAACCCACGGTAAC<br>ATTT | 59.7                             | 466                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_43011755  | Ca7                                     | 43011755                      | TTATATATATATATATATAT/TTATAT<br>ATATATATAT                                                                                                    | TGCCAATTTTTCAAAGG<br>TTTTT | GCCCAAGTTCGAAATG<br>TTGT | 59.9                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_43208355  | Ca7                                     | 43208355                      | CTTTTT/CTTTT                                                                                                                                 | CACAGGCACAAAATTT<br>TCTCAA | TGAATTGAGATCGTTG<br>GCAC | 60.1                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_43209769  | Ca7                                     | 43209769                      | TACACACACACACACACAC/TACA<br>CACACACACAC                                                                                                      | GGAAGAAAGGATGGGT<br>TCCT   | TGAGAGGAATCTGGGA<br>TTGG | 59.4                             | 689                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_4323147   | Ca7                                     | 4323147                       | CTT/CTTT                                                                                                                                     | AATTCGGGTGTGAGA<br>GGTG    | GCAACTCGGATTGGTG<br>ATTT | 60.0                             | 800                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_43375115  | Ca7                                     | 43375115                      | CAAAA/CAAA                                                                                                                                   | CCAATATCTCGTGTTT<br>CCGT   | CATTCAAGTTGGGGC<br>AGTT  | 59.8                             | 335                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_4339580   | Ca7                                     | 4339580                       | TTTTTTATTTTTATTTTTATT/TTTTT<br>ATTTTTATTTTTATTTTTATT                                                                                         | GCTAGTGCCTCCCTTG<br>AGTG   | TCACGGGTGCATTGAA<br>CTTA | 60.0                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_4354610   | Ca7                                     | 4354610                       | CTT/CTTT                                                                                                                                     | TATTTTCAACAGGCGC<br>AGTG   | GTTGTTCCACGGAAC<br>TGAT  | 59.9                             | 788                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                       | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                     |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_43606803  | Ca7                                     | 43606803                      | TATAAATAAATAAATAA/TATAAATA<br>AATAAATAAATAAA                                                        | TTTGGCCATGTCTCAG<br>CTTG   | TCTCCTCATTCCCAAG<br>TGG     | 60.0                             | 814                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_43607952  | Ca7                                     | 43607952                      | GTTCTTCTTCTTCTTC/GTTCTTCTT<br>CTTCTTCTTCTTC                                                         | AATGAGGAGATGGGAC<br>AACG   | AAGACCAAGGCACGAA<br>ACAC    | 59.9                             | 731                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_43633041  | Ca7                                     | 43633041                      | TAAAAAAA/TAAAAAAA                                                                                   | CTAGAACTCGCCCCAA<br>CAAC   | TTTATCGCAATTGGTTC<br>GGT    | 59.7                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_43705565  | Ca7                                     | 43705565                      | TAA/TAAA                                                                                            | CATTCCGATTGTGGCT<br>TCTT   | CCACAACACAATCACAA<br>CCC    | 60.1                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_43806008  | Ca7                                     | 43806008                      | CAAAAAAAAA/CAAAAAAAAA                                                                               | CACTCTTAGCCTTGGA<br>CACAAA | CGTTTTGGGAGAGAAA<br>TGCT    | 59.4                             | 780                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_43806200  | Ca7                                     | 43806200                      | GAAAAA/GAAAAA                                                                                       | TTCCGGATAAGGAGGG<br>TGAT   | ATCCACCTTGATGCCTT<br>CAC    | 60.7                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_4385687   | Ca7                                     | 4385687                       | GAAAAA/GAAAAA                                                                                       | TTTAATGGGGCCTAAG<br>GGAG   | GTGAGAGAGTGCCCC<br>AATA     | 60.3                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_43889969  | Ca7                                     | 43889969                      | GAAAAA/GAAAAA                                                                                       | TAGCACCTACGACAT<br>CCGT    | CGTAGCTTTGATTCTT<br>CATCACA | 60.5                             | 227                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_43984680  | Ca7                                     | 43984680                      | AATATATATATATATATATATATAT<br>ATATATATATATATA/AATATATAT<br>ATATATATATATATATATATATA<br>TATATATATATATA | TTTTGAAGGTCGCGAG<br>AAGT   | TGGACATGATTTGTG<br>GATG     | 60.0                             | 264                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_44001226  | Ca7                                     | 44001226                      | GAAA/GAA                                                                                            | GAACACCACACGCAA<br>GAAA    | TTTGTCCAATGGCAGTT<br>TCA    | 59.7                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                             | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                           |                             |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_4448677   | Ca7                                     | 4448677                       | CATATATATATATATATAT/CATAT<br>ATATATATATATAT                                                               | TGAAAACATGCAGTG<br>GGAA     | CGGTAATGAGTTGATT<br>GTTCAAA | 60.1                             | 381                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_4450160   | Ca7                                     | 4450160                       | T/TTTA                                                                                                    | TTTGCAAAAAACCTGT<br>ACCA    | ATGGTTATCCGATGCC<br>TGAC    | 59.1                             | 781                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_44681117  | Ca7                                     | 44681117                      | GTTTT/GTTTTT                                                                                              | AATGATGTTAGAAACC<br>GCCG    | GTTTCCAGCCATCCAA<br>CACT    | 60.0                             | 166                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_4473592   | Ca7                                     | 4473592                       | TAAAAAAAAAAAAAAAA/TAAAAAAAAA<br>AAAA                                                                      | GCAAAACAAATGAAT<br>GTAAACAA | TGGAGAAAAGAGGGGA<br>AGAGA   | 58.2                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_44903250  | Ca7                                     | 44903250                      | ATTTTTTTTT/ATTTTTTTTTT                                                                                    | AACCCCATATCCCCAA<br>ATGT    | CCCTGCCTCCACAATT<br>TTTA    | 60.1                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_45169614  | Ca7                                     | 45169614                      | ATTTTTTTTT/ATTTTTTTTT                                                                                     | TGTCCAATTGGCAATA<br>CAAAA   | AAAGAAGCTCGCTTGT<br>ATTGA   | 58.9                             | 678                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_45170609  | Ca7                                     | 45170609                      | ATTTTTTTTT/ATTTTTTTTTT                                                                                    | AAAGGGTTATTGCCAG<br>CTTTT   | AGGCATAGTTAGACGC<br>CCCT    | 59.2                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_45206871  | Ca7                                     | 45206871                      | GTATATATATATATA/GTATATATATA<br>TATATA                                                                     | AGGAGGTTTGTGTTTG<br>ACGG    | TTTGGATTTTGACTCG<br>GAGG    | 60.0                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_45219689  | Ca7                                     | 45219689                      | GTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAA/GTAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA | TGCCACAAGTGTTTA<br>TTGC     | TTTCTCTTTTGGTGTT<br>GCC     | 59.6                             | 769                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_45241477  | Ca7                                     | 45241477                      | TA/T                                                                                                      | TTTACCCCAACACGTA<br>AGCC    | CAGATCGGCGCTACAC<br>TACA    | 59.9                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_45271219  | Ca7                                     | 45271219                      | GAGAGAGAAAGAGAGA/GAGAGAG<br>A                                 | TGCATGCACAAAACA<br>CATT  | TCTTTTGAGGGGAGTG<br>AGGA   | 58.6                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_45407833  | Ca7                                     | 45407833                      | TGG/TG                                                        | CCGTCCTTCCTTCTTTC<br>TCA | GTGTGCATTGGACCAG<br>ATTG   | 59.4                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_4562422   | Ca7                                     | 4562422                       | ATT/ATTT                                                      | TCTCCGATTTCCTCCT<br>CAAA | ACATCTTGGATGATGT<br>GGCA   | 59.7                             | 283                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_45738190  | Ca7                                     | 45738190                      | ATTT/AT                                                       | TAACCCCAATAGCATC<br>CGAG | AAATTAAAGTTTCAAC<br>CACGG  | 59.9                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_46025180  | Ca7                                     | 46025180                      | AACA/AA                                                       | CTATCACGGCCCGTAC<br>TGTT | TTCGCAACTCCACTCTT<br>CCT   | 60.0                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_46075915  | Ca7                                     | 46075915                      | CTATATATATATATATATA/CTATATA<br>TATATATATATATA                 | AAACAATCCAGACCAG<br>TGGC | TCAAGCCAAACCCTTAT<br>CTTTT | 60.0                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_4616950   | Ca7                                     | 4616950                       | CTTTTTTTTTTT/CTTTTTTTTTTT                                     | GTGGGAGGTATAATTG<br>GGGG | CATGAATTTGGGAATTT<br>GGG   | 60.3                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_46252887  | Ca7                                     | 46252887                      | CATATATATATATATATATAT/CAT<br>ATATATATATATATATATAT             | CATATGGGTTGGGTCA<br>CTCC | CATCCATCCCGAGAG<br>AGTA    | 60.1                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_46319212  | Ca7                                     | 46319212                      | TTATATATATATATATATA/TTATA<br>TATATATATATATATA                 | ACAAGCGATTATGGTA<br>CCGC | AATTGCGGCGAGAGAA<br>GATA   | 60.0                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_46332309  | Ca7                                     | 46332309                      | GAACACAA/GAACACAATCAACACA<br>A                                | AACGTACTGCCTATCA<br>CGGG | TTCGCAACTCCACTCTT<br>CCT   | 60.0                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                 |                              |                            |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_46354851  | Ca7                                     | 46354851                      | CTATATATATATATATATATATATAT<br>ATGTATATATATAT/CTATATATATAT<br>ATATATATATATATATATGTATATAT<br>ATAT | TATCGTTGGACGAATG<br>GACA     | TTCATGAGCAACTTTCC<br>ACAA  | 59.9                             | 486                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_4645962   | Ca7                                     | 4645962                       | CTATTATTATTATTA/CTATTATTATT<br>ATTATTA                                                          | CCTTGCCCTTAAACCA<br>GTCA     | GCTTACCCACCGCAAC<br>TAAA   | 60.1                             | 769                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_46514929  | Ca7                                     | 46514929                      | ATTTTTTTTT/ATTTTTTTTTT                                                                          | TTGCTAGTGTAACACC<br>CCGA     | CGAGGGTATGAGCGAT<br>GTTT   | 59.2                             | 221                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_46559587  | Ca7                                     | 46559587                      | TAAAA/TAAAAA                                                                                    | GGGAGAAATTAGCCTA<br>TTGCC    | GAAGTGTGCACCAGGG<br>ATTT   | 59.1                             | 798                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_46560466  | Ca7                                     | 46560466                      | AATATATATATATATATA/AACATA<br>TATATATATATATATATATATATAT<br>A                                     | GGAGGCATTGTTTCCT<br>CAAA     | AGGAAGAGTGGAGTTG<br>CGAA   | 60.1                             | 658                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_46573334  | Ca7                                     | 46573334                      | TATAATAATAATAATAATAATAA<br>TAATAATAATAA/TATAATAATAATAA<br>TAATAATAATAATAATAATAATAA<br>A         | GGCACGACATCATCAT<br>CATC     | CTTTTAGGCCGGGTTA<br>CCAT   | 59.9                             | 597                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_46621054  | Ca7                                     | 46621054                      | TATAATAATAATAATAATAA/TATAAT<br>AATAATAATAA                                                      | ACGAAAACAATGCGAT<br>AGGG     | GGGAAATGTTCTGTCTG<br>AGGA  | 60.0                             | 255                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_4663386   | Ca7                                     | 4663386                       | TAATTCAGAATTCA/TAATTCAGAAT<br>TCAGAATTCA                                                        | TAATTATGCGGTGGCG<br>TGTA     | GCAATTTAGTAGCATC<br>GCCC   | 60.0                             | 260                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_4664246   | Ca7                                     | 4664246                       | ATT/ATTT                                                                                        | CCAACATGCGTTTCA<br>ACAACA    | TCACACACAATTGTAA<br>GTTTCG | 59.8                             | 463                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca7_P4_4664736   | Ca7                                     | 4664736                       | ATTTT/ATTT                                                                                      | CAATTGTGTGTGAGTT<br>TTTGATGA | ATGCACGATGGCACTT<br>GTAG   | 59.9                             | 604                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                           |                            |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_46654338  | Ca7                                     | 46654338                      | ATTTTTTTTT/ATTTTTTTTT                                                                     | TGGAATGTTGGTCAA<br>CAAAAG  | GCTTGTGCATTATTGTT<br>ACAAGTTC | 59.9                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_46657551  | Ca7                                     | 46657551                      | CAAA/CA                                                                                   | GTGATCGTCTTCGGAT<br>TGGT   | TGAATCTTGGGACGGA<br>AAAG      | 59.9                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_46657639  | Ca7                                     | 46657639                      | GAGTAAATTAAGTAA/GAGTAA                                                                    | ACGATTCATGCGTGTG<br>TGAT   | TGAATCTTGGGACGGA<br>AAAG      | 60.0                             | 171                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_4670868   | Ca7                                     | 4670868                       | AATATATATATATATATATATAT<br>/AATATATATATATATATATATAT                                       | AGCTGAAGCAGAGAGG<br>CAAC   | GAGTGGTGTGGAGTC<br>ATGTTT     | 59.9                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_46722519  | Ca7                                     | 46722519                      | ATTTTT/ATTTTT                                                                             | CAATATTCATTGGATC<br>CACCA  | CGACTAGGGGTATTTT<br>GGACG     | 59.5                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_46736089  | Ca7                                     | 46736089                      | ATTTTTTTTT/ATTTTTTTTT                                                                     | TAAATCGCGGTATGA<br>GGAC    | GTTTTCATTGTTGGCTG<br>CCT      | 59.9                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_46739794  | Ca7                                     | 46739794                      | CATAAT/CAT                                                                                | CATCACCGACGAACAA<br>ACAC   | GAATCAACGCATCAAG<br>CTCA      | 60.0                             | 621                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_46903175  | Ca7                                     | 46903175                      | AATATATATATATATATATATAT<br>AT/AATATATATATATATATATATA<br>TATATATATAT                       | AAGTTCGACCGAACAC<br>TTTTAT | CCACAAAAATTTGGGG<br>AAAG      | 57.0                             | 917                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_47010986  | Ca7                                     | 47010986                      | AATTATTATTATTATTATTATTAT<br>TATTATTATTATT/AATTATTATTAT<br>ATTATTATTATTATTATTATTATT<br>ATT | GAACCTTCGCAGAAAC<br>TTCG   | TGGTTTGGTAATTGGG<br>AGGA      | 60.0                             | 712                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_47032360  | Ca7                                     | 47032360                      | GAAAA/GAAAATAAAA                                                                          | CATTTCAGTTGGGGC<br>AGTT    | ACACCCACATCTCTCG<br>TTCC      | 60.0                             | 343                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                 |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_47065322  | Ca7                                     | 47065322                      | T/TAG                                                                           | CACAAGCCATTGGCAA<br>ACTA  | TTGATCCATAGCTCGT<br>GCAG    | 59.7                             | 348                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_47089790  | Ca7                                     | 47089790                      | TACAC/TAC                                                                       | CACATACACTCCCCAA<br>TCCC  | ACGGTTCAGAAAGAGAA<br>GGCA   | 60.1                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_47155072  | Ca7                                     | 47155072                      | A/AAGAG                                                                         | AGGAGGGGTGCGATT<br>TTAT   | TTATGCGTGGTTGTTG<br>CATT    | 59.8                             | 166                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_47160099  | Ca7                                     | 47160099                      | ATTATTTATTTATTTATTTATTT<br>ATTTATTTATTTAT/ATTATTTATTTA<br>TTTATTTATTTATTTATTTAT | TGATACCCGATCCGTC<br>TCTC  | TGGGTTTTAATCTTTTG<br>GGG    | 60.0                             | 408                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_47270756  | Ca7                                     | 47270756                      | GTTTTTTTTT/GTTTTTTTTT                                                           | TTCCCCATGCAAAGTT<br>AGG   | CTTAGGCAACCGCAAG<br>GATA    | 59.9                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_47286553  | Ca7                                     | 47286553                      | GATAATAATAATAATAATAATAA<br>TAA/GATAATAATAATAATAATAA<br>TAATAATAA                | CTGAAGGTGCAAAACAC<br>GAGA | CAAGGACTAAATTGAAA<br>CCCAAA | 60.0                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_47462097  | Ca7                                     | 47462097                      | TCTTCNNNNNNNNNNCTTC/TCTT<br>C                                                   | ATTGGCGACAAAGATT<br>CACC  | CACATTGTGATTGGCT<br>CCG     | 59.9                             | 249                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_47680703  | Ca7                                     | 47680703                      | TAAAAAAAAA/TAAAAAAAAA                                                           | TCAATGAAGTTGCCAC<br>CAAA  | CCTGCACAGCTTGCA<br>TTT      | 60.1                             | 885                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_47683251  | Ca7                                     | 47683251                      | CTTTT/CTTTT                                                                     | TCCTTTTCTGCCTTTGT<br>GCT  | TTCAAACCATCTCG<br>TCG       | 60.0                             | 681                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_47715158  | Ca7                                     | 47715158                      | T/TAC                                                                           | AGCACACGCCCTTTGT<br>ACTT  | TGTGAGGAAATGGAA<br>CACA     | 59.8                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                               | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                             |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_4775529   | Ca7                                     | 4775529                       | TAAAAAAAAA/TAAAAAAAAA                                                                       | TGCACATTGCACACTA<br>CCAA | GTGCATTGGAAGAAAG<br>AGCC    | 59.7                             | 619                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_47791893  | Ca7                                     | 47791893                      | TCCCCCCCCC/TCCCCCCCCCCC                                                                     | TGAGGATCCCCACAAA<br>CAGT | CCTAGGATCCATGGAC<br>AACG    | 60.4                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_47927082  | Ca7                                     | 47927082                      | AATATATATATATATATATATATA/<br>AATATATATATATATATATATATAT<br>A                                 | TATTTTGGATTTTGGCT<br>CGG | CACCGTAGTGTGGTGG<br>TGAG    | 59.9                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_48311764  | Ca7                                     | 48311764                      | GAAA/GAA                                                                                    | TTCAGATCTGGGATGC<br>CTCT | GGTACGTCCAGTCCTC<br>TTGC    | 59.8                             | 402                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_48312562  | Ca7                                     | 48312562                      | TAAAA/TAAAAA                                                                                | CGAAGCACAAGGAGAT<br>GACA | CAGTGATGCGGAAAAA<br>CTCA    | 60.0                             | 196                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_48312616  | Ca7                                     | 48312616                      | AT/ATATCT                                                                                   | CGAAGCACAAGGAGAT<br>GACA | TTCCGAGTGCTGTCA<br>AATG     | 60.0                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_48390576  | Ca7                                     | 48390576                      | CTTTATTTATTTATTTATTTATTTAT<br>/CTTTATTTATTTATTTATTTATTTAT<br>TTATT                          | TGTCATGGCAACCAT<br>GTCT  | TTGCTCCTACGTATTT<br>CCG     | 60.0                             | 938                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_48392684  | Ca7                                     | 48392684                      | TAAAAAAAAA/TAAAAAAAAA                                                                       | TGATTCCCCAACATCC<br>AACT | ATGATATTGGAGTTTGC<br>GCC    | 60.2                             | 165                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_48429143  | Ca7                                     | 48429143                      | AATATATATATATATATAT/AATATAT<br>ATATATATATATAT                                               | AACACCGGGTTCAGAT<br>GTGT | GGCCAAATACGTTGGA<br>AATG    | 60.3                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_48436958  | Ca7                                     | 48436958                      | TTATATATATATATATATATATATA<br>TATATATATAT/TTATATATATATATA<br>TATATATATATATATATATATATAT<br>AT | AATCCTCAATGCGGA<br>GAAA  | AAATTTTAGGAAACTC<br>AAGTTCG | 59.6                             | 384                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                       | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                     |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_48489925  | Ca7                                     | 48489925                      | C/CACTATCAAT                                                                                        | CCACAACTAAGATCC<br>TGCCA   | GCCTCCAAAACCGATA<br>TTCA    | 60.1                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_4867122   | Ca7                                     | 4867122                       | AATATATATATATATATATATATATAT<br>ATTTATATATATATAT/AATATATATA<br>TATATATATATATATATATTTATAT<br>ATATATAT | AGGTGGTGAGCGTTTT<br>TGAA   | TTGATGATGTGAAGGA<br>ATGACAG | 60.7                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_48806824  | Ca7                                     | 48806824                      | GAAAAAAAAAAAAA/GAAAAAAAAA<br>AAA                                                                    | CAAGAACGCATGCATT<br>AGGA   | GGGAGGCAACCCAATT<br>TTAT    | 59.8                             | 615                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_48845811  | Ca7                                     | 48845811                      | TAAAAAAAAA/TAAAAAAAAA                                                                               | GACTTGACGGATATTT<br>CACGC  | TACATCCCTAGGATGC<br>GACC    | 59.6                             | 421                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_48858448  | Ca7                                     | 48858448                      | TAGA/TAGAATGAGGTGGCAGAGA                                                                            | GCATGGTTGAGAAGGG<br>AGAA   | TCAGCCAAAAAGCTGA<br>TGTG    | 60.2                             | 174                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_48873547  | Ca7                                     | 48873547                      | AATATATATATATATATAT/AATATAT<br>ATATATATAT                                                           | AAGGGAGGACGTGGA<br>GAACT   | CGAAGGTTTTGGAAGA<br>GCTG    | 60.1                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_48932820  | Ca7                                     | 48932820                      | AT/ATGGAAACCCTTT                                                                                    | ACATGCTGTTTTTGCT<br>GCTG   | CAAGTCTCCAAGTTC<br>CCAA     | 60.1                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_48950591  | Ca7                                     | 48950591                      | CTTTTTTTTT/CTTTTTTTTT                                                                               | TTGTTGGCTTAATTGCA<br>TTTTT | CACGACTGCACCACTT<br>GACT    | 58.7                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_4904641   | Ca7                                     | 4904641                       | CTTTTT/CTTTTT                                                                                       | TTCTAATATTCGCGTTG<br>GGC   | TCATGTGTGTCGTGT<br>GTGC     | 60.1                             | 763                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_4974042   | Ca7                                     | 4974042                       | CAAAAAAAAA/CAAAAAAAAA                                                                               | ATTGGTGGGGTTTAT<br>GGGT    | GTGAGGGGTTTCATAGG<br>TCCA   | 60.2                             | 293                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5009997   | Ca7                                     | 5009997                       | A/AAAAACAT                                                    | CACAACTCCGCGTAA<br>CTTT     | TTTGGGGTTTTGTTTC<br>GTGT   | 60.2                             | 900                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5011126   | Ca7                                     | 5011126                       | GAAAAAAAAAAAAA/GAAAAAAAAA<br>AAAA                             | TCATCAAATCCGTAAC<br>GCAA    | TGCAAGCATGAGAAGT<br>TGTTG  | 60.1                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5014340   | Ca7                                     | 5014340                       | CAA/CAAA                                                      | AATACCACCACCGACC<br>ACAT    | AATGAGCTCCAACGGT<br>CATC   | 60.0                             | 787                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5026355   | Ca7                                     | 5026355                       | TAAAA/TAAA                                                    | GTCACCCCTCAAGAC<br>ACAT     | TTGAGAAGAATGGGG<br>TGAG    | 59.8                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5029422   | Ca7                                     | 5029422                       | ATT/AT                                                        | GTGCCAAATTGGACCT<br>ATGC    | GAGTCACACACCCG<br>AGAA     | 60.3                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5030934   | Ca7                                     | 5030934                       | ATTT/ATTTT                                                    | AACTGGTCAGATTGGT<br>TGAGAAA | CATCCAATTCTTCACT<br>CCGA   | 60.0                             | 585                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5034485   | Ca7                                     | 5034485                       | ATTTTTTTTT/ATTTTTTTTTT                                        | CCCACCTGCAACGGTT<br>TATT    | TGAGGTAAGCTTTGCA<br>TCATGT | 59.9                             | 837                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5044562   | Ca7                                     | 5044562                       | ATT/AT                                                        | CCAACAACACAGATGC<br>AACC    | GCGCTTAGAGTTCCAA<br>CCAG   | 60.0                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5076726   | Ca7                                     | 5076726                       | GTTTTT/GTTTTTTT                                               | CATGCTGCAAGTTGT<br>GAAT     | CTTCTAAAAACGCGCT<br>GCT    | 59.7                             | 700                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5081329   | Ca7                                     | 5081329                       | ATTTTTTT/ATTTTTTTT                                            | GGGGGATTTGACCTG<br>ATT      | TGTTTCGTTTACTTTTG<br>ACGGA | 60.0                             | 750                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5081699   | Ca7                                     | 5081699                       | AC/A                                                          | TTACTGGTGGGCCTTA<br>CACC     | TTATCTTTCCAACGCCT<br>GCT  | 59.9                             | 793                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5136940   | Ca7                                     | 5136940                       | TAAAAAAAAA/TAAAAAAAAA                                         | GGCTTAAGAGAGGGG<br>GCTTA     | TCGAAGTTTTTGGTAGG<br>GTGG | 59.8                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5157175   | Ca7                                     | 5157175                       | CATATATATATATATATA/CATATATA<br>TATATATATATA                   | TGGGGAAGAGTTCCCT<br>TCTT     | AGTGTGTGCGTTGCC<br>CTTA   | 60.0                             | 903                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5178298   | Ca7                                     | 5178298                       | ACC/ACCC                                                      | TGAGCCGTAGAATCCC<br>TATGA    | TTCCAGGAAAAATCCA<br>GACA  | 59.7                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5180934   | Ca7                                     | 5180934                       | ATTTTTTT/ATTTTTTTT                                            | TTGAGACATTTTGTA<br>TCTAATGGA | GCAATTTTGGTACCGC<br>TGTT  | 58.3                             | 842                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5191824   | Ca7                                     | 5191824                       | TAAAAAAA/TAAAAAAA                                             | ACGAATTTTCGGGAT<br>CTTG      | TTTCCCAGTTGGTCG<br>TTTA   | 59.0                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5212385   | Ca7                                     | 5212385                       | AC/A                                                          | TATTGCGGGCTTTTAG<br>GACA     | TCAAGCAATTTTGTGCG<br>GAG  | 60.6                             | 852                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5302889   | Ca7                                     | 5302889                       | TTATATATATATA/TTATATATATATA<br>TA                             | AAGCATTGTAAAAATT<br>ACGCCA   | ATTCATTGCTTCGGA<br>GTCG   | 59.9                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5343899   | Ca7                                     | 5343899                       | CTTTTTTTTT/CTTTTTTTTTT                                        | TGAGGTGATGTGTCCA<br>TTGAG    | TGCAGAGAACAAGCAC<br>ATTG  | 59.5                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5387713   | Ca7                                     | 5387713                       | TATTTAAATTTAAAT/TATTTAAAT<br>T                                | TGCATATAATTGGATCA<br>TTGGTG  | ATGGAAATGGTGGTGA<br>TGGT  | 59.6                             | 607                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5405644   | Ca7                                     | 5405644                       | AATATAT/AATATATAT                                             | GCGATGGAAGAAAAGT<br>TGGA    | AACGTGCAACAATATC<br>GCAA  | 60.2                             | 245                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5407056   | Ca7                                     | 5407056                       | A/AT                                                          | AAAAAGGCTGCAAAAG<br>CAAA    | CGGTGAAAATCCACTC<br>CCTA  | 60.0                             | 782                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5407517   | Ca7                                     | 5407517                       | TCTAAC/TCTAACTAAC                                             | AAATTAGGGAGTGGAT<br>TTTCACC | GTTTGGGTTGAGACG<br>TGGT   | 59.6                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5414070   | Ca7                                     | 5414070                       | ACTCTCTCT/ACTCTCT                                             | TGACAAATTCAAACTCC<br>CGA    | GGTGACCTGGGAAAT<br>CCTT   | 59.1                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5429372   | Ca7                                     | 5429372                       | ATT/ATTT                                                      | AAAGGCGAGATGGAAG<br>GTTG    | TTGGTGTGATTTCGTGA<br>CCAT | 59.3                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5434482   | Ca7                                     | 5434482                       | TAAAAA/TAAAA                                                  | CCAATTATGCCATTGG<br>AATTT   | TGTCGGGTTGATCCTC<br>TTTC  | 58.7                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5440132   | Ca7                                     | 5440132                       | TCAAAAG/T                                                     | GCTAAACTGCCATTTTC<br>TTTTCA | TTGGTAATGTCGTGGG<br>AACA  | 59.8                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5443791   | Ca7                                     | 5443791                       | TATAAATAAATAAATAA/TATAAATAA<br>ATAA                           | TATTTGCGAGCGTGTC<br>TTCA    | TTTTGATGCTTTTCCA<br>CCA   | 60.5                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5445444   | Ca7                                     | 5445444                       | ATTTTTTTTTTT/ATTTTTTTT                                        | AATCCACATGTTGGAG<br>GGAC    | GCACGAAGAATGAGAG<br>GGAG  | 59.6                             | 745                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5445507   | Ca7                                     | 5445507                       | AA/AAGA                                                       | AATCCACATGTTGGAG<br>GGAC    | GCACGAAGAATGAGAG<br>GGAG  | 59.6                             | 745                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5445796   | Ca7                                     | 5445796                       | CAAAAAA/CAAAAA                                                | CGAATATTTATGAACGT<br>GGTCC | GCACGAAGAATGAGAG<br>GGAG   | 58.4                             | 185                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5458475   | Ca7                                     | 5458475                       | TAAAA/TAA                                                     | ACAATTACGTGAAGGC<br>CACA   | TTCGGATTGCAACCTTT<br>TTC   | 59.1                             | 391                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5458536   | Ca7                                     | 5458536                       | ACTAG/ACTAGCTAG                                               | ACAATTACGTGAAGGC<br>CACA   | TTCGGATTGCAACCTTT<br>TTC   | 59.1                             | 391                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5461647   | Ca7                                     | 5461647                       | GCTTTTCTTTTCTTTT/GCTTTT<br>CTTTT                              | CTTTTGTGCCAAGTG<br>GGTT    | CAAACAAACCCGATC<br>GAAA    | 60.0                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5461787   | Ca7                                     | 5461787                       | GAAAAAA/GAAAAAA                                               | CTTTTGTGCCAAGTG<br>GGTT    | CAAACAAACCCGATC<br>GAAA    | 60.0                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5461973   | Ca7                                     | 5461973                       | TG/T                                                          | TTTCGATCGGGGTTAG<br>TTTG   | TTGGAAAATGTCAATC<br>GATTCT | 59.9                             | 180                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5468199   | Ca7                                     | 5468199                       | GATGATGATTA/GA                                                | AACTCGGTGAGCCTCT<br>CAAA   | CCCACGCATCTTGTTT<br>CTTC   | 60.0                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5468429   | Ca7                                     | 5468429                       | TGG/TG                                                        | GCGAAGCAATTTTGAG<br>AAGG   | TTTATGACGGGCAATC<br>CAAT   | 60.0                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5470006   | Ca7                                     | 5470006                       | TTATATATATAT/TTATATATAT                                       | GGGATCTATTAACAA<br>CGAACCA | TGGAATTGTCCACCAC<br>AACA   | 60.4                             | 632                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5470397   | Ca7                                     | 5470397                       | GAAAAA/GAAAA                                                  | TTTGATCACATCCATTG<br>TCCT  | TATCACTTCCAATTTCC<br>GGG   | 57.8                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5472392   | Ca7                                     | 5472392                       | AC/A                                                          | CCCTCACCCCTTTCTTC<br>ACA       | CGGAAGTCATAACCGT<br>CGTT    | 60.1                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5480065   | Ca7                                     | 5480065                       | TAAAAAAA/TAAAAA                                               | TGGAGTCGGTTACGTG<br>AGTG       | CCTACCCAAACCCTAC<br>CCAT    | 59.7                             | 820                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5481672   | Ca7                                     | 5481672                       | ATTTTTTT/ATTTTTTTT                                            | GGTGTCCACTGAGTTT<br>GGGT       | TGCTTGTGATTACCTT<br>AATTCC  | 59.9                             | 812                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5482693   | Ca7                                     | 5482693                       | TATT/TATTTTATAATT                                             | TTCGTGTAGTTGATTCA<br>AACCAT    | AACAAAAGGCAATAAAT<br>GAACGA | 58.6                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5482708   | Ca7                                     | 5482708                       | ATTTT/ATTT                                                    | TTCGTGTAGTTGATTCA<br>AACCAT    | AACAAAAGGCAATAAAT<br>GAACGA | 58.6                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5484348   | Ca7                                     | 5484348                       | TTATATATATATA/TTATATATATA                                     | AAAGAAGAAGAAAATAA<br>AGCAAATCA | TTTTTGGCAGACACGG<br>AGTA    | 58.3                             | 216                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5486002   | Ca7                                     | 5486002                       | ATTTTTTT/ATTTTTTTT                                            | TCATCATTTATCCAAG<br>CATCA      | AAGGACAAATTTGATTC<br>GGTTT  | 58.1                             | 200                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5487626   | Ca7                                     | 5487626                       | ATCTCTCTCTCTCTCT/ATCTCTC<br>TCTCTCTCTCTCTCTCTCTCTCT           | AAACGGAGAGAAAACG<br>ACGA       | AGGTGACGGAAAAGGA<br>GGTT    | 59.9                             | 261                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5492251   | Ca7                                     | 5492251                       | AT/A                                                          | TGGACATGTTCCATTG<br>GTTG       | GCTCCTCCAAAATTGAT<br>TGG    | 60.2                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5518891   | Ca7                                     | 5518891                       | GTTTTTTTTT/GTTTTTTTTT                                         | TTGTTGATTTGGGCC<br>AGAT        | AGCATGTCATTGATGG<br>AGCA    | 60.3                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5525528   | Ca7                                     | 5525528                       | AT/ATT                                                        | AATGTCAAGGCATT<br>GGTC    | CGTTTTTGGACATGA<br>GAAA  | 59.8                             | 624                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5532508   | Ca7                                     | 5532508                       | GAAAAAAAA/GAAAAAAAA                                           | AGCGGTGAAGTCAATA<br>TGGG  | TGAAATGAGTTCGTCT<br>GCG  | 60.0                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5539537   | Ca7                                     | 5539537                       | ACC/ACCC                                                      | TTCTCAAATCCGTTTC<br>CAC   | AAATCAAATTTGCCGC<br>TTG  | 59.9                             | 955                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5572175   | Ca7                                     | 5572175                       | TAAAAAAAAAAAAAAAAA/TAAAAAAAA<br>AA                            | TGTCAAATGTGAGGAA<br>GCCA  | TAGGGACCCATATGCA<br>AAAA | 60.2                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5572652   | Ca7                                     | 5572652                       | ATTTTTTT/ATTTTTTTTT                                           | AAAAATGGCGTTCATC<br>AAATG | TTTGCCAAATTTTAGGG<br>ACC | 59.8                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5572958   | Ca7                                     | 5572958                       | TAAAAAAAA/TAAAAA                                              | ATGGGTCCCTAAAAAT<br>TGCC  | CGAGACGCGTCAACA<br>CATA  | 60.0                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5576452   | Ca7                                     | 5576452                       | TAAAAAAAA/TAAAAAAAA                                           | ATCGTGTGATGCGTTT<br>GTGT  | TCTTGCTTCGGACCTC<br>TGAT | 60.0                             | 562                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5628001   | Ca7                                     | 5628001                       | ATTTT/ATTT                                                    | CTGATGCTACAGCCAC<br>TGGA  | TCCAATAAATACCAAC<br>CCG  | 60.0                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5628019   | Ca7                                     | 5628019                       | CAAAAA/CAAAAA                                                 | CTGATGCTACAGCCAC<br>TGGA  | TCCAATAAATACCAAC<br>CCG  | 60.0                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5628193   | Ca7                                     | 5628193                       | TAAAAAAAA/TAAAAAAAA                                           | TGTTTCGTTTTTGCTT<br>CAG   | TCCAATAAATACCAAC<br>CCG  | 58.9                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5628630   | Ca7                                     | 5628630                       | GAAAAAAAA/GAAAAAAAA                                           | CGGGTTGGTATTTATT<br>GGGA  | ATTGAGTTGATCACTC<br>GGGG   | 59.5                             | 678                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5629123   | Ca7                                     | 5629123                       | GAAAAAAAA/GAAAAAAAA                                           | CCCCGAGTGATCAACT<br>CAAT  | TGCACTCTTATGTGTG<br>GGAAA  | 59.9                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5648526   | Ca7                                     | 5648526                       | TAAAAAAAA/TAAAAAAAA                                           | TGTGCACCAACAAC<br>ATCA    | TGGGGGATGACATGTA<br>CCTT   | 59.6                             | 448                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5649774   | Ca7                                     | 5649774                       | CTTTTTTTTT/CTTTTTTTT                                          | AAGGGAATGCATTGTC<br>TCTCA | TTGTATTGTGTGGCTT<br>GTAGTA | 59.7                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5650363   | Ca7                                     | 5650363                       | AAATAATAATA/AAATAATAATA<br>TAATA                              | TCGTTCCCTCTGAAAT<br>GAAA  | TCGAGTGAACGTGGAA<br>GATG   | 58.3                             | 239                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5651939   | Ca7                                     | 5651939                       | TATTAAT/TATTAACAATTAAA                                        | CGGAGAACAACAATC<br>CACC   | AGCATTGCGCCTCTGT<br>AGAT   | 60.4                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5663307   | Ca7                                     | 5663307                       | ATCCATTAGT/AT                                                 | CGGAGCCTATTGCTGC<br>TATC  | TATCCACGGACACGAG<br>TTCA   | 60.0                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5668000   | Ca7                                     | 5668000                       | TAAAAAAAAA/TAAAAAAAA                                          | TCATACTCGTATTCGT<br>GCCG  | CAGGGTCCTTGTCGTG<br>ATTT   | 59.7                             | 764                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5688390   | Ca7                                     | 5688390                       | GTT/GTTTT                                                     | TTGGTTAAAGGGTCGA<br>GTGG  | TGCTAATTGAACCCC<br>AAAA    | 60.0                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5689310   | Ca7                                     | 5689310                       | ATTTTTTTT/ATTTTTTTT                                           | CAAGTGAACACGGCG<br>TGAA   | GTGCTCATAGGCCCA<br>TGTT    | 59.9                             | 422                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5694761   | Ca7                                     | 5694761                       | TAAAAAA/TAAAAAA                                               | GGAATTCTGTTTGCAAGGGA    | AACCCATCACTTGCTGATCC    | 60.1                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5697428   | Ca7                                     | 5697428                       | TAAAAAAAAA/TAAAAAAAAA                                         | AATGTTGTAAGGTGGGCGAG    | AAGTTAAGGGACCACGAGTGA   | 60.0                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5697927   | Ca7                                     | 5697927                       | A/ATT                                                         | TCACTCGTGGTCCCTTAACCTT  | TTGCCATTCCATGGATACAC    | 58.7                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5699413   | Ca7                                     | 5699413                       | CAAAAAAAAA/CAAAAAAAAA                                         | TTTGAATTGCTTTTAAAGGGG   | ACGTTTTTGTATCACGAATCA   | 59.4                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5703031   | Ca7                                     | 5703031                       | GTTTTTT/GTTTTTT                                               | TGGCCACAAAATAAAGGTG     | CTTCTACGACGCATCGAACC    | 58.7                             | 492                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5704766   | Ca7                                     | 5704766                       | ACTT/ATT                                                      | TGCAACAAAAGGCAAACTAGAA  | AATCATTTCAATTCCGCTGC    | 59.9                             | 259                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5715370   | Ca7                                     | 5715370                       | TAAAAAA/TAAAAAA                                               | ACGAGCTTGGCTTACTGGAC    | AAGCCCTCTCCCTCTCACAT    | 59.5                             | 744                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5716940   | Ca7                                     | 5716940                       | TAAAAAAAAA/TAAAAAAAAA                                         | ACCAAACTCTATCCCCTTAAAA  | AACGTGGATACATTTGATTCTCA | 57.4                             | 400                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5717190   | Ca7                                     | 5717190                       | CTTTTTTTTTTTTT/CTTTTTTTTTTT                                   | ACCAAACTCTATCCCCTTAAAA  | CCACTCTCAAAGTCAATGGC    | 57.4                             | 620                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5717490   | Ca7                                     | 5717490                       | TAAAAAAAAA/TAAAAAAAAA                                         | TGAGAATCAAATGTATCACGTT  | CGTAGCATTTGCCTTCCAAT    | 58.5                             | 702                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5719119   | Ca7                                     | 5719119                       | CTATA/CTATATA                                                 | GAGTCCACCGAACATT<br>TTGA       | TTGGGTCTGTGTGTT<br>CCAA         | 60.0                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5740792   | Ca7                                     | 5740792                       | TGAAGAAGAAGAA/TGAAGAAGAAG<br>AAGAA                            | ACTCCCACTTCCACCA<br>CAAG       | TCGGGGGACTAGTCAA<br>GAAA        | 60.0                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5761200   | Ca7                                     | 5761200                       | TC/TCC                                                        | GCATCCAAACATACCA<br>TCCC       | CTTGACCCAAAATGTG<br>GCTT        | 60.0                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5775928   | Ca7                                     | 5775928                       | TAAAAAAAAA/TAAAAAAAAA                                         | TTGGATTCAGTGTGG<br>TGGA        | CGACCACATGTCTGTC<br>TCGT        | 59.9                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5785819   | Ca7                                     | 5785819                       | TATTTTTTTTTA/T                                                | TGCGGAGAGATAGAGA<br>GCGT       | TGCAACGATTTAACTT<br>CCAA        | 60.3                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5786240   | Ca7                                     | 5786240                       | TAAAAAAAAA/TAAAAAAAAA                                         | TTGCATTGGAAAGTTA<br>AATCG      | TCCAAAATTGAGTGG<br>CACA         | 59.2                             | 753                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5787059   | Ca7                                     | 5787059                       | AT/ATTGTTATT                                                  | TTTGACCTCAAGCAAA<br>CCC        | ATTTGGATGAGATCG<br>GGTG         | 60.1                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5798029   | Ca7                                     | 5798029                       | TAAAAAA/TAAAAAA                                               | ATAACCGAGCCGCAAC<br>TAAA       | TTCTTTTAATGTTTAT<br>ATTGTGCCA   | 59.7                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5803545   | Ca7                                     | 5803545                       | ATA/ATAGTA                                                    | CAATCGAATTCTGGAA<br>TTGTCA     | AAAATGGGGAGTTTAA<br>CATAGTACAAA | 59.9                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5803964   | Ca7                                     | 5803964                       | CTCCCCATT/CT                                                  | TCAGCGAAATATTTAT<br>TTTATTCCTT | ATGAGCCGTCGTCGTA<br>TCTC        | 59.1                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5807623   | Ca7                                     | 5807623                       | TTATA/TTATATA                                                 | TAATTGAGGCTTGTG<br>CGTG    | GTTTCTTGCCTTGC<br>TCC        | 59.9                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5813343   | Ca7                                     | 5813343                       | ATTTTTTTT/ATTTTTTTTT                                          | AATGAAAAGAGGAGTG<br>GCGA   | ACGGTTTTCCGGTAGT<br>TTCC     | 59.8                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5817548   | Ca7                                     | 5817548                       | AAATA/AAATAATA                                                | TACGAACCAACACGTG<br>GAAA   | ACATTTCCGCGCTTAC<br>AGAT     | 60.0                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5818691   | Ca7                                     | 5818691                       | ATTT/ATTTTT                                                   | TACACATTTATGTGCG<br>CCGT   | TGATTTGGATGTGATT<br>GCC      | 60.0                             | 292                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5818847   | Ca7                                     | 5818847                       | TA/TAA                                                        | TACACATTTATGTGCG<br>CCGT   | GGGCAACAACATGT<br>CTCAA      | 60.0                             | 402                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5819215   | Ca7                                     | 5819215                       | GAT/GATAT                                                     | TGGCAAATCACATCCA<br>AATC   | TGGCCTTGAGTGCTCA<br>GTAG     | 59.3                             | 957                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5820802   | Ca7                                     | 5820802                       | A/AG                                                          | TGAGGCCAACATAAAA<br>ATCAT  | ACGGATTGGTGGATG<br>GTAA      | 57.1                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5838661   | Ca7                                     | 5838661                       | AGG/AG                                                        | CGAACTATCTTCTGTT<br>TGACCG | TTCTTGTTTTTAATTT<br>CTCCTCTG | 60.2                             | 387                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5839571   | Ca7                                     | 5839571                       | A/AT                                                          | GGCGGTGAATCTTTGT<br>CATT   | TGGCATCACAACTTC<br>CAAA      | 59.9                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5843643   | Ca7                                     | 5843643                       | AT/ATT                                                        | GGTGAGTTTTTCTCTC<br>CCCC   | TTCATCGTCTGAAGTCA<br>CGG     | 59.9                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5858952   | Ca7                                     | 5858952                       | ATTTTTTTTT/ATTTTTTT                                           | AAAGATGTTCAATTGAG<br>CCAAA | TGGGTTTCAAAAAGGC<br>AAAG | 58.7                             | 696                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5864797   | Ca7                                     | 5864797                       | GTCTCTCTCTCTCTCTC/GTCTCT<br>CTCTCTCTCTCTCTCTCTCTC             | CCAGAAAAGGAGGAGC<br>TCAA   | GACTGTGAGGTGGGAA<br>TGCT | 59.5                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5864882   | Ca7                                     | 5864882                       | AAGAGAGAGAGAGAGAGAGA/AA<br>GAGAGAGAGAGAGAGAGA                 | AGCATTCCACCTCAC<br>AGTC    | TGGAAGAAAATGGGTA<br>ACGG | 60.1                             | 230                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5870704   | Ca7                                     | 5870704                       | AAG/AAGAG                                                     | CACTACAAAAGTGCAA<br>GCCC   | CACAACCTCCAGAGC<br>CAAA  | 58.4                             | 747                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5871390   | Ca7                                     | 5871390                       | T/TAGTG                                                       | TTTGGCTCTGGAGAGT<br>TG TG  | TAAGCTAGAGCAGGG<br>GAGG  | 59.0                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5874353   | Ca7                                     | 5874353                       | GA/G                                                          | TTTGGTACAACGAGGT<br>CCAC   | TTGGCTTGTCACATCA<br>GCTT | 58.5                             | 268                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5874667   | Ca7                                     | 5874667                       | CAAA/CAA                                                      | AAGCTGATGTGACAAG<br>CCAA   | TTATAAACATGGGCGA<br>ACCC | 59.4                             | 391                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5875142   | Ca7                                     | 5875142                       | AATTTATTTATTTATTT/AATTTATTT<br>ATTT                           | CTATAAATTGGGGTTC<br>GCCC   | ATCTTTGTCGTTCAAGT<br>GCC | 60.5                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5875186   | Ca7                                     | 5875186                       | CTTT/CTTTT                                                    | CTATAAATTGGGGTTC<br>GCCC   | ATCTTTGTCGTTCAAGT<br>GCC | 60.5                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5875322   | Ca7                                     | 5875322                       | A/AG                                                          | GCTTTGTCGGCTCAAA<br>GACT   | ATCTTTGTCGTTCAAGT<br>GCC | 59.6                             | 115                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5876334   | Ca7                                     | 5876334                       | AAG/AAGTTAG                                                   | GCTTTCGGCTCAACTT<br>TTTG | ATGAAGTGAATGGAA<br>TGGC       | 60.0                             | 679                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5876688   | Ca7                                     | 5876688                       | GAGGGAAAAATAAGGGAA/GAGG<br>GAA                                | ACGCGTCTTTTCGAG<br>TCAT  | CGCCATTCTTATTTGG<br>GGTA      | 59.9                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5884631   | Ca7                                     | 5884631                       | ATTTTT/ATTTTTTTT                                              | TCTTGTTGCCTGTCT<br>CGTG  | ATGCGAAGGAGCAATT<br>ATGG      | 60.0                             | 832                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5884732   | Ca7                                     | 5884732                       | CAA/CA                                                        | ACATGGCTTTACTTGG<br>TGGA | ATGCGAAGGAGCAATT<br>ATGG      | 58.1                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5884765   | Ca7                                     | 5884765                       | AC/A                                                          | ACATGGCTTTACTTGG<br>TGGA | ATGCGAAGGAGCAATT<br>ATGG      | 58.1                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5885014   | Ca7                                     | 5885014                       | CAAA/CAAAA                                                    | CCATAATTGCTCCTTC<br>GCAT | CAGCCGAATACGCTGC<br>TACT      | 60.1                             | 213                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5886738   | Ca7                                     | 5886738                       | ATTTTT/ATTTTTTT                                               | GAGCATGTAGGTGCTG<br>GGTT | TTCATTGCATCTATTT<br>GTTACCTTT | 60.1                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5891630   | Ca7                                     | 5891630                       | TGG/TG                                                        | GCTGGGATAATAGGCG<br>CTTC | AAATGGGTGAGATCAG<br>CGAC      | 59.9                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5893840   | Ca7                                     | 5893840                       | CAAAAA/CAAAAAAAA                                              | AAATGAAAGCAGGCCT<br>CAAA | CGGTGTTGTCCGTTTT<br>TCTT      | 59.8                             | 411                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5894005   | Ca7                                     | 5894005                       | GTTTTTTTTT/GTTTTTTTTTT                                        | AAGAAAAACGGACAAC<br>ACCG | TGTTGTGCATGACTTG<br>AAGG      | 60.0                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5894071   | Ca7                                     | 5894071                       | CTT/CT                                                        | AAGAAAAACGGACAAC<br>ACCG   | TGTTGTCATGACTTG<br>AAGG   | 60.0                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5894442   | Ca7                                     | 5894442                       | ATTTTTTT/ATTTTTTTT                                            | CAAGTCATGCACAACA<br>TTTGG  | TGTC AACCTGATTGAA<br>CCGA | 60.0                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5895925   | Ca7                                     | 5895925                       | TCC/TC                                                        | CGTTTGTAAGTTGCGG<br>GATT   | GGCTCAAAGTGGGTGA<br>ATGT  | 60.0                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5895955   | Ca7                                     | 5895955                       | CAAAAAAAAA/CAAAAAAAAAA                                        | CGTTTGTAAGTTGCGG<br>GATT   | GGCTCAAAGTGGGTGA<br>ATGT  | 60.0                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5896488   | Ca7                                     | 5896488                       | GAGTAG/GAG                                                    | ACATTCACCCACTTTGA<br>GCC   | GGTCCCTGAAGCAATC<br>TTTG  | 60.0                             | 481                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5897121   | Ca7                                     | 5897121                       | CT/CTTTGTT                                                    | CAAAGATTGCTTCAGG<br>GACC   | CCACTGTTTAAAATGTG<br>CCG  | 59.7                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5899902   | Ca7                                     | 5899902                       | TGG/TG                                                        | TTTCATGCATTTGGTTT<br>CCA   | TCTCTAATGCATGGCA<br>GCAC  | 59.9                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5900049   | Ca7                                     | 5900049                       | CA/CAA                                                        | TTTCATGCATTTGGTTT<br>CCA   | TCTCTAATGCATGGCA<br>GCAC  | 59.9                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5900811   | Ca7                                     | 5900811                       | CTC/CTCGATC                                                   | TGGAAGAGTCCAATGA<br>AAATCA | TTCGGTTCTTCTCTAAA<br>TCC  | 59.5                             | 823                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5901013   | Ca7                                     | 5901013                       | TAAAAA/TAAAAA                                                 | AAATTTGTGCTAAATTC<br>CCCA  | TGAAACAGTTGAGGTC<br>GCTG  | 58.5                             | 881                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5901378   | Ca7                                     | 5901378                       | CAAA/CAAAA                                                    | TAGGAAGGAACCGAAG<br>TGGA     | TGAAACAGTTGAGGTC<br>GCTG    | 59.7                             | 132                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5902065   | Ca7                                     | 5902065                       | ATTTTTTTTT/ATTTTTTTTTT                                        | TACACCGGTTCAATTG<br>GGAT     | TTACACTGACGGACG<br>AAGA     | 60.1                             | 886                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5902114   | Ca7                                     | 5902114                       | TAAAAAAAA/TAAAAAAAA                                           | TTCATCCTTGCAAATAT<br>GTTTTGT | TCAACTTGACCCAAC<br>GCAA     | 59.8                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5926131   | Ca7                                     | 5926131                       | AC/A                                                          | TCATTTGCTTTGTGCTT<br>TGC     | AAAAAGGATTTAGGCT<br>GATCAAA | 60.0                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5936262   | Ca7                                     | 5936262                       | GTTTTT/GTTTTTTT                                               | AAGAGCAACTTAGTCC<br>GCGA     | AAGGTAGCGGCTCACA<br>ACAC    | 60.2                             | 421                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5936337   | Ca7                                     | 5936337                       | GTTTT/GTT                                                     | AAGAGCAACTTAGTCC<br>GCGA     | AAGGTAGCGGCTCACA<br>ACAC    | 60.2                             | 421                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5936505   | Ca7                                     | 5936505                       | TAAAAAAAAAAAAAAAA/TAAAAAAAA<br>AAAAA                          | AAGAGCAACTTAGTCC<br>GCGA     | ATCACAGTTTGTTCG<br>CTTG     | 60.2                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5936706   | Ca7                                     | 5936706                       | T/TTAGATAA                                                    | GACCGACGACAGATT<br>GTGA      | TTGTTCGCTTGACAAC<br>GTC     | 59.7                             | 319                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5936794   | Ca7                                     | 5936794                       | TA/T                                                          | GACCGACGACAGATT<br>GTGA      | TTGTTCGCTTGACAAC<br>GTC     | 59.7                             | 319                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5938033   | Ca7                                     | 5938033                       | TTG/TTGTG                                                     | AAATAGTGGAGGCAGC<br>GAAC     | CATTCAATTTGGTGATC<br>GCC    | 59.3                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5996383   | Ca7                                     | 5996383                       | CTTTTT/CTTTT                                                  | GGTGCGCCAATAAACT<br>CAAT      | TCTTTCACTTTCACCAC<br>CCC     | 60.0                             | 287                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_5999036   | Ca7                                     | 5999036                       | CTTTTTTTT/CTTTTTTT                                            | GAATCGATTGGCTTCC<br>ACAT      | GAGGAAGTCAAACATG<br>CGGT     | 59.9                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6002838   | Ca7                                     | 6002838                       | A/AT                                                          | GAAAACCATCTTCAAC<br>CCGA      | ACGGACGATACTTTGA<br>ACGC     | 59.9                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6005760   | Ca7                                     | 6005760                       | T/TA                                                          | TGTTGCCGTATAACCG<br>TTGA      | TTACGAGGCCTAAAGC<br>GAAA     | 60.0                             | 180                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6006122   | Ca7                                     | 6006122                       | ATTTTTTTTTT/ATTTTTTTT                                         | TGTTGCCGTATAACCG<br>TTGA      | TCTTCTATTTTGGCGGT<br>GGT     | 60.0                             | 701                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6007513   | Ca7                                     | 6007513                       | TAAAA/TAAA                                                    | TGAAGCTTTATTGGAAA<br>GAAATCA  | TGACAGGGTCATGCGT<br>GTAT     | 59.3                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6015163   | Ca7                                     | 6015163                       | ATTTTTTTT/ATTTTTTTT                                           | ACACGCAGCTCCTTTT<br>CAAC      | TCCAATTTTAAACAATA<br>CCACAGC | 60.4                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6015189   | Ca7                                     | 6015189                       | TAAAA/TAAAAA                                                  | ACACGCAGCTCCTTTT<br>CAAC      | TCCAATTTTAAACAATA<br>CCACAGC | 60.4                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6015584   | Ca7                                     | 6015584                       | GTTTTTTTTTTT/GTTTTTTTTTT                                      | GCTGTGGTATTGTTTA<br>AAATTGGA  | TTCCACTGAATGGTGC<br>AGAA     | 59.4                             | 805                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6017174   | Ca7                                     | 6017174                       | TAA/TA                                                        | TGCACCTTGTCAAAATG<br>AGTTAAGG | CGTGTCTCGTAACTCA<br>ATCCA    | 60.5                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_6018381   | Ca7                                     | 6018381                       | T/TG                                                          | CGAAAATGTGTGCAC<br>CTCG      | AAAAGGAAGGAACAGA<br>CAAGACC | 60.2                             | 171                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6020210   | Ca7                                     | 6020210                       | GTTTTTTTT/GTTTTTTTTT                                          | AATCCGTTGAGATTGG<br>GATG     | TCATTTTGTCTTTCC<br>TTTGTT   | 59.8                             | 379                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6033100   | Ca7                                     | 6033100                       | TAA/TA                                                        | AAAAAGAAAAATCCATG<br>ATTGTGA | AAACAACACCGCACCA<br>AAAT    | 58.9                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6045136   | Ca7                                     | 6045136                       | CAAAAAAAAA/CAAAAAAAAAA                                        | CCCCTGATCTTGAAAT<br>GGA      | TTGTCACTGTTACTTCG<br>CCG    | 59.9                             | 352                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6047570   | Ca7                                     | 6047570                       | TAAAAAAAAAAAA/TAAAAAAA                                        | CATGTTGTACACTGAC<br>CCGC     | TGCACAACGACATTTAC<br>GGT    | 60.0                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6047617   | Ca7                                     | 6047617                       | CA/CAA                                                        | GAGATAGGCGGTGGA<br>ATGA      | TGCACAACGACATTTAC<br>GGT    | 60.0                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6049845   | Ca7                                     | 6049845                       | T/TTTC                                                        | TCTTACTCCGAAATTCC<br>CCC     | TTATGCCCAACCATCT<br>CTC     | 60.3                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6049898   | Ca7                                     | 6049898                       | GAAAAA/GAAAAAA                                                | CCATGAGCTGCACATC<br>AAAC     | TGGATTTCCTTTGAAA<br>CGA     | 60.3                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6053559   | Ca7                                     | 6053559                       | CAAAAAA/CAAAAAAAA                                             | ATCGGAGTTTGCAT<br>TTTG       | TTCAAACCAACACGT<br>TCA      | 59.9                             | 687                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6054349   | Ca7                                     | 6054349                       | TC/T                                                          | CGGTATCGCTATTCGA<br>CACA     | TGGGCCTCTGTTCTCT<br>CACT    | 59.7                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_6054380   | Ca7                                     | 6054380                       | T/TG                                                          | CGGTATCGCTATTCGA<br>CACA    | TGGGCCTCTGTTCTCT<br>CACT  | 59.7                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6080588   | Ca7                                     | 6080588                       | GAAAAAAAA/GAAAAAAAAA                                          | CGGTGATGAGAGAAAC<br>AGCA    | CGTGTGAATCATGTGC<br>AAAA  | 60.0                             | 930                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6080886   | Ca7                                     | 6080886                       | TAAAA/TAAAA                                                   | TGAAATGGATATTGG<br>GCGT     | CGTGTGAATCATGTGC<br>AAAA  | 60.2                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6082788   | Ca7                                     | 6082788                       | AGTG/A                                                        | TGCAGTGCATGACT<br>CTGTGT    | ATTTGACAGCAAAACG<br>GTCC  | 59.4                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6086243   | Ca7                                     | 6086243                       | AATA/AA                                                       | TCGGAAGTTTGGTCTT<br>CAATG   | AAAAATCGGTGCACCTT<br>CAA  | 60.1                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6087806   | Ca7                                     | 6087806                       | CTTTTTTTTTT/CTTTTTTTTT                                        | ATGTTGGGGAGGTTAG<br>GGAC    | GGCCAACCAACCTCA<br>GTTA   | 60.1                             | 337                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6094916   | Ca7                                     | 6094916                       | TTCACAT/TT                                                    | ATGAGGCCATGGAAAA<br>TGAA    | AGGTGATTGAATCGTG<br>GAGG  | 60.3                             | 796                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6102449   | Ca7                                     | 6102449                       | TA/T                                                          | CGAATGAAACGTGTAC<br>TCGAAA  | GGTCGTAAGATGGAGA<br>AACGA | 60.2                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6102476   | Ca7                                     | 6102476                       | CTTTT/CTTTT                                                   | CGAATGAAACGTGTAC<br>TCGAAA  | GGTCGTAAGATGGAGA<br>AACGA | 60.2                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6103166   | Ca7                                     | 6103166                       | AAAAT/A                                                       | TTTCGTTTAACTCACA<br>CATTCTG | CCTTATTGCCCCATTTC<br>CTT  | 59.2                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_6121180   | Ca7                                     | 6121180                       | A/ACTTCC                                                      | TTAAATTCACCGCACACG      | CGACGTTGTGGTTTCATGTC    | 59.6                             | 771                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6122315   | Ca7                                     | 6122315                       | TAGAGA/TAGA                                                   | TGGGTTTCGAGCCTAATTTTG   | CCGATTCATCCAAAGCCTTA    | 60.1                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6125384   | Ca7                                     | 6125384                       | TAAATTC/TAAATTCAAAATTC                                        | TCAACTTCCACACTTGTCTAAA  | TCAACTATCATCCCTTGTCTTT  | 57.6                             | 902                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6141449   | Ca7                                     | 6141449                       | TTATATATATATA/TTATATATATATA                                   | GAAGGCATAAACTCCACGTCA   | ATTTTGGCATGTCCGCTAC     | 60.1                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6143029   | Ca7                                     | 6143029                       | GAAAAAAAA/GAAAAAAAA                                           | CGGTTTCGGTTCAGTTTGATT   | GGTCGATCTTACATCTGGGC    | 60.0                             | 953                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6148450   | Ca7                                     | 6148450                       | TG/T                                                          | ACTTTCCCCAAACGTATCCC    | GGAACATTGAGGGGTGTCAG    | 60.1                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6156302   | Ca7                                     | 6156302                       | TTAT/TTATAT                                                   | TGAACCTAACGGTGGTAGCC    | TAAGGGCTTGGTGAGAGCAT    | 60.0                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6159448   | Ca7                                     | 6159448                       | ATTT/ATT                                                      | GGGCAAAGTGAGTGTGAGGT    | TGCCATGAAAAGCATAATGG    | 60.2                             | 332                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6159652   | Ca7                                     | 6159652                       | GTA/GTATATA                                                   | CACGTGGGGCTGATATTCT     | CTCCCCCTATCTTCGATCC     | 60.0                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6165770   | Ca7                                     | 6165770                       | ATTTTT/ATTTTTTTT                                              | GGATTTTCGATTTTCAATAGCCA | CTGTTCCGTGTCTCCATT      | 60.3                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                           |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_6166062   | Ca7                                     | 6166062                       | TAAAAAAAA/TAAAAAAAA                                                       | TCAACACATGAATTGC<br>ACAAAA  | CTGTTTCCGTGTCTCC<br>CATT   | 60.0                             | 269                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6172273   | Ca7                                     | 6172273                       | GTATATATATATATATATATATAT<br>ATATATATAT/GTATATATATATATAT<br>ATATATATATATAT | TTATTGCTTTGGCAAG<br>GCTC    | TTTTTCGACACAGCCTT<br>TTT   | 60.3                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6268277   | Ca7                                     | 6268277                       | TAAAAAAAA/TAAAAAAAA                                                       | TCAGCAGGGGTCAACT<br>TACA    | CCCACCAACATGAAG<br>TCCT    | 59.3                             | 878                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6269578   | Ca7                                     | 6269578                       | CTTTTTTT/CTTTTTTT                                                         | GGGCCGACTATTGAGT<br>ATGC    | TGCGGCAAAATACAAT<br>AAAAA  | 59.6                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6301584   | Ca7                                     | 6301584                       | ATATA/ATATACTTATA                                                         | TCTTCAACAATGGTC<br>CTCAGA   | CAAGTTCATGCCGGGA<br>TAGT   | 59.7                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6311074   | Ca7                                     | 6311074                       | TATATATA/TATATATAATATATA                                                  | CGCAACAAATGATTTAA<br>ACGAA  | CCGCATGTATGAGACT<br>AGAGCA | 60.0                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6383568   | Ca7                                     | 6383568                       | TAAAAAAAA/TAAAAAAAA                                                       | ACACTGGCATGAAGAA<br>TCTTTT  | ACGGAACATTCCATCA<br>CCAA   | 57.9                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6614224   | Ca7                                     | 6614224                       | TAAAAAAAA/TAAAAAAAA                                                       | AGCGCTGCAATAGGCT<br>TTTA    | TGAAGATGGTTTGCAA<br>TGGA   | 60.1                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6614899   | Ca7                                     | 6614899                       | CATATATATATATATATATATATA/<br>CACATATATATATATATATATATA<br>TATATATA         | TCCATTGCAAACCATCT<br>TCA    | TTGTTAGTTTGACGAG<br>GGCA   | 60.0                             | 443                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_666161    | Ca7                                     | 666161                        | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATATA<br>T               | GGAGTCAACAAATTTT<br>GAACCTA | GAAATCACATCAATGC<br>CCA    | 57.4                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                           | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                         |                              |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_6743906   | Ca7                                     | 6743906                       | GTTATTATTATTATTATTATTATT<br>ATTATT/GTTATTATTATTATTAT<br>TATTATTATT                                                      | TGGTCTTTGAAAAGAA<br>AATGACAA | TGATTCACCAATGCAA<br>GTCA     | 60.0                             | 824                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6745128   | Ca7                                     | 6745128                       | ATTTTTTTTT/ATTTTTTTTT                                                                                                   | TGAGATGAAGAAAAAC<br>GCGA     | CGAGAGCGTAATAGAG<br>AGTTTGAA | 59.5                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6746268   | Ca7                                     | 6746268                       | AATATATATATATATATA/AATATATA<br>TATATATATATA                                                                             | TCAACAATGCTTCCTT<br>CCC      | TTCGAAATGTGGGGAT<br>TAAAA    | 60.1                             | 356                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6799187   | Ca7                                     | 6799187                       | CAAAAAAAAA/CAAAAAAAAA                                                                                                   | AACGACTCTCGTCGTT<br>CCAT     | ATGTTGTCGCACTCTC<br>ATCG     | 59.7                             | 647                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6879569   | Ca7                                     | 6879569                       | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA<br>AAA                                                                                    | TTTGAGACCTCACAGT<br>TGTTGA   | ATTTGATCCAACCCACC<br>AAA     | 59.8                             | 366                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6894038   | Ca7                                     | 6894038                       | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAA/AAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAA | GCCAACTGGCTCCTCA<br>ATTA     | TCAAAGCCAACATGG<br>CATA      | 60.2                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6912264   | Ca7                                     | 6912264                       | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATAT                                                                     | TGCACCTGCACATGTT<br>GAATAA   | AATCCCTGCAATTGTG<br>GAAG     | 60.2                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6929292   | Ca7                                     | 6929292                       | GTATATATATATA/GTATATATATATA<br>TA                                                                                       | ATCTGCGCCTCACATT<br>TCTT     | CCTCGAACTATTTCGC<br>AACC     | 59.8                             | 443                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_6986107   | Ca7                                     | 6986107                       | AATATATATATATATATATAT/AA<br>TATATATATATATATATATAT                                                                       | CCCAAACTGCAACAAA<br>TCCT     | TTTATTGTGAGCACGG<br>GTGA     | 60.0                             | 283                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7021774   | Ca7                                     | 7021774                       | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                                                                           | AGAGGGTGGATGTTGC<br>GTAG     | TTTGACGCACACCAC<br>TAAT      | 60.1                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_7034358   | Ca7                                     | 7034358                       | TAAAAAAAAA/TAAAAAAAAA                                         | TCTCCATTGACATTGAG<br>CTCC   | TTTCCCTCATTCTAAG<br>TCCTCC  | 60.2                             | 101                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7150970   | Ca7                                     | 7150970                       | TAAAAAAAAA/TAAAAAAAAA                                         | GCTGGGGAGAACCACT<br>ATCA    | AAAGAGAGTGGGTGTG<br>GGTG    | 60.1                             | 326                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7362000   | Ca7                                     | 7362000                       | ATTTTTTTTT/ATTTTTTTTT                                         | TGCTTTTTCGGTGGAA<br>TTGT    | TGCCAATAACAAAAGTA<br>ATGCAA | 60.5                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_745192    | Ca7                                     | 745192                        | TAAAAAAAAAAAAA/TAAAAAAAAA<br>AAA                              | CCACATCCAACAACATT<br>AAAAA  | GGACCTGACGGAATGA<br>AAAA    | 57.5                             | 762                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7458735   | Ca7                                     | 7458735                       | A/AT                                                          | TTTTGCAATTGACCGT<br>CTTT    | GACCCACATAGTGAGG<br>GGTG    | 59.6                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7487564   | Ca7                                     | 7487564                       | TTC/TTCATC                                                    | GCTCCAGCTCATGTTG<br>TTGA    | CTCCAACTCCAACCTAA<br>GGG    | 60.0                             | 377                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7512410   | Ca7                                     | 7512410                       | GATATATATATATATATATA/GATA<br>TATATATATATATATATATA             | TCCGCCTTAGTGCCGT<br>ATTA    | TTCCGTGCCATACCGT<br>TTAT    | 60.6                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7535397   | Ca7                                     | 7535397                       | GTTTTTTTTT/GTTTTTTTTT                                         | CGGTAAAAGGGTGCAA<br>ATGT    | AAAAATTCCTTCACCA<br>AAGTC   | 59.9                             | 840                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7559321   | Ca7                                     | 7559321                       | CAGAGAGAGAGAG/CAGAGAGAGA<br>GAGAGAGAGAGAGAG                   | TCGAGTCAACCAAAAT<br>AACCG   | TCTCATCCCTTTCCTTC<br>CCT    | 60.0                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7571540   | Ca7                                     | 7571540                       | AAATAATAATAA/AAATAATAATAA<br>ATAA                             | AACATTCTGATGCAACT<br>CCATTT | ATCTCTTCCCTCTGCC<br>CATT    | 59.9                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                     | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                                                                   |                              |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_7621945   | Ca7                                     | 7621945                       | TAAAAA/TAAAA                                                                                                                                                      | TTGCCAAACACTTATTG<br>AAGAAAA | GAGGGAAATGAACGAA<br>CGAA     | 60.0                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7638200   | Ca7                                     | 7638200                       | GTTT/GTT                                                                                                                                                          | CATTATTTCGGTGTGA<br>CGCA     | AACACCATAGAGCCAC<br>TTTTTAGA | 60.5                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7738038   | Ca7                                     | 7738038                       | TC/T                                                                                                                                                              | GATTCCATTGGGATTG<br>GTTG     | CACGTTTTAGAGATGT<br>CCATTTTG | 60.0                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7738228   | Ca7                                     | 7738228                       | AAAAAA/AAAAATAGAAAAA                                                                                                                                              | GATTCCATTGGGATTG<br>GTTG     | CACGTTTTAGAGATGT<br>CCATTTTG | 60.0                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7738595   | Ca7                                     | 7738595                       | GTATATATATATATATATATATAT<br>A/GTATATATATATATATATATATA                                                                                                             | CAAAATGGACATCTCT<br>AAAACGTG | TCTCTACCCAATCACC<br>AAA      | 59.9                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7954535   | Ca7                                     | 7954535                       | TAAAAAAAAA/TAAAAAAAAA                                                                                                                                             | TGGGAGAAATTTTGAG<br>TGGG     | AAATGGGAGATCCAAA<br>ATTGC    | 59.9                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7957533   | Ca7                                     | 7957533                       | GATATATATATATATATATAT/GATAT<br>ATATATATATATATATAT                                                                                                                 | AAGACTTTGCGAGGGT<br>CTGA     | ATCCTCACCTTTGATGC<br>TCG     | 60.0                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7974267   | Ca7                                     | 7974267                       | TTTATTATTATTATTATTGTTATT<br>ATTACTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>TTATTATTATTATTATTATTATT<br>TTACTATTATTATTATTATTATT<br>TTATTATTATTATTATTATTATT | TCTCAAACTGTCACC<br>GCAG      | TTCGGTCAATTTGTCC<br>CTT      | 60.0                             | 771                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_7977507   | Ca7                                     | 7977507                       | CATACTATATAAT/CATACTATATAAT<br>ACTATATAAT                                                                                                                         | ACTGTCTTTTTCGCGC<br>ATTG     | TGCTTTGAATCACGCA<br>GTTG     | 60.3                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_8148654   | Ca7                                     | 8148654                       | GATACATACATA/GATACATA                                                                                                                                             | GCAAGTCATGCATGCT<br>CCTA     | TCTTGGGGGAATTGGT<br>GTAA     | 60.0                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                         | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                       |                              |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_820016    | Ca7                                     | 820016                        | A/ACGAGGGAATG                                                                                         | TGTATCAATGTGTTTT<br>AGGAAATG | TGAAGAAGAAAAACATT<br>GGTGG  | 57.3                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_824115    | Ca7                                     | 824115                        | T/TATTATTA                                                                                            | ACATGCATTGTTTACG<br>CCA      | TATTAAGCAAATTTGGC<br>CCG    | 60.0                             | 332                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_8247693   | Ca7                                     | 8247693                       | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATAT                                                     | AGTACACGTGCTTCCA<br>TCCC     | GAAGCAAAGCAAAGCA<br>AAGG    | 60.0                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_8272785   | Ca7                                     | 8272785                       | ATTTTTTT/ATTTTTTTT                                                                                    | GTGTCCTTTGCTGGAG<br>TGGT     | CCACCACTATCTCTCTT<br>TAACGG | 60.2                             | 960                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_8367160   | Ca7                                     | 8367160                       | TAAAAA/TAAAAA                                                                                         | CACCTTAATCGGTTTAT<br>AATTCCA | AAGACCCTTGATTGAC<br>GGTG    | 59.6                             | 808                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_8503724   | Ca7                                     | 8503724                       | TAAAAAAAAA/TAAAAAAAAA                                                                                 | TCGCTGAAACGTGCAA<br>CTAC     | GAGCTCTTGACAAGGC<br>GAAG    | 60.1                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_8522491   | Ca7                                     | 8522491                       | CAA/CAAA                                                                                              | GGATTCGTTTTTCCCC<br>AAAT     | TTCGCAACTCCACTCTT<br>CCT    | 60.0                             | 343                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_85654     | Ca7                                     | 85654                         | TAAAAAAAAA/TAAAAAAAAA                                                                                 | TGCATCCCTTGCTTTTC<br>TCT     | TAAGCCACATTGCATC<br>CCTT    | 60.0                             | 887                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_8578840   | Ca7                                     | 8578840                       | AATATATATATATATATAT/AATATAT<br>ATATATATAT                                                             | GAGTGGTGTTGGAGTC<br>GATG     | ATTTTGCATGGGGTG<br>TTGT     | 59.1                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_85847     | Ca7                                     | 85847                         | CTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATT/CTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATT | TCTTTCGCAAAATCCAA<br>TCA     | AACGTTGTAGCCGCAA<br>AAGT    | 59.2                             | 900                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                               | Forward primers (5'-3')     | Reverse primers (5'-3')   | Anneling temperature<br>(0C) | Expected amplified product size<br>(bp) | Structural annotation                          |                                  | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------|-----------------------------|---------------------------|------------------------------|-----------------------------------------|------------------------------------------------|----------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                             |                             |                           |                              |                                         | Sequence components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_8964622   | Ca7                                     | 8964622                       | AATATATATATATATATATATATATATATATATATATATATATATATAT/AATATATA<br>TATATATATATATATATATATATATAT                                   | TTCGATGAGTTGGAGA<br>CTCG    | AGTTGCCGTTACGGAT<br>TGAA  | 60.0                         | 575                                     | INTERGENIC                                     | --                               | --                    | --  |
| Ca7_P4_8975890   | Ca7                                     | 8975890                       | TATTATTTAATTATTTAATTATTTT/TA<br>TTATTTAATTATTTAATTATTTAATTAA<br>TTT                                                         | TGCCTCCATAGGATTC<br>TTCG    | TGTTTGTTGTGAAGCT<br>CGC   | 60.2                         | 611                                     | INTERGENIC                                     | --                               | --                    | --  |
| Ca7_P4_8993316   | Ca7                                     | 8993316                       | GTT/GTTTAGTGGCTACTGATTT                                                                                                     | GGATTGATAAAGCAGA<br>GCCG    | GACGCAGCTCAAGTGA<br>AAAA  | 59.8                         | 381                                     | INTERGENIC                                     | --                               | --                    | --  |
| Ca7_P4_8995733   | Ca7                                     | 8995733                       | ATTTTTTTTT/ATTTTTTTTTTT                                                                                                     | AACCGCTCTAGAGGAG<br>GATTAAA | AACAAATAGGTCGCGC<br>ATTC  | 59.8                         | 146                                     | INTERGENIC                                     | --                               | --                    | --  |
| Ca7_P4_9100875   | Ca7                                     | 9100875                       | TC/T                                                                                                                        | TGCAGTGTCGTTTTGT<br>TGGT    | TCTAAAGGCGTCCAAT<br>CACAA | 60.2                         | 506                                     | INTERGENIC                                     | --                               | --                    | --  |
| Ca7_P4_9134592   | Ca7                                     | 9134592                       | TAAAAA/TAAAAA                                                                                                               | TTTTCTGGGAGATGGA<br>TAAAAA  | ACATTGCGAGTCCAAA<br>CACAA | 57.7                         | 503                                     | INTERGENIC                                     | --                               | --                    | --  |
| Ca7_P4_9180941   | Ca7                                     | 9180941                       | TA/TAGA                                                                                                                     | ATGATTTCACGAGCC<br>AAC      | TGCAACATTTCTGATG<br>AGC   | 59.9                         | 322                                     | INTERGENIC                                     | --                               | --                    | --  |
| Ca7_P4_9181858   | Ca7                                     | 9181858                       | CT/C                                                                                                                        | TATTACCCAACCAAGC<br>CAGC    | TGAACTTTGATTGCCG<br>CTAA  | 60.0                         | 554                                     | INTERGENIC                                     | --                               | --                    | --  |
| Ca7_P4_9182870   | Ca7                                     | 9182870                       | CATATATATATATATAT/CATATAT<br>ATATATATAT                                                                                     | TGCAATTGATGCTTGG<br>TGAT    | AAAGGGCATATTTGCA<br>ATCG  | 60.1                         | 857                                     | INTERGENIC                                     | --                               | --                    | --  |
| Ca7_P4_9261419   | Ca7                                     | 9261419                       | TATAATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAA/TATAA<br>TAATAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAATAAT<br>AA | TCATTCGTGTTGAGAA<br>AAATTG  | TGCATGCTAGGTTTAT<br>GTCCC | 57.8                         | 350                                     | INTERGENIC                                     | --                               | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                   |                               |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_9302708   | Ca7                                     | 9302708                       | GTTTTTTTTTTT/GTTTTTTTTTTT                                         | ATGGAATGGATTCAAG<br>GAAG      | TTAATGGGCCTGTGGA<br>TAGC   | 60.0                             | 775                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_9332729   | Ca7                                     | 9332729                       | T/TTCAAAATGA                                                      | ACCAATCCAAATGCCA<br>TCAT      | TCATCTTTTGATTGTG<br>GCG    | 60.0                             | 201                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_9339636   | Ca7                                     | 9339636                       | TTATATATATATATATATATATATA<br>TATAT/TTATATATATATATATATA<br>TATATAT | ATGCAATTGTTGGCGA<br>TTTT      | AGGCATGGTGTGGAG<br>TCAT    | 60.3                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_9358512   | Ca7                                     | 9358512                       | TG/T                                                              | TTGAGTTTGATTAGGT<br>CAATGATGA | TTTGCCAAATATTTTC<br>TTCAA  | 59.9                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_9404184   | Ca7                                     | 9404184                       | ATTT/ATT                                                          | TTTTCTTGGAACGA<br>AGTG        | AAACGAGTGCGTGAAA<br>CTGA   | 60.1                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_9406854   | Ca7                                     | 9406854                       | TTATATATATATATATATA/TTATA<br>TATATATATATATATA                     | CACTGAAATGCACAAG<br>GGAA      | GATTCAATTCTCATAAC<br>GCACG | 59.7                             | 866                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_942479    | Ca7                                     | 942479                        | AAATAATAATAATAATAATAAA/AA<br>ATAATAATAATAATAATAATAA               | TTAAACCGTGACCG<br>CCTC        | TCTCTCAAGGGGAAAT<br>AGCAA  | 60.0                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_9425893   | Ca7                                     | 9425893                       | TATAAATAAAT/TATAAATAAATAAT<br>AAAT                                | GAATGAGGGGCTCATG<br>TGTT      | TTTGACAAATATGCGT<br>TGG    | 59.9                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_9578967   | Ca7                                     | 9578967                       | AAAAATTAAAA/AAAAATTAAATTA<br>AA                                   | ACTCCACAACACTTAC<br>GCCC      | CGGAATACGGCGAATT<br>AAGA   | 60.0                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_9595573   | Ca7                                     | 9595573                       | CACCTAAGAGCGAGTGAA/CA                                             | CTTCGCCACAACACT<br>CAAA       | GCAGAAATCCTATGGT<br>GGGA   | 59.9                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                       | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                     |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_966494    | Ca7                                     | 966494                        | AATA/AA                                                                                             | TCAACTTGGGTTCCAT<br>GTCA    | CTGTCAACCGGAGTGA<br>TGTG | 59.9                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca7_P4_9909690   | Ca7                                     | 9909690                       | AATATATATATATATATAT/AATATAT<br>ATATATATATATATAT                                                     | CGTTTTGCCAGAACAA<br>ATGA    | ACACGCCCACTAATCT<br>GACC | 59.7                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_10051845  | Ca8                                     | 10051845                      | AATATATATATATATATATATATAT<br>ATATATATATATATAT/AATATATATA<br>TATATATATATATATATATATATAT<br>ATATATATAT | GCTAAATTACATTGGG<br>TCAAAAA | CACGTGTACAAAAGCA<br>GCGT | 57.4                             | 686                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_10092385  | Ca8                                     | 10092385                      | AACAGGGAGAC/AAC                                                                                     | ATTTCCAGCTTCCAAA<br>GCCT    | CTCCATAAGCCTTTTGC<br>TCG | 60.2                             | 879                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_10161190  | Ca8                                     | 10161190                      | GAAAAAAAAA/GAAAAAAAAA                                                                               | GCAGATGTGCTCATTG<br>CTTT    | GCTCCCAGCCCACTA<br>TTTT  | 59.0                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_103414    | Ca8                                     | 103414                        | GATATATATATATATAT/GATATATAT<br>ATATATATAT                                                           | TTGATTGTCCGAACCT<br>CTTTGC  | GATGATGGGACCGAGA<br>CAGT | 59.3                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_10364033  | Ca8                                     | 10364033                      | TG/T                                                                                                | AAATGGTGGTTGGTTG<br>TGGT    | TGCTGTCTTTTCTGCTT<br>TGC | 60.0                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_10366674  | Ca8                                     | 10366674                      | CTT/CT                                                                                              | CAAGAAGACGCCGATG<br>AAAT    | GTCGAACGTTCTCCGT<br>TTGT | 60.2                             | 571                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_10366831  | Ca8                                     | 10366831                      | GTTTT/GTTT                                                                                          | CCCTCAACAAAAATG<br>CACC     | GTCGAACGTTCTCCGT<br>TTGT | 60.3                             | 400                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_10375574  | Ca8                                     | 10375574                      | CG/CGG                                                                                              | TGGTCTCTCGATCAGA<br>TTTTTG  | GATGATGTGGCACAGT<br>GGAC | 59.3                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_10519205  | Ca8                                     | 10519205                      | CTTTTTTTTTTT/CTTTTTTTTTTT                                     | TGAAGGGTGTAAAGCGA<br>ACAA | TGTAGGCTGCATCCAT<br>TTTT      | 59.3                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_10590161  | Ca8                                     | 10590161                      | ATTTTT/ATTTTTTT                                               | AACGGAGGAGGAACAA<br>ACAC  | TTAGAAGGCCTTGCAT<br>ACGA      | 59.0                             | 212                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_10591108  | Ca8                                     | 10591108                      | CAAAAAAAAA/CAAAAAAAAAAAAA                                     | TCCCGAGCATATCAAC<br>ATCA  | TGTGGGAGTTTGTCTT<br>GCAG      | 60.0                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_10612849  | Ca8                                     | 10612849                      | CTTTT/CTTT                                                    | AGTGGGAGTTTCGTCC<br>ATTG  | AGCACATGGAACCAAA<br>GAGG      | 60.0                             | 299                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_10671859  | Ca8                                     | 10671859                      | TTGTTGGTG/TTG                                                 | TGCGCAACTATTTGGT<br>CCTT  | TTTGATTGCGTTCAGA<br>GCAA      | 60.6                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_10686546  | Ca8                                     | 10686546                      | ATTTT/ATTT                                                    | TGCTATCGGTACCAAT<br>TTTGC | TCCGTTGTCTCATTGCA<br>TCA      | 60.0                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_10701972  | Ca8                                     | 10701972                      | ATGTT/AT                                                      | TCAACGGTTATACGGC<br>AACA  | TTTTATCTATGAAAAAT<br>GCCTCACA | 60.0                             | 373                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_10743637  | Ca8                                     | 10743637                      | TAATAAATAAATAAATAAATAA<br>ATA/TAATAAATAAATAAATAA<br>TA        | TTGAGCTTGAGCAACA<br>ATGG  | AAACACCCCTTCCTGG<br>CTTT      | 60.0                             | 815                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11070760  | Ca8                                     | 11070760                      | AG/A                                                          | GCTTCTAGCTGGTGCT<br>GCTT  | AGGGAATCAATTGTAG<br>GGGG      | 59.9                             | 900                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11079278  | Ca8                                     | 11079278                      | GAAAAAAAA/GAAAAAAAAA                                          | GTTTTGGGGGTGAGTC<br>GTGA  | GGTCTAATTGGTTGGG<br>GTGA      | 59.8                             | 667                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                                |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_11088512  | Ca8                                     | 11088512                      | ATTTT/ATTT                                                    | TGGTGCTCTTCAAAT<br>CCAA        | GATTGCATGCACATATT<br>TTGGT | 59.2                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11098303  | Ca8                                     | 11098303                      | CAAA/CA                                                       | TCCTTGCGAGGCTCTG<br>ATAC       | TGAGAAACCAACCCAA<br>GTCC   | 60.5                             | 647                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11110298  | Ca8                                     | 11110298                      | ATTTTTTTTT/ATTTTTTTTTT                                        | ACAATGATGCAAAACAC<br>GGAA      | AAACCCATGCACCACA<br>AAAT   | 60.0                             | 923                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11110509  | Ca8                                     | 11110509                      | CTAAG/CTAAGTAAG                                               | TCTCATAACGGATTGA<br>CTCTGTG    | CAAACCCATGGTGATT<br>GTGA   | 59.3                             | 764                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11113946  | Ca8                                     | 11113946                      | GA/GAATA                                                      | CCAGAAAACGAAAACC<br>AAACA      | TTTGATTTTGAGGCAGA<br>GCA   | 60.0                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11114905  | Ca8                                     | 11114905                      | GTT/GT                                                        | TTCTAAACACCATCTTA<br>ATCGAATTG | GGGGAAAATTTAGGGG<br>TGAA   | 59.8                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11129783  | Ca8                                     | 11129783                      | TAAAAAAA/TAAAAAAA                                             | CAAAGCCAACCACTAA<br>TCGG       | GTGGCATTGGAAGTT<br>GTTT    | 60.5                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11132594  | Ca8                                     | 11132594                      | TAAGAAGA/TAAGA                                                | CGCGCGGACCATAATC<br>TAGT       | CGGATTTGACAACAAA<br>ACTGAA | 62.4                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11136187  | Ca8                                     | 11136187                      | ATTTTTTTTTT/ATTTTTTTTTT                                       | AATTTTGGGTGAATTC<br>GGTG       | TGACAACCGTGAATGA<br>ATCAA  | 59.7                             | 802                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11145618  | Ca8                                     | 11145618                      | TTTATTA/TTTATTATTA                                            | TCTTTCTGGTTGCAAA<br>TGTTTT     | CATGCTTTAAAGAGCC<br>AATGC  | 60.0                             | 758                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                 |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_11346093  | Ca8                                     | 11346093                      | TGGAATTCAAGGGAATTCAA/TGGA<br>ATTCAA                             | TCATTCCGTTGAATCG<br>AACA   | AGCAATTCATGGCAG<br>CTCT     | 60.0                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11508469  | Ca8                                     | 11508469                      | TTATATATATATATATATATATATA<br>TATAT/TTATATATATATATATATA<br>TATAT | TGTCCAATGAAGTTAAA<br>GCGAA | TTGATGTGGTTGAATG<br>GGAA    | 59.8                             | 811                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11559010  | Ca8                                     | 11559010                      | ANNNNNNNNN/ANNNNNNN                                             | TGGAAGGCAAAGAAGG<br>AGAA   | CACATCACCTCGTTT<br>GAGA     | 59.9                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11561185  | Ca8                                     | 11561185                      | AATATATATATATATATATATAT<br>A/AATATATATATATATATATAT<br>ATATATA   | TTAGTGGCGGAGTTTG<br>AACA   | CGCATAATACTCAAACA<br>AAACCC | 59.3                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11753116  | Ca8                                     | 11753116                      | GAA/G                                                           | GACCGCCATGATAAGA<br>ATGC   | CGCAAAGACAACGAAC<br>AAAA    | 60.4                             | 309                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11769671  | Ca8                                     | 11769671                      | C/CCCTTACCAA                                                    | TCATTGGTCCTACCCT<br>CGTC   | TTTGGCAATCGACATT<br>GTGT    | 59.9                             | 154                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11772813  | Ca8                                     | 11772813                      | ATCTC/ATC                                                       | TTTTAACTTGC GCCTC<br>CAAC  | GGCCTTCAACAACCAC<br>CTAA    | 60.2                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11784506  | Ca8                                     | 11784506                      | AAGAGAGAGAGAGAGA/AAGAGAGA<br>GAGAGAGAGA                         | TCTCCGACTTTTAAAGA<br>GCCAA | ACGTGGGTCACTTGTG<br>CAAT    | 60.4                             | 266                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_1184414   | Ca8                                     | 1184414                       | GAAAAAAAAA/GAAAAAAAAA                                           | TTCGTACCGTTCTCTC<br>CTCAA  | TTGTACACAACCTCCCTT<br>GCG   | 59.9                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11955442  | Ca8                                     | 11955442                      | T/TG                                                            | GGCCGATTACTGCTC<br>ACAT    | GTTGCCACTTGCGTA<br>AAAT     | 60.1                             | 430                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_11955768  | Ca8                                     | 11955768                      | CTAATAATAA/CTAATAA                                                      | CTAATGCCCCCACTC<br>ACAT  | TTGTTTGGTGAAGGCT<br>CTTG  | 59.8                             | 307                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11975713  | Ca8                                     | 11975713                      | CT/C                                                                    | TATACTCGTGCACTAC<br>GCGG | GGATGGAGACAATGAT<br>GAGGA | 59.9                             | 135                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_11975949  | Ca8                                     | 11975949                      | AATTTATGTGTAGATGTATTTAT/AA<br>TTTATGTGTAGATGTATTTATGTGTA<br>GATGTATTTAT | TATACTCGTGCACTAC<br>GCGG | TTGTGGGGTGAACCT<br>AATCG  | 59.9                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_12048375  | Ca8                                     | 12048375                      | ACC/ACCC                                                                | TTCCCCCTAAACAGA<br>ACCA  | GTTGTTGCTGCCCTTT<br>GTTT  | 59.4                             | 723                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_12048632  | Ca8                                     | 12048632                      | CTTTCTCTCTTTTCTCT/CTTTCTCT                                              | TTCTTTCCACCTTCTT<br>CCA  | GTTGTTGCTGCCCTTT<br>GTTT  | 59.6                             | 474                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_12056555  | Ca8                                     | 12056555                      | A/AT                                                                    | GTGAAAGCGCTGTAA<br>AGGC  | ACTGGCTGACCACTCT<br>CGTT  | 60.0                             | 872                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_12801785  | Ca8                                     | 12801785                      | GA/GAA                                                                  | AGGTCATTTTCGTCT<br>CCCT  | GGCCTGACTTGTCAA<br>TTTT   | 59.9                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_12875576  | Ca8                                     | 12875576                      | GGAT/GGATGGAGAT                                                         | TGTATGATCGATCTGG<br>GCAA | TGCATGTGCCTTCTGA<br>AATG  | 60.0                             | 731                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_12979016  | Ca8                                     | 12979016                      | C/CG                                                                    | ATATGTTGGGGTGAT<br>GGAA  | GGGGTCGGACATTTAC<br>TAGC  | 59.9                             | 921                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_12979079  | Ca8                                     | 12979079                      | TTTA/TTTAATTA                                                           | CGTGCAGTTTAGGGAA<br>GGAT | GGGGTCGGACATTTAC<br>TAGC  | 59.2                             | 873                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_12983474  | Ca8                                     | 12983474                      | ATTTTT/ATTTT                                                  | TGCAGATGCACGAATC<br>TCTT  | TGCACTAATTTATCGG<br>GACCA | 59.6                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_12983910  | Ca8                                     | 12983910                      | TAA/TA                                                        | TTGGTCCCGATAAATTA<br>GTGC | CCCCAAGTTAAGACAA<br>CCCA  | 59.0                             | 442                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_12984097  | Ca8                                     | 12984097                      | CGTGTGT/CGTGT                                                 | AGTGTAAACCGGGATC<br>AAACA | CCCCAAGTTAAGACAA<br>CCCA  | 59.3                             | 301                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_12988606  | Ca8                                     | 12988606                      | AG/A                                                          | CTCGCTCAAGATTTC<br>AAGG   | GTTGTGGGAGGATCGA<br>AAGA  | 59.9                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_12990010  | Ca8                                     | 12990010                      | CTA/CTATA                                                     | TGGCTAATAAATTGTG<br>CCCAT | TCATGTCCCCTCCTTG<br>AATC  | 59.3                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_12998724  | Ca8                                     | 12998724                      | ATTTTTTTTT/ATTTTTTTTTT                                        | TCACACCTCTTCACTT<br>CATGG | CAAAGTTGTTGGGCAA<br>GGTT  | 60.1                             | 138                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13076511  | Ca8                                     | 13076511                      | TTCCCTCCCT/TTCCCT                                             | TGAAGGTGCTGGAAAA<br>CACA  | CCAACCCTCTCACCCA<br>TAAG  | 60.3                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13144318  | Ca8                                     | 13144318                      | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATAT             | TTGGTGTCACAAGGA<br>ACGA   | ACGCCACAATAAAGGT<br>GTCA  | 60.1                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13186978  | Ca8                                     | 13186978                      | ATTCAGTTC/ATTCAGTTCAGTTCA                                     | TCGTCGTTGTTGCCA<br>TGTT   | AATGTGAATCCCACCA<br>GGAA  | 60.0                             | 411                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13297997  | Ca8                                     | 13297997                      | TA/TAA                                                        | AAATTGATTGGATGGT<br>GGGA  | AAATGCAGAGGCACCA<br>CTCT  | 60.0                             | 442                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                       | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                     |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_13298358  | Ca8                                     | 13298358                      | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATATATAT<br>TATATAT                                    | AGGAGGGGTCCCTGTT<br>TCTA    | ACACGAAATTGCTCA<br>GCCT    | 59.9                             | 548                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13338881  | Ca8                                     | 13338881                      | ATTTTTTT/ATTTTTTTT                                                                                  | TGTGAGGTACCGAGTT<br>CCAA    | TTATAACGGGTGGAAA<br>CGGA   | 59.1                             | 689                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13388397  | Ca8                                     | 13388397                      | CAATAATAATAATAATAATAATA<br>ATAATAATAATAATAAT/CAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAATAAT | TACCAACATACCCCTT<br>CCCA    | GCGGTTGAATAAATGT<br>GACAAA | 60.0                             | 835                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13475860  | Ca8                                     | 13475860                      | TGG/TG                                                                                              | AGGAAGAGTGGAGTTG<br>CGAA    | TATTTTGGATTTTGGCT<br>CGG   | 60.0                             | 300                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_1347851   | Ca8                                     | 1347851                       | CAAAAAAAAA/CAAAAAAAAA                                                                               | CCAACATTTGATTGGC<br>ATTG    | TTCTTTTAAATTGCCGT<br>CGTTT | 59.8                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_1355185   | Ca8                                     | 1355185                       | CTTTTTTTTT/CTTTTTTTTTT                                                                              | TTTATTTCTTCACGTG<br>GGC     | ATGTGTTGGGTGGGT<br>CACT    | 59.9                             | 125                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13719839  | Ca8                                     | 13719839                      | TAAAAAAAA/TAAAAAAAA                                                                                 | TCTCTTGAGGTTCTTAA<br>TGGTGG | CGTTGTTTTTCAAACA<br>CCTAA  | 59.6                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13751146  | Ca8                                     | 13751146                      | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATA              | GATGGAGGGAGAAGCT<br>GAAA    | CATCTGACCATTGAATT<br>GCG   | 60.1                             | 293                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13757181  | Ca8                                     | 13757181                      | ACCCCCC/ACCCCCC                                                                                     | AATTCAGCTCCTACGA<br>GGCA    | GCATTTTGGGCATTTT<br>GATT   | 60.0                             | 326                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13767395  | Ca8                                     | 13767395                      | ATTTTTTTTT/ATTTTTTTTTT                                                                              | GGCAACGAATGTGGTC<br>TTCT    | GTATGGTTTGGTGGGG<br>TCTG   | 60.1                             | 753                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                               | Forward primers (5'-3')         | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------|---------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                             |                                 |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_13774     | Ca8                                     | 13774                         | CAAAAA/CAAAA                                                                                | CGAGGCACAACATCATC               | TGGTGCTTCAATGAAC<br>TTGG  | 60.1                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13815011  | Ca8                                     | 13815011                      | AAA/AATAA                                                                                   | CACAATTGCCACCAAC<br>ACTC        | TTTTTGCCACCATTTTC<br>ACA  | 60.0                             | 220                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13815063  | Ca8                                     | 13815063                      | TG/TGGAAGG                                                                                  | CACAATTGCCACCAAC<br>ACTC        | GCACCATCATGTATCC<br>TGCTT | 60.0                             | 275                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13817368  | Ca8                                     | 13817368                      | AAATAATAATAA/AAATAATAA                                                                      | TTTTTGCCCATTCAAAC<br>ACA        | CACCTTTTTCTCACCCC<br>CAC  | 59.9                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13844941  | Ca8                                     | 13844941                      | AATATATATATATATA/AATATATATA<br>TATATATA                                                     | GGCTCTCCATCTCCT<br>CAAA         | TTTCTTCGAGAGGTGCG<br>CTTC | 59.4                             | 607                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13899612  | Ca8                                     | 13899612                      | GATATATATATATATATATATATATA<br>TATATATATA/GATATATATATATATATA<br>TATATATATATATATATATATATA     | TTGGAGTCATGTTTT<br>CATCAG       | CGTTGCACGGAACAT<br>TTTA   | 60.0                             | 224                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_13899770  | Ca8                                     | 13899770                      | TAAAAAAAAA/TAAAAAAAAA                                                                       | GTGCAACGCACCGGTT<br>ATAC        | ATTTGGCAGACACGTG<br>ACAA  | 61.3                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14035508  | Ca8                                     | 14035508                      | GA/GAATA                                                                                    | TGAAATATTTTAAGCAT<br>TCACTGATAA | CATGCCTTCTTGCTTCA<br>ACA  | 57.7                             | 466                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14036236  | Ca8                                     | 14036236                      | CATATATATATATATATATATATATA<br>TATATATATA/CATATATATATATATA<br>TATATATATATATATATATATATAT<br>A | TCCAACCGTCCAATCA<br>AAAT        | GGTATCCATGGGAGCT<br>TTGA  | 60.2                             | 652                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14048687  | Ca8                                     | 14048687                      | ATTTTTTT/ATTTTTTTT                                                                          | CCACCGAAAAATTTCAT<br>CCA        | CCGGAAAACTTCATTC<br>CAAA  | 60.7                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_14064085  | Ca8                                     | 14064085                      | CATATATATATATATATA/CATATATA<br>TATATATA                       | TGTGTGTGTGTGTCCA<br>GAGG  | GGTATCCATGGGAGCT<br>TTGA  | 59.1                             | 804                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14064155  | Ca8                                     | 14064155                      | AA/AATTTCATA                                                  | TTAACCCTATGGGGGT<br>TGATT | GGTATCCATGGGAGCT<br>TTGA  | 59.4                             | 467                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14073516  | Ca8                                     | 14073516                      | A/AT                                                          | TTCTTCTCAACCAACA<br>GGC   | GAAGTTGATGAACCCG<br>TCGT  | 60.2                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14111238  | Ca8                                     | 14111238                      | C/CA                                                          | TGAACGGTTGGTCACC<br>ATAA  | CACCCCAACCATCAAAT<br>TCT  | 59.8                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14111879  | Ca8                                     | 14111879                      | GTTAATT/GTT                                                   | GGATTTGATGATCGAT<br>TCGG  | CAACCAGCAGTAGACG<br>CAAA  | 60.2                             | 796                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14112533  | Ca8                                     | 14112533                      | TAA/TAAA                                                      | TGTCAAGATCCGCCAA<br>TGTA  | TCATTGCGGTAGACAA<br>ACACA | 60.1                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14112769  | Ca8                                     | 14112769                      | CTTTTTTT/CTTTTTTTT                                            | TTGCGTCTACTGCTGG<br>TTGT  | GTGCCTCCAAGCCAAA<br>ACTA  | 59.5                             | 922                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14113684  | Ca8                                     | 14113684                      | TAAAAAA/TAAAAA                                                | AACACGCCTCACACCA<br>CATA  | CCAATTCACAAAATCG<br>GTCC  | 60.0                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14131243  | Ca8                                     | 14131243                      | GATAT/GATATAT                                                 | CCGTTTGAAAAATGTT<br>GGCT  | TTGGACAAGTTGAGTC<br>GGTG  | 60.0                             | 705                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14157701  | Ca8                                     | 14157701                      | ATTTTTTTTT/ATTTTTTTTTT                                        | CCTTGCATCAACATCA<br>ACCA  | TGGTCGTCAGTAGTCA<br>ACGG  | 60.5                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_14163137  | Ca8                                     | 14163137                      | ATTTTT/ATTTTTT                                                | CTTTCAAACGACCTG<br>CCAT    | TTTTCATTTTCGCCTT<br>TGA   | 60.1                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14164932  | Ca8                                     | 14164932                      | GAAA/GAAAA                                                    | CAAGGCCCAAGTCAAA<br>AGAT   | CCAAGCATGTTGCTTT<br>GACA  | 59.2                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14169234  | Ca8                                     | 14169234                      | ATTTTTTTTT/ATTTTTTTT                                          | TTGGGGGTTACATGTT<br>CTGA   | CAACAATTAGGCCTCAT<br>CCA  | 58.8                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14170722  | Ca8                                     | 14170722                      | GAAAA/GAAAATAAATAAAA                                          | AAAGGACCAATCGGG<br>AAGA    | CCAAAACTGCCATTG<br>CTTT   | 60.8                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14170739  | Ca8                                     | 14170739                      | CTTTTT/CTTTTTT                                                | AAAGGACCAATCGGG<br>AAGA    | CCAAAACTGCCATTG<br>CTTT   | 60.8                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14182954  | Ca8                                     | 14182954                      | ATTTTTTT/ATTTTTT                                              | CGTAGAGGCATCAACA<br>CTCG   | GAAGGTGCTTTGTTGT<br>TTGGA | 59.5                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14186957  | Ca8                                     | 14186957                      | TT/TTCAAT                                                     | ATAAAGCAGCAACTCG<br>GGAA   | GTTGCTTGCTGGCTTT<br>GAAT  | 59.8                             | 684                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14194998  | Ca8                                     | 14194998                      | AATGAT/AAT                                                    | CCTTAATGTGGAGAC<br>TTGAGGA | TTTCTTGCAATTGTGG<br>AGA   | 59.6                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14212046  | Ca8                                     | 14212046                      | TTTTTAATT/TTTTTAATTATTTAATT                                   | TTCTCTTTGAAATTC<br>CGGT    | ACTTGTTGGGGTTGCT<br>CATC  | 59.9                             | 243                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14218109  | Ca8                                     | 14218109                      | A/AAT                                                         | TCTCCACAAATGCAAG<br>GAAA   | AAGCCTGGCCCACTA<br>ATTT   | 59.2                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_14218237  | Ca8                                     | 14218237                      | A/AT                                                          | TCTCCACAAATGCAAG<br>GAAA  | AAGCCTGGCCCACTA<br>ATTT    | 59.2                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14222158  | Ca8                                     | 14222158                      | CTGTGT/CT                                                     | TGATTCTTCGTGCTCTT<br>TCG  | CTTCAAGTTTGACCACT<br>TCTGG | 59.1                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14244514  | Ca8                                     | 14244514                      | CAAA/CAA                                                      | ATCTTAAGCATCCCC<br>TCGT   | TCAATGGTGTCATCC<br>CTTT    | 59.9                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14244924  | Ca8                                     | 14244924                      | GA/GAAAA                                                      | AAAGGGATGGACACCA<br>TTGA  | CCTTTGGCTTAGCATT<br>AGGG   | 60.2                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14252000  | Ca8                                     | 14252000                      | TAAAAA/TAAAAA                                                 | ACCCCAAAGGAAAGAA<br>AGGA  | GTCGGCGGTGCATATA<br>GATT   | 59.9                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14261406  | Ca8                                     | 14261406                      | ATTTTTTTTT/ATTTTTTTTT                                         | TGGAGATTGTGGATT<br>GCAG   | GATTCACCATCCCATTT<br>GATTT | 59.6                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14262685  | Ca8                                     | 14262685                      | ATTTTT/ATTTTT                                                 | GGATTGTGGCTTGAAG<br>TGGT  | CAAAGGTAGCAAGGCC<br>CATA   | 60.0                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14266837  | Ca8                                     | 14266837                      | GTTTTTTT/GTTTTTTT                                             | TCTTCAGGAATTTGGG<br>TTGG  | CGCATCTATTCGCAAT<br>TCAC   | 59.9                             | 298                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14269495  | Ca8                                     | 14269495                      | ATTTGATTTTGATTTTGATTTGATT<br>TTGA/ATTTGATTTTGATTTTGA          | GCCATTGTCACCGTA<br>TGCT   | TGTGCTTTTCCAAATC<br>CAA    | 60.9                             | 863                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14290921  | Ca8                                     | 14290921                      | GATATATATATATATATATATA/GA<br>TATATATATATATA                   | TCAATCTCATGTCCACA<br>TCGT | GTCCGCACAACCTTGC<br>AATG   | 58.9                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_14291937  | Ca8                                     | 14291937                      | CT/C                                                          | TTCAAAACGGTGTCTTA<br>TGCC    | CCTTCCCACTTTACAAC<br>GTCA  | 60.0                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14292407  | Ca8                                     | 14292407                      | ATTTTTT/ATTTTTTT                                              | TGACGTTGTAAAGTGG<br>GAAGG    | CATTGCAGAAACAAAA<br>GCCT   | 60.0                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14302846  | Ca8                                     | 14302846                      | AT/ATATTT                                                     | GGTCAACAATGATCGT<br>ATTGAAAA | GAACGTCTTTGACCAA<br>ATTGAA | 60.1                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14308135  | Ca8                                     | 14308135                      | CATA/CATATATA                                                 | GCAATGAAGAGTGACC<br>TGACC    | TCTCCATTCAAACATTG<br>CCA   | 59.7                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14310126  | Ca8                                     | 14310126                      | CTT/CT                                                        | TGGTACCTTTTCCTCCT<br>CCA     | GGCATCCTCAACTTAA<br>CTCCA  | 59.5                             | 248                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14311611  | Ca8                                     | 14311611                      | ATT/AT                                                        | TTTGAGCGTACAAAGA<br>TCCAA    | AAATTTATCACCCGCAA<br>AGA   | 58.4                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14313181  | Ca8                                     | 14313181                      | TAAAA/TAAA                                                    | TGCTGCACGAGTATTT<br>TACCA    | TTGGGTTGGTCAAATG<br>TGATT  | 59.4                             | 259                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14319609  | Ca8                                     | 14319609                      | A/AG                                                          | CCTTGATGCACCATGC<br>TAGA     | GTCAATTTCCGGTGCAAT<br>GTG  | 59.8                             | 257                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14319897  | Ca8                                     | 14319897                      | CATT/CATTAATTTTTTAATATT                                       | CACATTGCACCGAAAA<br>TGAC     | AAATAAATGCCCCATC<br>GACA   | 60.0                             | 352                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14320208  | Ca8                                     | 14320208                      | TA/TAA                                                        | TGTCGATGGGGCATT<br>ATTG      | GCTGCATGTTACTGCC<br>ATTG   | 60.2                             | 434                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_14337762  | Ca8                                     | 14337762                      | A/AT                                                          | TGTGTCGTTAAATCTC<br>TTTAGCA   | CCATTAAGGGCCCAT<br>CTAT   | 58.2                             | 782                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14337821  | Ca8                                     | 14337821                      | TAAAAAAAA/TAAAAAAAAA                                          | CCAAATTTAATTGTCAA<br>GGTTCCTC | CCATTAAGGGCCCAT<br>CTAT   | 59.4                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14363248  | Ca8                                     | 14363248                      | TTTTTATTTTATTTTATT/TTTTTATT<br>TATTTTATTTTATT                 | AGCGCCCCTAATATTT<br>CGTT      | GTGGGAAAGGAATCCA<br>AGGT  | 60.0                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14363459  | Ca8                                     | 14363459                      | ATTTTTTTTTTT/ATTTTTTTT                                        | AGCGCCCCTAATATTT<br>CGTT      | GTGGGAAAGGAATCCA<br>AGGT  | 60.0                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14363844  | Ca8                                     | 14363844                      | CTATATA/CTATA                                                 | GTTGCCACTTGACCTT<br>GGAT      | TGGACTTCATCCAAAA<br>GGG   | 60.0                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14365585  | Ca8                                     | 14365585                      | TAA/TAAA                                                      | GGACACTATCCCCTCA<br>CCCT      | TAAATTCCTGTTTGGGC<br>TGG  | 60.2                             | 288                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14365858  | Ca8                                     | 14365858                      | A/AC                                                          | CCAGCCCAAACAGGAA<br>TTTA      | CCTTTGTTCTTGACCC<br>ATT   | 59.9                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14369827  | Ca8                                     | 14369827                      | T/TGGTA                                                       | ATGGCACCTTCACCAT<br>TAGG      | AAAACGTTACAAACAG<br>GGCA  | 59.8                             | 731                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14370711  | Ca8                                     | 14370711                      | A/AAAT                                                        | GGCCAATCAATTTTGA<br>TGC       | TGGGAGATTGGAGCAT<br>GATT  | 60.3                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_1442767   | Ca8                                     | 1442767                       | GTATATATATATATATAT/GTATATAT<br>ATATATAT                       | ACGACCTGGAATACGA<br>CCTG      | CATTCCTCAAAGTAAGG<br>CGAA | 60.0                             | 562                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                              |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_14458401  | Ca8                                     | 14458401                      | CTATTTATTTATTTATTTATTTATTTA<br>TTTATTTATTTATTTATTT/CTATTTAT<br>TTATTTATTTATTTATTTATTTATTTA<br>TTTATTTATTTATT | GAGGCAGCAAAATGGA<br>AATC   | TTTTCATGAAACATG<br>CCA    | 59.7                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_1452383   | Ca8                                     | 1452383                       | CAAAAAAAAA/CAAAAAAAAA                                                                                        | TTGCAAGGGAAGGAAA<br>CAAC   | CGGGCTACCTAGAATC<br>CCTC  | 60.1                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14564939  | Ca8                                     | 14564939                      | AAT/AATGTCTGGAT                                                                                              | TTGATTCGTTGACCA<br>TTGA    | ACTAAGCAAATTGTGC<br>GCCT  | 60.0                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14568257  | Ca8                                     | 14568257                      | TAAAAAAAA/TAAAAAAAAA                                                                                         | AACGCGCGGGTTATAT<br>TCTA   | GGCAAAGGGTTTTGC<br>AATC   | 59.6                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14568852  | Ca8                                     | 14568852                      | TG/T                                                                                                         | TGCAAAAACCTTTGC<br>CTAT    | TCAACAATCAACGTCAA<br>CCAA | 59.6                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14569590  | Ca8                                     | 14569590                      | GTTATTATTATTATTATTATT/GTTAT<br>TATTATTATTATT                                                                 | TCCAAATAAGCCAAC<br>AAAAA   | GGGGCACAATTGAAGA<br>TAATG | 57.4                             | 800                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14575137  | Ca8                                     | 14575137                      | TTATTAATAA/TTATTAATAAAATATT<br>AATAA                                                                         | TGATTGGAGGGTTGTT<br>CTCTG  | TACAAGCCAATCACCC<br>ACCT  | 60.1                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14575369  | Ca8                                     | 14575369                      | TCAA/T                                                                                                       | TCGGAGGAAGAGAATA<br>GAATGA | TCCACGAGAAAATAGC<br>CACC  | 58.0                             | 770                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14585860  | Ca8                                     | 14585860                      | TTCTT/TTCTTGAATATCTT                                                                                         | TGAATTGATTGTCGCTT<br>TCG   | ATGATGGTTTTAGCG<br>ATGC   | 59.8                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14617610  | Ca8                                     | 14617610                      | CATTTAT/CATTTATATTTAT                                                                                        | GCTCCAACCGTAAAC<br>CAAA    | TGCAGGGAGAAGAGG<br>GAGTA  | 60.0                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_14630693  | Ca8                                     | 14630693                      | CA/CAA                                                        | GCGTTTTCCAGAACTG<br>CTTC      | AGATTGACTGGTTGGT<br>TCGC       | 60.0                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14630745  | Ca8                                     | 14630745                      | ATTTTTTT/ATTTTTTT                                             | GCGTTTTCCAGAACTG<br>CTTC      | AGATTGACTGGTTGGT<br>TCGC       | 60.0                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14631000  | Ca8                                     | 14631000                      | TC/TCC                                                        | GCGAACCAACCAGTCA<br>ATCT      | TCGTTTGAGGAATTTT<br>AAACC      | 60.1                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14631294  | Ca8                                     | 14631294                      | TAAAAAAA/TAAAAAAA                                             | GCGAACCAACCAGTCA<br>ATCT      | TGAAAAGGGAGTGGA<br>TTGG        | 60.1                             | 869                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14645076  | Ca8                                     | 14645076                      | TAAAAAAA/TAAAAAAA                                             | CCCCACCCATGTTCTT<br>AGTG      | CGGATATGACATTGATT<br>CTCAAATTA | 60.2                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14647157  | Ca8                                     | 14647157                      | GTTT/GTTTT                                                    | TTGCTTGCCATGACG<br>TAGG       | TCTGCAACGAAGATTAA<br>ACCAA     | 59.7                             | 297                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14657093  | Ca8                                     | 14657093                      | GAAA/GAA                                                      | CCAAGCCAATTCACAC<br>AAAA      | GGTAGAGGTACAACCC<br>CCGT       | 59.6                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14660502  | Ca8                                     | 14660502                      | TAA/TAAAA                                                     | TGCATGCATTTTAAAT<br>TATGTTTT  | CATGTACCGATATGTT<br>GGTCT      | 59.0                             | 788                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14660730  | Ca8                                     | 14660730                      | A/AGT                                                         | TGAAGTGTTTTTGGTA<br>CATCAATTT | CATGTACCGATATGTT<br>GGTCT      | 58.9                             | 339                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14661963  | Ca8                                     | 14661963                      | AT/A                                                          | TGTTGTTGTGAAATCG<br>ACGAA     | TGTTAGGTGGCCAAAG<br>GAAG       | 60.1                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_14662017  | Ca8                                     | 14662017                      | A/AG                                                          | TGTTGTTGTGAAATCG<br>ACGAA   | TGTTAGGTGGCCAAAG<br>GAAG     | 60.1                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14665010  | Ca8                                     | 14665010                      | TAAAAAAA/TAAAAAAA                                             | AATCTCAAGCAAAGCC<br>GAAA    | AATATCAGGGGCATCA<br>AGGA     | 60.0                             | 636                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14665510  | Ca8                                     | 14665510                      | CTAAGTTTTT/CTAAGTTTTTAAGTTT<br>TT                             | TCCTTGATGCCCTGA<br>TATT     | CCACTTCCTCGCTTTCA<br>AGT     | 59.3                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14666923  | Ca8                                     | 14666923                      | CTTCAT/CTTCATGCTAATTCAT                                       | ATGGCCGTTTTGAACA<br>ACAT    | CTTGTTGCGGATGAGA<br>GACA     | 60.2                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14669635  | Ca8                                     | 14669635                      | CAAAAAA/CAAAAAA                                               | TTACAATGCATGGCAC<br>CACT    | TTTTTGGTTGGATTTTT<br>GGG     | 60.0                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14671081  | Ca8                                     | 14671081                      | T/TG                                                          | TACAACATGTAGGCTC<br>CGCC    | AAAGGATCAAATCGGG<br>AAGG     | 61.1                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14671445  | Ca8                                     | 14671445                      | TAAAAAAA/TAAAAAAA                                             | CCTTCCCGATTGATC<br>CTTT     | TCGACAACCTACATTTT<br>ATCATCC | 60.3                             | 831                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14675237  | Ca8                                     | 14675237                      | ATTTTTTT/ATTTTTTTT                                            | TGTTGCTTGTTCAAAT<br>GGA     | GTCGTGGCATTGAAA<br>AGTT      | 60.1                             | 940                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14678752  | Ca8                                     | 14678752                      | CATATGGATATG/CATATGGATATG<br>GATATG                           | TTCACCGACTATTGTAT<br>TGATGC | CAAAGCGTATCCCTT<br>TTCA      | 59.0                             | 270                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14680791  | Ca8                                     | 14680791                      | AAA/AAATAA                                                    | AATCGAAGATGGGCTC<br>AATG    | TCGTTTGACAATCCAC<br>CGTA     | 60.0                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')         | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|---------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                     |                                 |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_14684651  | Ca8                                     | 14684651                      | GTTTTTTT/GTTTTTTT                                                   | TTTtagaggtgtcagc<br>TAAACACAA   | TGTGACTCGTGAAT<br>GCTG      | 60.0                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14687938  | Ca8                                     | 14687938                      | CTATTATTATTATTATTATTATTA<br>TTATTATTATT/CTATTATTATTATTA<br>TTATTATT | AATGGGAATCCAATGC<br>AAAA        | TGCGTAAGTACAGCGT<br>AAAGAAA | 60.1                             | 849                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14688210  | Ca8                                     | 14688210                      | ATTTTTTTTT/ATTTTTTTTT                                               | TTTTCTTAAGGTGAAAA<br>TAACATTCAT | TGCGTGATCGATGCAT<br>ATAGA   | 57.9                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14688901  | Ca8                                     | 14688901                      | T/TA                                                                | TATGCATCGATCACGC<br>AATG        | TCAAACAATTCGATTGA<br>ACCA   | 61.6                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14700657  | Ca8                                     | 14700657                      | GAA/GAAA                                                            | TTTGTGACTTAGGCAT<br>CACGA       | TCCATACCTTTTCCAAC<br>CCA    | 59.3                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14701078  | Ca8                                     | 14701078                      | TATAATA/TATA                                                        | TGGGTTGGAAAAGGTA<br>TGGA        | CCATCTCCCCTTGATCT<br>TTG    | 60.2                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14746565  | Ca8                                     | 14746565                      | CTT/CTTT                                                            | GCTTCACCAACCAAAA<br>CACA        | GGGGGAAAAATTGAAA<br>CCAC    | 59.6                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14758563  | Ca8                                     | 14758563                      | GTTTTTTTTT/GTTTTTTTTT                                               | GTAGCTAATCGAACGG<br>CGAG        | GCTCCAAACAAGGAAC<br>CAAA    | 60.0                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14759364  | Ca8                                     | 14759364                      | CA/CAA                                                              | TTTGGTTCCTTGTTTG<br>GAGC        | CAAATTCAGTTGGCTC<br>AGCA    | 60.1                             | 694                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14764083  | Ca8                                     | 14764083                      | CATA/CATATA                                                         | ATGCATGCACACCACA<br>CTCT        | TGGTTTGCAACCTTTTC<br>TTG    | 60.2                             | 935                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_14774361  | Ca8                                     | 14774361                      | T/TAA                                                         | TCGATCCTTACGGTTA<br>ACATCA | GAATATCCGTGTGGGA<br>TTGC    | 59.5                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14775134  | Ca8                                     | 14775134                      | TTAT/TT                                                       | AGAGCAATCCCACACG<br>GATA   | TTGGACCATTGTAGTT<br>GCG     | 60.5                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14776665  | Ca8                                     | 14776665                      | T/TTAA                                                        | CCAACTCTGGTGGTTG<br>GTCT   | GCTTGGGGGTTGTAA<br>TACG     | 60.0                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14776722  | Ca8                                     | 14776722                      | A/AT                                                          | CCAACTCTGGTGGTTG<br>GTCT   | GCTTGGGGGTTGTAA<br>TACG     | 60.0                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14781231  | Ca8                                     | 14781231                      | T/TG                                                          | ATCGTTGGTCCTTGTT<br>TTGG   | AAATGGCAGGACACAT<br>TGTT    | 59.8                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14788651  | Ca8                                     | 14788651                      | ATTTTTTTT/ATTTTTTTT                                           | TCATGAAAAACCAATG<br>CATCA  | TCAGAACTCATCACGA<br>CCAA    | 59.9                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14809231  | Ca8                                     | 14809231                      | AA/AAAATA                                                     | TCGCCAACAACAATAT<br>CAAA   | CTTGCAGCATTTTCACC<br>AAA    | 57.6                             | 744                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14811835  | Ca8                                     | 14811835                      | GAAAAAAAA/GAAAAAAAA                                           | GCAATTGCAACCACTT<br>CAAA   | AGGACATTGTGTGGTG<br>GTGA    | 59.7                             | 189                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14813828  | Ca8                                     | 14813828                      | ATTAGTTGT/ATTAGTTGTAGTTAGT<br>TGT                             | CTCTCCACCATGACCC<br>ATTT   | TGTGATGGAGAACACA<br>CAATACC | 59.8                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_14814179  | Ca8                                     | 14814179                      | ACTTTTTATTAT/A                                                | AAATTGCAAGTTGCCA<br>AAAC   | TCCATTTTCGAGTTAGC<br>TTTGA  | 57.8                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                     | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                                   |                             |                             |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_14814560  | Ca8                                     | 14814560                      | CAAAAAAAAA/CAAAAAAAAA                                                                                             | TTTCAAAGCTAACTCGA<br>AAATGG | TTCTCCTTGGTGCTTCT<br>CCA    | 59.8                             | 651                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca8_P4_14815814  | Ca8                                     | 14815814                      | ATTTTTT/ATTTTTTT                                                                                                  | GCACATGTGGTTGGTC<br>TTGT    | TCCAATCGAAGAGAAA<br>ATCAAAA | 59.4                             | 319                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca8_P4_14848528  | Ca8                                     | 14848528                      | TTATATATATATATATATATATATA<br>/TTATATATATATATATATATATAT<br>ATATATATA                                               | TATTTCTCCCATGCG<br>CTAC     | TCTAAATCCGCCTCTCT<br>CCA    | 60.1                             | 440                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca8_P4_14855137  | Ca8                                     | 14855137                      | CATATATATATATATATATATATA<br>T/CATATATATATATATATATATAT                                                             | TCATGTGAACCTCACC<br>CAAA    | TCATGTCCATCCATCCA<br>TTG    | 59.9                             | 816                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca8_P4_14894600  | Ca8                                     | 14894600                      | AATATATATATATATA/AATATATA<br>TATATATATATA                                                                         | TCAAAGCCCACCAGAT<br>TCTC    | TCCGCGTCTGAGCTTT<br>TATT    | 60.2                             | 569                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca8_P4_14900024  | Ca8                                     | 14900024                      | CTAATAATAATA/CTAATAATAATAAT<br>AATA                                                                               | AAATGACATAATCGCAA<br>TGAAAA | CGTGGACTTTTTGTTC<br>AAATG   | 58.6                             | 561                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca8_P4_14921456  | Ca8                                     | 14921456                      | TAAAAAAAA/TAAAAAAAA                                                                                               | CCATGGTTGAGTTGAC<br>CAAA    | ATGTGTGGAGGAGTTG<br>GGAG    | 59.4                             | 626                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca8_P4_14922109  | Ca8                                     | 14922109                      | GTTTTTTTT/GTTTTTTTT                                                                                               | CTCCCAACTCCTCCAC<br>ACAT    | GAGTTTGTGTCAGCG<br>AGCA     | 60.0                             | 569                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca8_P4_14934606  | Ca8                                     | 14934606                      | CATATATATATATATATATATATA<br>TATATATATATATATATATAT/CATAT<br>ATATATATATATATATATATATATA<br>TATATATATATATATATATATATAT | ATGCAAGGACTGATTG<br>AGGG    | GAAACGGAAAGCCGAT<br>ATGA    | 60.1                             | 336                                           | INTERGENIC                                           | --                                  | --                    | --  |
| Ca8_P4_15092448  | Ca8                                     | 15092448                      | TTATATATATATATATATATATATA<br>TATA/TTATATATATATATATATATAT<br>ATATATATATATATA                                       | GGTCCAAATCATCTCC<br>TCCA    | GTGGGCACATCATTCT<br>TCCT    | 59.9                             | 242                                           | INTERGENIC                                           | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3')       | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|-------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                           |                               |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_15162330  | Ca8                                     | 15162330                      | TTAATAATAATAATAATAAA/TTAA<br>TAATAATAATAATAA                                              | TTCGTCGTGTAGGTCC<br>AGTG      | GGGAAACCCACCTCTT<br>GATT     | 59.7                             | 757                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15177027  | Ca8                                     | 15177027                      | GTTTTTTTTT/GTTTTTTTTT                                                                     | CCAAACGCATTATGGT<br>CAACT     | CATTGTCTTGACACCT<br>GTGTTT   | 59.9                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_1523715   | Ca8                                     | 1523715                       | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATA<br>TATAT                           | TTGGCTTTTCAGTTCC<br>CATC      | AAAAATCCTTGCCATA<br>CAA      | 60.1                             | 801                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_1524117   | Ca8                                     | 1524117                       | ATTTTTTTTT/ATTTTTTTTT                                                                     | TTCAATTGTATGGGCA<br>AGGA      | GTGAAGGAGCACGCAT<br>GTAA     | 59.0                             | 276                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15313993  | Ca8                                     | 15313993                      | ACC/ACCTCC                                                                                | TGTTGTGGAGTTCTAG<br>GGGC      | TGGACCTTTTGGTCC<br>TTCT      | 60.1                             | 180                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15387864  | Ca8                                     | 15387864                      | TTCTCTCTCTCTCTCTCTCTCTCT<br>CTCTCTCTCTCTCTCT/TTCTCTC<br>TCTCTCTCTCTCTCTCTCTCTCT<br>CTCTCT | TTTCTTTTTCACCGCAA<br>ACC      | AACAGAGAGCTCCGAA<br>TCCA     | 60.1                             | 324                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15458098  | Ca8                                     | 15458098                      | G/GGGAAAAGGTTATTA                                                                         | GGTTCAAGCTGCCATT<br>GATT      | GTTGTGGTGTGCTTC<br>CTGA      | 60.1                             | 263                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_1548216   | Ca8                                     | 1548216                       | ATTTTTTTTT/ATTTTTTTTTTT                                                                   | TTGGAGTTGTGCCAAT<br>GTGT      | ATGCCACGTCACCCTA<br>AATC     | 60.0                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15508     | Ca8                                     | 15508                         | G/GAAT                                                                                    | ACACGTGTGCAAAGTG<br>CAA       | TTTTTACGGGTACCTG<br>GTCG     | 59.9                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15564348  | Ca8                                     | 15564348                      | ATTTTT/ATTT                                                                               | TGTCAAATTGATATCTGT<br>TGCAATG | TTTTTACCTCAAAGCT<br>AAAACAGA | 59.9                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_15578880  | Ca8                                     | 15578880                      | TT/TTTCT                                                      | TGGATGAGGATGAACC<br>ACAA | ACAAAATTTGCATTGAA<br>AAGAAT | 59.9                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15580121  | Ca8                                     | 15580121                      | A/AATTTAATTT                                                  | TCCTCAATTTTGAGCAC<br>ACG | TGGACACCACACTTCA<br>AATCA   | 59.8                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15685035  | Ca8                                     | 15685035                      | T/TAAA                                                        | TGCCAGGATGTAACCC<br>TTTC | ACTTGGTTCTGTTGTTG<br>GGC    | 59.9                             | 177                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15685177  | Ca8                                     | 15685177                      | AGG/AG                                                        | GCCCAACAACAGAACC<br>AAGT | GACTCCAAAACCTGT<br>GCAT     | 60.0                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15685330  | Ca8                                     | 15685330                      | AT/A                                                          | GCCCAACAACAGAACC<br>AAGT | GACTCCAAAACCTGT<br>GCAT     | 60.0                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15685626  | Ca8                                     | 15685626                      | T/TA                                                          | ATGCACAGGGTTTGG<br>AGTC  | ACTTGGTTCTGTTGTTG<br>GGC    | 60.0                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15685828  | Ca8                                     | 15685828                      | TAAAAAAAA/TAAAAAAAAA                                          | ATGCACAGGGTTTGG<br>AGTC  | ACTTGGTTCTGTTGTTG<br>GGC    | 60.0                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15685888  | Ca8                                     | 15685888                      | A/AG                                                          | ATGCACAGGGTTTGG<br>AGTC  | ACTTGGTTCTGTTGTTG<br>GGC    | 60.0                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15788537  | Ca8                                     | 15788537                      | TAAAAAAAAA/TAAAAAAAAA                                         | TCGGTTCCTTCAACTT<br>TGG  | ATCAATGCTTCCACCCT<br>TTG    | 60.1                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15788948  | Ca8                                     | 15788948                      | ATT/ATTT                                                      | GACATTCCAAAGGGTG<br>GAAG | GGTTTCCAAAACCAGA<br>ATCG    | 59.4                             | 422                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_15791303  | Ca8                                     | 15791303                      | AATATATATATATATATATAT/AA<br>TATATATATATATATATATAT             | GCGAGCATGAGAAGTT<br>GTTG   | CCGACTAATCACTCCTA<br>AATATCG | 59.6                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15854737  | Ca8                                     | 15854737                      | ATT/AT                                                        | CTCGCTAGTGACCGGT<br>TTTC   | TGCATTTGACTTCAACG<br>CAC     | 59.9                             | 727                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15879806  | Ca8                                     | 15879806                      | TATA/TATAGATA                                                 | TACGTCGCACAGAAAG<br>AACG   | TTCAAAAAGGCATAGG<br>GTTGA    | 60.1                             | 233                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15880009  | Ca8                                     | 15880009                      | CAAAAA/CAAAAA                                                 | TACGTCGCACAGAAAG<br>AACG   | TGCCCACTTGATACAA<br>CAAAA    | 60.1                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15881213  | Ca8                                     | 15881213                      | AC/ACC                                                        | TTATTAGGACGGGCAA<br>CAGC   | ACCGTTGAGAATTGAG<br>TGGC     | 60.1                             | 903                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15884757  | Ca8                                     | 15884757                      | GTTTTTT/GTTTTT                                                | TGCATAGTGTGAACAA<br>CTCACG | AAATGGCCCATCACTC<br>TTTG     | 59.8                             | 753                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15890497  | Ca8                                     | 15890497                      | TAAAAA/TA                                                     | GTCGACATAAGCCAAG<br>CCAT   | TTCAAGCTTTTGATGTT<br>GGG     | 60.1                             | 322                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15892786  | Ca8                                     | 15892786                      | AAAGA/AAAGAAGA                                                | AGCAGTTGAACTTGCC<br>TCGT   | CGATGATTCATTCCCAA<br>ACC     | 60.1                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15893508  | Ca8                                     | 15893508                      | GTTAC/GTTACAAATTTGAAATTAT<br>TAC                              | CCGAAAAACACATTATC<br>CGAA  | CGAAAAATTTTGCCAAAG<br>TGAA   | 59.8                             | 275                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15893957  | Ca8                                     | 15893957                      | ATTTTTTTTT/ATTTTTTTT                                          | TTCGAAACTTTTGCATT<br>TCG   | AATCCACGGAATTAGT<br>CCCC     | 58.9                             | 719                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                  |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_15896000  | Ca8                                     | 15896000                      | TAAAAAAA/TAAAAAAA                                                | CAAAGAGTGATGGGCC<br>ATT    | TTTTGTTGGGGACA<br>AAAG     | 59.9                             | 345                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15899043  | Ca8                                     | 15899043                      | CAAAAAAAAA/CAAAAAAAAA                                            | TGACGAAAATGCAACT<br>ACGC   | CCCATTGACCTGAA<br>ACTT     | 59.9                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15925648  | Ca8                                     | 15925648                      | TAAATGAAAAAT/TAAATGAAAA<br>TGAAAAAT                              | GCTTGATTCTTTGTG<br>GGGA    | AGCACTGCATTTCTCA<br>CCC    | 60.1                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15928480  | Ca8                                     | 15928480                      | TAA/TAAA                                                         | CGAACCATGTGAAAGC<br>ACAC   | GCACGGCCTATTGTTC<br>AGAT   | 60.2                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_15976346  | Ca8                                     | 15976346                      | CATATATATATATATATATA/CATA<br>TATATATATATATA                      | GACGTTGGAGTCATGT<br>TTTTCA | ACAACGCAGAGAGCA<br>GAAT    | 60.0                             | 365                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_16066420  | Ca8                                     | 16066420                      | AATATATATATATATATAT/AAAT<br>ATATATATATATAT                       | TATTTTGGGATTTTGG<br>CTCG   | AGGAAGAGTGGAGTTG<br>CGAA   | 59.9                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_1619554   | Ca8                                     | 1619554                       | TT/TTAT                                                          | AAGGATGGGTTGCTGA<br>GAGA   | TGTCACGTCCCTTGTC<br>CTTT   | 59.8                             | 189                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_16236582  | Ca8                                     | 16236582                      | TTTTATTTATTTATTTATTTATTT<br>TATTT/TTTTATTTATTTATTTATTT<br>TTATTT | AGCATCACACCGACCC<br>TATC   | TCATTAGCCAATTGTGT<br>GGC   | 60.0                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_16315020  | Ca8                                     | 16315020                      | TAAAA/TAAA                                                       | AATGCAAAGCAACAAG<br>GTTTC  | TTGTATGCATGTGTGAT<br>GTGTG | 59.3                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_16315069  | Ca8                                     | 16315069                      | CTGATGAT/CT                                                      | AATGCAAAGCAACAAG<br>GTTTC  | GCACATTGAACCCCAT<br>ACAA   | 59.3                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                 |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_16315111  | Ca8                                     | 16315111                      | GAT/G                                                                                           | AATGCAAAGCAACAAG<br>GTTTC  | GCACATTGAACCCCAT<br>ACAA  | 59.3                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_16316035  | Ca8                                     | 16316035                      | CAAAA/CAAAAA                                                                                    | GGCATCACCCCAAGAC<br>ATAG   | CCCTTGATTTTCAATC<br>ACTCC | 60.3                             | 352                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_16467464  | Ca8                                     | 16467464                      | CTTTTTTTTTT/CTTTTTTTTTT                                                                         | TTTGTAACCATCGTG<br>CAGTG   | AGTGCATGAGTTTT<br>GGTCA   | 59.6                             | 763                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_16467871  | Ca8                                     | 16467871                      | ATTTTTTTTTT/ATTTTTTTTTT                                                                         | TTTTCCGACTTGGTC<br>CTTT    | AGTGCATGAGTTTT<br>GGTCA   | 58.7                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_1654587   | Ca8                                     | 1654587                       | AC/A                                                                                            | TGGCAATTCTGTCAGT<br>TGGA   | GAGCCCATCTGCATT<br>CATT   | 60.2                             | 245                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_1770210   | Ca8                                     | 1770210                       | GTTTTTTTTTTTTT/GTTTTTTTTTT<br>TTT                                                               | TGCTGCTAAAATATGTC<br>CCTCA | AGCCACAACATGAAC<br>CACA   | 59.7                             | 857                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_1805720   | Ca8                                     | 1805720                       | TAAAAAAAAA/TAAAAAAAAA                                                                           | GAACCACGATCTCCAG<br>GTGT   | ATTTGGAGTGCATGGG<br>AAAC  | 60.0                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_1833301   | Ca8                                     | 1833301                       | TTAATAATAATAATAATAATAAT<br>AATGATAATAATAATA/TTAATAATA<br>ATAATAATAATAATAATAATGAT<br>AATAATAATAA | AGCTTAGCGTGCGGTT<br>AAAA   | TGCACTCATCCATGCC<br>ATAA  | 60.0                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_18339     | Ca8                                     | 18339                         | CAAA/CAAAA                                                                                      | TGGCACACTGTCTTGT<br>CCTC   | GTGTGCCAATTGAGGA<br>AGGT  | 59.9                             | 268                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_1870873   | Ca8                                     | 1870873                       | CNNNNNNNNN/CNNNNNNNNN                                                                           | GCAAACCCATCCTTT<br>CTCA    | TGATCTCTGTGAGTCC<br>GTCG  | 60.1                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                            | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                          |                               |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_1919955   | Ca8                                     | 1919955                       | GAAAAAAAAA/GAAAAAAAAA                                                                    | AAAAGGAGTACCTACC<br>AAATGTTCC | GTTGAATCAATGCCAT<br>GTCG  | 60.1                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_2021031   | Ca8                                     | 2021031                       | CAAAAAAAAAAAAA/CAAAAAAAAAA<br>A                                                          | GGGTTGCCTTTAGAAA<br>TGGG      | CCACATGTAGCAGTGG<br>CCTA  | 60.7                             | 217                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_2033135   | Ca8                                     | 2033135                       | TC/TCC                                                                                   | ACGCTCGATTCCGAG<br>AGTA       | CACTGTGTGGGTTGTT<br>CGAC  | 60.0                             | 828                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_2097207   | Ca8                                     | 2097207                       | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAA/AAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAA | CACGACTTTCACCAAC<br>ATGG      | CTCACCTGCTTCCTTC<br>CAG   | 60.0                             | 775                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_2099514   | Ca8                                     | 2099514                       | TAAAAAAAAAAAAA/TAAAAAAAAA<br>AA                                                          | AAGGTTAAATTGCACC<br>CGC       | AGATGGCCAAAAATCA<br>CCAA  | 60.0                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_2295637   | Ca8                                     | 2295637                       | TAAAAAAAAAAAA/TAAAAAAAAA                                                                 | CCACCCTATCGAGAAG<br>ACCA      | AACTGACAGCCATAAAA<br>GCCA | 60.1                             | 864                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_2319568   | Ca8                                     | 2319568                       | ATTTTTTT/ATTTTTTTT                                                                       | TCATCACAGCCGGATA<br>TCAA      | TGATGATGCCGATTTTT<br>CAA  | 60.0                             | 254                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_2428087   | Ca8                                     | 2428087                       | CATTATTATTATTATTATTATTAT<br>TAT/CATTATTATTATTATTATTATTA<br>TTAT                          | TTATTTACCGTCGTGT<br>CCA       | TATTGGACTGTCGTGT<br>CCGA  | 60.0                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_24399     | Ca8                                     | 24399                         | TGTTTAGGGTTTAGGGTTTAGG/TG<br>TTTAGGGTTTAGG                                               | CGGATTTAGGGTTTTG<br>GGAT      | GCGTCCGACAACCATT<br>TACT  | 60.0                             | 448                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_2507807   | Ca8                                     | 2507807                       | TTATATATATATATATATAT/TTAT<br>ATATATATATATATAT                                            | CGGACTGGAATCAAAA<br>GCTC      | AGCTAAATGCGATTTG<br>CAGG  | 59.8                             | 852                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                     | Forward primers (5'-3')        | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------|--------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                   |                                |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_3645706   | Ca8                                     | 3645706                       | GATATATATATATATATATATATA/<br>GATATATATATATATATATATATA<br>TA                                       | GGTTATTTAGGCACCTC<br>GTTATTGTG | TCACAATCAATTGCGA<br>GAATTT  | 60.2                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_3834738   | Ca8                                     | 3834738                       | CATATATATATATATATATATATA<br>TATATATATATATAT/CATATATATAT<br>ATATATATATATATATATATATATA<br>TATATATAT | GGGACAAACATTTGTT<br>ATTGCAT    | GTGCGTAAAGCAAAC<br>CACG     | 60.0                             | 874                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_3960211   | Ca8                                     | 3960211                       | TTATATATATATATATATA/TTATATA<br>TATATATATA                                                         | AAAACCTCGTGCCTTG<br>ACGTG      | AACCATTGTGAAAATTT<br>AAGGGA | 60.2                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_3964540   | Ca8                                     | 3964540                       | GAAAAAAAAA/GAAAAAAAAA                                                                             | AAACGTCATAAATTCGA<br>AATGC     | GGCGTCAACAATCCAT<br>CTTT    | 58.2                             | 194                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4071945   | Ca8                                     | 4071945                       | TG/T                                                                                              | GAGGGGTGGTAACTGA<br>CTCG       | ATGCACAAATTCTCGCA<br>CAG    | 59.6                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4114988   | Ca8                                     | 4114988                       | CTTTTTTT/CTTTTTTT                                                                                 | GCAGCCCGAGTGATAA<br>AGAA       | TGGCTCAATCACACAA<br>AGGA    | 60.4                             | 261                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_414617    | Ca8                                     | 414617                        | ATTTTTTTTT/ATTTTTTTTT                                                                             | TTTGC GTTACGAATTTG<br>ATGA     | TTTCCCGACTTGGTCC<br>TTTA    | 59.2                             | 178                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4179867   | Ca8                                     | 4179867                       | AATATATATATATATATATAT/AAT<br>ATATATATATATATATATATAT                                               | AGTAGGAGCGGTTGAG<br>GGAT       | ACCGGCAAAGATTGAT<br>GAAC    | 60.1                             | 652                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4181622   | Ca8                                     | 4181622                       | C/CT                                                                                              | TGTAGATGAGATGCTC<br>CCCC       | ATGGAAGTCGGTGAGT<br>ACGG    | 60.0                             | 265                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4186334   | Ca8                                     | 4186334                       | CAATAATAATAATAATAATAA/CA<br>ATAATAATAATAATAATAATAAT<br>AA                                         | CCTCGAGTTTTAGTCG<br>GCTG       | TAAAGGGGCATGCAGT<br>CATT    | 60.0                             | 835                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                  | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_4221957   | Ca8                                     | 4221957                       | CG/C                                                                           | AGCAACCAGCTGAAGG<br>AAGA     | GGATTTTGTGTGCGAC<br>AGATT   | 60.1                             | 313                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4222042   | Ca8                                     | 4222042                       | AATATATATATATATATA/AATATA<br>TATATATATATATATA                                  | AGCAACCAGCTGAAGG<br>AAGA     | GGATTTTGTGTGCGAC<br>AGATT   | 60.1                             | 313                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4230851   | Ca8                                     | 4230851                       | ATTTTTTTT/ATTTTTTTT                                                            | CCTAGCCTTAAATTCA<br>GGTCAGAT | CGAAGATTGGAATTCG<br>GAAA    | 59.2                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_425245    | Ca8                                     | 425245                        | TATAAA/TA                                                                      | ACGAGCTAGTCGGTGA<br>AGGA     | TGCGATATTAAATTTTG<br>GTTTGG | 60.0                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4264902   | Ca8                                     | 4264902                       | GTATATATATATATATATATATAT<br>ATATAT/GTATATATATATATATAT<br>ATATATATATATATATAT    | TAGCATTGGGGAACAT<br>GACA     | TCCACCAATTCAATGGA<br>CAA    | 59.9                             | 843                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4371201   | Ca8                                     | 4371201                       | ATTTTTTTTT/ATTTTTTTTT                                                          | TGGTGGGGACTAAGAA<br>GGTG     | CCTCGTTGAAAAGAGG<br>TTGG    | 60.0                             | 691                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4384084   | Ca8                                     | 4384084                       | ATTTTTTTTT/ATTTTTTTTT                                                          | TCCCTTTTCCATGAACA<br>TTTG    | TTGCGTTATGGATTTG<br>ATGA    | 59.8                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4399889   | Ca8                                     | 4399889                       | AAATAATAATAATAATAATAATA<br>ATA/AAATAATAATAATAATAATA<br>ATA                     | CAACCTCCCAAAGGGT<br>TTTT     | AGGTGTGGTAAGATTG<br>TTTGAA  | 60.2                             | 372                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4399931   | Ca8                                     | 4399931                       | AAATAATAATAATAATAAT/AAAT<br>AATAATAATAATAATAATAAT                              | CAACCTCCCAAAGGGT<br>TTTT     | AGGTGTGGTAAGATTG<br>TTTGAA  | 60.2                             | 372                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4400447   | Ca8                                     | 4400447                       | GTATTATTATTATTATTATTATTA<br>TTATTATTAT/GTATTATTATTATTA<br>TTATTATTATTATTATTATT | TTTTCAAAACAATCTTA<br>CCACACC | TATTGGGCCAATGCTT<br>CTC     | 59.3                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_444103    | Ca8                                     | 444103                        | CT/CTAT                                                       | TCGGTCCTACGGTACG<br>AAGT   | CGCATATTCGTGGAGA<br>TTGA   | 59.6                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4586301   | Ca8                                     | 4586301                       | CAAAAAAAAA/CAAAAAAAAA                                         | CCTTCACTCAAAAGAT<br>CGTCG  | CCTACTGCGTGATTCT<br>CAACC  | 59.9                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4601932   | Ca8                                     | 4601932                       | ATCTCTCTCTCTCTC/ATCTCTCT<br>CTCTCTCTCTCTC                     | ACACGTTGGATTGTTG<br>GGTT   | TGGATTGGACCTGTTT<br>CCTC   | 60.1                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4642153   | Ca8                                     | 4642153                       | AAATAATAATAATAA/AAATAATA<br>ATAATAATAATAA                     | ATAGTCGGCCCTGCTA<br>TTGA   | TGATTTTAAAGCGGAA<br>ACAA   | 59.7                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_465058    | Ca8                                     | 465058                        | TAAAAAAAA/TAAAAAAAA                                           | CCCAAACCTAAACGTT<br>CACC   | ACATGGGACATGTGCA<br>AAAA   | 60.4                             | 863                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4651594   | Ca8                                     | 4651594                       | TT/TTTAATGTTTTCTGCT                                           | AACGTTCGGATTTTCC<br>TGTG   | GCAGAACAATTACTTG<br>CGGA   | 60.0                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_46677     | Ca8                                     | 46677                         | TT/TTAT                                                       | CAATCGGACACCAATT<br>CAAA   | TCTGTCTTGTCCCACTC<br>CAA   | 59.4                             | 251                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4691099   | Ca8                                     | 4691099                       | AATATATATATATATATA/AATATA<br>TATATATATATATATA                 | TAAGAGCCATGCAGAG<br>ACGA   | CCATATCCCTCATCTCA<br>TACCG | 59.7                             | 755                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4752741   | Ca8                                     | 4752741                       | TTATATATATATATATATATATA<br>TATAT/TTATATATATATATATATA<br>TATAT | TTTGGGCAGCATAAAT<br>AGGG   | TGCTAAAATTCCAGG<br>GGTG    | 59.9                             | 819                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_4787057   | Ca8                                     | 4787057                       | ATTTTTT/ATTTTTT                                               | TCCCCGACAAATGTTA<br>ATTCTT | GGTATTGCCAATTGGT<br>GCTT   | 59.7                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                           |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_5364370   | Ca8                                     | 5364370                       | GATTTATTTATTTATTTATTTATTTAT<br>TTATTTATT/GATTTATTTATTTATTT<br>ATTTATT     | CACATTGGCACAACTC<br>CAAC     | AAAACAATCAGGGCAC<br>CAAA    | 60.0                             | 457                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_5366435   | Ca8                                     | 5366435                       | GTTTTTTTTTTT/GTTTTTTTTTTT                                                 | CTGATGAAGGGAAGGG<br>AACA     | CTTCATCATTGGTGG<br>GAGAA    | 60.0                             | 652                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_5378899   | Ca8                                     | 5378899                       | ACCCCC/ACCCCC                                                             | CCTTTTGGATGTATTGA<br>ATTGAGA | CAATGGGTGTTTTTCAT<br>GGTG   | 59.4                             | 805                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_5464595   | Ca8                                     | 5464595                       | TTTTTATTTATTTATTTTA/TTTTTA<br>TTTTATTTATTTATTTTA                          | ACTTCCCTTTCGAGAC<br>CGAT     | CGAAGTACAATGGTTT<br>GTAAGCA | 60.1                             | 870                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_5543964   | Ca8                                     | 5543964                       | GATATATATATATATATATATATAT/G<br>ATATATATATATATATATATAT                     | AGTGGTGCTGGAGTCA<br>TGC      | CGTCCACGGAACAA<br>GATA      | 59.8                             | 215                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_5596170   | Ca8                                     | 5596170                       | GATATATATATATATATATATATATA<br>TATAT/GATATATATATATATATATAT<br>ATATATATATAT | AGTCCTAACAATCTGG<br>CACGA    | CTATGGTGAATGCGCA<br>AAAA    | 59.7                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_5601429   | Ca8                                     | 5601429                       | TAAAAAAAA/TAAAAAAAAA                                                      | ATGCGAAAATTGACAA<br>CGTG     | CCGGTACCCTAAACTG<br>CAAA    | 59.6                             | 724                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_5635625   | Ca8                                     | 5635625                       | TATAGATAGATAGATA/TATAGATAG<br>ATAGATAGATA                                 | CGCCACTTTTCTAGTC<br>CACC     | CCCTCAAGCCATCGTG<br>TATT    | 59.7                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_5704254   | Ca8                                     | 5704254                       | TTATATATATATATATATATATATAT/<br>TATATATATATATATATATATA                     | GTCGCACACCAATCC<br>TTTT      | GGCTAACAAGTGCCTA<br>TCACG   | 60.0                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_5719968   | Ca8                                     | 5719968                       | TTGTGTG/TTGTG                                                             | GTTCCATTCCAACCCC<br>AAT      | AAAGTCGTGTGCTCGT<br>GTTG    | 59.4                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                 |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_5719997   | Ca8                                     | 5719997                       | C/CGTTAAA                                                                                       | AATTGTGTGGTTGCAG<br>GACA | TTTTCATCCAATTGGC<br>ACA  | 60.0                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_5724554   | Ca8                                     | 5724554                       | TAATAAATAAATAA/TAATAAATAA<br>TAAATAAA                                                           | CTGCCGACAAGGACAA<br>TGTA | AACAAGAACATCCTGG<br>TCGC | 59.7                             | 906                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_5733091   | Ca8                                     | 5733091                       | TAC/TACTTTTAAC                                                                                  | TGATTCTCAGGGAGGG<br>TGTC | GAGGGGATGAGAACGA<br>CAAA | 60.0                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_5774679   | Ca8                                     | 5774679                       | CTATATATATATAT/CTATATATAT<br>ATATATAT                                                           | TTCTTCGTCGTCTCA<br>CGTA  | TGATGCAACCGGTATA<br>TGGA | 59.4                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_5862916   | Ca8                                     | 5862916                       | CTT/CTTT                                                                                        | GGCCTTGTAACATTTG<br>AGGG | GCTCGCCTTTGCTATG<br>AGTC | 59.4                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_6097515   | Ca8                                     | 6097515                       | AAATAATAATAATAATAATAATA<br>ATAATAATAATAAA/AAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAA | GTTGGTGATTGGAAT<br>TGGG  | TTCCCTCTATTTTGCA<br>TCC  | 60.0                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_6124309   | Ca8                                     | 6124309                       | TAAAAAAAA/TAAAAAAAAA                                                                            | AAAACCATGGCACCTC<br>TTTG | GACGATCGCGTTAAG<br>AAGA  | 60.0                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_6136556   | Ca8                                     | 6136556                       | CTATTATTATTATTATTATT/CTA<br>TTATTATTATTATTATT                                                   | GAACGCAAAGGACATG<br>GATT | CCAAAGCATCAACAT<br>CAGA  | 59.9                             | 715                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_6253206   | Ca8                                     | 6253206                       | TTATATATATATATATATAT/TTAT<br>ATATATATATATATAT                                                   | ACCCGTTATGAAACGA<br>GTGC | CAGTAATCGGAGAAAA<br>CCCG | 60.0                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_6306502   | Ca8                                     | 6306502                       | AAATAATAATAATAATAATAATA<br>ATAATAATAATA/AAATAATAATAA<br>ATAATAATAATAATAATAATAAT<br>A            | TGGACTTCGATTGTCC<br>AAAA | TTGCATTTTCGTTGAAT<br>TGC | 59.1                             | 287                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                  | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_6307113   | Ca8                                     | 6307113                       | ATAATACATGTAATACATGTAATA/<br>TAATACATGTAATA                                                    | GCAATTCAACGAAAT<br>GCAA    | CCACTAAGTCATTGCA<br>AGGC     | 59.7                             | 942                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_6492546   | Ca8                                     | 6492546                       | CAAAA/CAAA                                                                                     | CGTAAGCAACCCACCA<br>ATCT   | TTGTCAACAACCTCAGC<br>GTAAAAA | 60.0                             | 142                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_6492603   | Ca8                                     | 6492603                       | ATTTTTTTTTTTT/ATTTTTTTTTTT                                                                     | CGTAAGCAACCCACCA<br>ATCT   | TTGTCAACAACCTCAGC<br>GTAAAAA | 60.0                             | 142                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_6492758   | Ca8                                     | 6492758                       | ATTTTTTT/ATTTTTTTT                                                                             | CGTAAGCAACCCACCA<br>ATCT   | TGGACATCATACGTTAT<br>CAATCG  | 60.0                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_6567143   | Ca8                                     | 6567143                       | AAGAGAGAGAGAGAGAGAGAGAGA<br>GAGAGAGAGAGAGAG/AAAGAGAGA<br>GAGAGAGAGAGAGAGAGAGAGAGA<br>GAGAGAGAG | GGAAAATTGAGGGAAG<br>AGGG   | GTGTGGGTCACCTTCAG<br>CAAA    | 59.9                             | 227                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_6651586   | Ca8                                     | 6651586                       | ATTATTATTGTTATTATT/ATTATTAT<br>T                                                               | TGCATGTGGGCACTAT<br>GATT   | TGGAATGGGTGAAC<br>AAAA       | 60.0                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_6991978   | Ca8                                     | 6991978                       | ATTTTTTTTTT/ATTTTTTTTTTT                                                                       | TTCAACATCTTGTTCT<br>TTATGC | ATTTCCAGTGGGATGG<br>TTGA     | 58.3                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7058455   | Ca8                                     | 7058455                       | TAAAAAAAAAAAAA/TAAAAAAAAAAA<br>AAA                                                             | CCAACGTATCTCTCAG<br>TGCG   | GCTGATGACATTCCCC<br>AAGT     | 59.5                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7065316   | Ca8                                     | 7065316                       | AATATATATATATATATATATATAT/<br>ATATATATATATATATATATATATAT                                       | TGGACCACAATTTAAG<br>TGCAA  | GGTTGAGTGGAAGGAT<br>GGAA     | 59.1                             | 448                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7106797   | Ca8                                     | 7106797                       | TAAAAAAAAA/TAAAAAAAAA                                                                          | AGGCTTTATGGGAAGC<br>AAAA   | TTTTCAGACCAACAC<br>CCA       | 58.8                             | 782                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_7200771   | Ca8                                     | 7200771                       | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATAT             | TTTGGGTTCAAGCATTTG<br>GATT    | TTTGACACCCGGTGAA<br>TTAT     | 60.3                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7203379   | Ca8                                     | 7203379                       | CATGTTA/CATGTTAATGTTA                                         | TGCCTTCAATTGTGCTT<br>TACC     | TTGGAGAAGCGACCT<br>TGTT      | 60.1                             | 423                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7284439   | Ca8                                     | 7284439                       | TAAAAAAAAA/TAAAAAAAAA                                         | ACGCCATTATCGTGAA<br>CACA      | GTGCCACGAGGTGAAG<br>ATT      | 60.0                             | 835                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7290942   | Ca8                                     | 7290942                       | GTTTTTTTTTTTT/GTTTTTTTTTT<br>T                                | CCTGACCTATTCAC<br>CCTT        | TTGACGTATTCAAGTGA<br>CACAATG | 60.2                             | 442                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7327814   | Ca8                                     | 7327814                       | CTATATATATATATA/CTATATATA<br>TATATA                           | TTGAATGATCTTCCTCA<br>TTTTCA   | TTCAACAAAGGTGGAA<br>AGGG     | 60.0                             | 983                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7338131   | Ca8                                     | 7338131                       | TAATA/T                                                       | GAAAAAGAGGGAGGGA<br>GAGAA     | TGGCCACTGCACTCAA<br>ATAA     | 58.9                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_75382     | Ca8                                     | 75382                         | ATTTTTTTTT/ATTTTTTTTTTT                                       | GAAATTTTCTTCGAG<br>GCCA       | CGGGACTTGAGGTGAA<br>TCAT     | 59.3                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7563428   | Ca8                                     | 7563428                       | ATA/ATAGGTTA                                                  | TCCGCTGCTAGCTCTT<br>CTTC      | TGGGAGGGAGTTCTTG<br>AATG     | 60.0                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_757289    | Ca8                                     | 757289                        | AT/ATGT                                                       | TGAGTTCAATTTTCTT<br>AAGTCAGAA | AAAACATGACATTGATT<br>TACGAGG | 59.7                             | 466                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7656693   | Ca8                                     | 7656693                       | TATGTGAATG/TATGTGAATGTGAAT<br>G                               | CCTAGTTCACCAAACT<br>CGGG      | GAAAGGTCAATGTCCC<br>GAAA     | 59.6                             | 441                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_7683519   | Ca8                                     | 7683519                       | TTGT/TT                                                       | AACCATTTGCTTTGGC<br>ACTC    | CAAGTTTGATTTGCACA<br>TTTGTT | 60.1                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7890414   | Ca8                                     | 7890414                       | CTTTTTTT/CTTTTTTTT                                            | TAGCCGCAAAGAAGAG<br>AAGC    | AATGGTGGTGAAGCA<br>AGTC     | 59.9                             | 769                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_789344    | Ca8                                     | 789344                        | GTATATATATATATATATATA/GTA<br>TATATATATATATATATATA             | CTGTCAACGCTCAAGG<br>ACAA    | CGCGGTTTTGCTTTTTA<br>GTC    | 60.0                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7895493   | Ca8                                     | 7895493                       | ATTTTTTTTT/ATTTTTTTTTT                                        | TGGCGTCACATTTGTT<br>CAAT    | CGTTGACGCTGAAAT<br>CGTA     | 60.0                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7896399   | Ca8                                     | 7896399                       | ATGTTGTT/ATGTTGTTGT                                           | TTTGATATGTTGCTTC<br>GCA     | CGATGCAGCCTCTTAG<br>GTGT    | 60.2                             | 689                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7901769   | Ca8                                     | 7901769                       | ATTTTTTTTT/ATTTTTTT                                           | CCTGGCCTACGGCCTA<br>TAAT    | TGGCCTACTTATGGTC<br>TGCC    | 60.3                             | 955                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7913547   | Ca8                                     | 7913547                       | A/AT                                                          | CCGATATGTCAGAAAA<br>CATCACA | GGCCTTCACTTCAAC<br>TTGCT    | 59.9                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7924797   | Ca8                                     | 7924797                       | TA/T                                                          | CGTTTGTCATCGTCT<br>TTCA     | TAATCTGCGGTTAAG<br>CAGA     | 59.7                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7938103   | Ca8                                     | 7938103                       | AT/ATTT                                                       | CACGGGGAAAAGTTGA<br>TTTG    | GAAGTCGCCATTTGGA<br>ACTC    | 60.3                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7938264   | Ca8                                     | 7938264                       | TTATATA/TTATATATA                                             | CACGGGGAAAAGTTGA<br>TTTG    | CACCAAATACCCCAT<br>TTG      | 60.3                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_7948182   | Ca8                                     | 7948182                       | TCA/TCACA                                                     | GCCGCAAAGAAGAGAA<br>GAGA    | TGCCCAAGTCACTAAT<br>GCTG  | 59.8                             | 443                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7950561   | Ca8                                     | 7950561                       | CAAAAA/CAAAAA                                                 | GTCTTTGGCCTCCAAT<br>CAAA    | TGGAGTTGGGCCAATA<br>ATTT  | 60.1                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7950841   | Ca8                                     | 7950841                       | AAAT/AAATAAT                                                  | TGTGTTGACCCAACCTC<br>CAAA   | AGCCACTTGTTGTGT<br>TTGA   | 60.0                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7952607   | Ca8                                     | 7952607                       | GAAAAA/GAAAAAAA                                               | CCTTCAAAATGGTGT<br>GCTCT    | GTCAATTTGCCGATCA<br>CCTT  | 59.2                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7953093   | Ca8                                     | 7953093                       | T/TC                                                          | AAGGTGATCGGCAAAA<br>TGAC    | CAGCCCTTCAGTGTCA<br>TGAGT | 59.9                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7953809   | Ca8                                     | 7953809                       | TACCTCAA/TACCTCAACCTCAA                                       | ACCTGCGACACGTGAA<br>CATA    | GAAAACGAGGCGTAA<br>CGAG   | 60.2                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7954393   | Ca8                                     | 7954393                       | TAA/TA                                                        | CTCGTTTACGCCTCGT<br>TTTC    | CCGTAGCATGAGAGTG<br>ACCA  | 59.9                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7954421   | Ca8                                     | 7954421                       | CATATATATATATATATATAT/CAT<br>ATATATATATATATATATATAT           | CTCGTTTACGCCTCGT<br>TTTC    | CCGTAGCATGAGAGTG<br>ACCA  | 59.9                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7954496   | Ca8                                     | 7954496                       | CATATA/CATATATA                                               | TTTCGTCGTATAAAGAC<br>GGAGAG | CCGTAGCATGAGAGTG<br>ACCA  | 59.8                             | 545                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_7955526   | Ca8                                     | 7955526                       | TCTC/T                                                        | CATGCAAGAGAAGGGA<br>AAGAA   | GTGTGGGAGAGAAAGC<br>ATCC  | 59.4                             | 296                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                               |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_7966081   | Ca8                                     | 7966081                       | CTTTTTTTT/CTTTTTTTT                                           | TCCGCTAGCGTTTCTC<br>TCTT      | GCCTAGCACAACTTTT<br>GGG     | 59.4                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8055205   | Ca8                                     | 8055205                       | CAATAAAGTAATA/CAATA                                           | TGATAAACATGATTTTC<br>CCTCATTT | TTGTTTGTTTGGAGAA<br>GGATCA  | 60.0                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8076052   | Ca8                                     | 8076052                       | TAAAA/TAAAAA                                                  | TAATGCCATTTTGGTGT<br>TGC      | TTTTCAACAAATGTGC<br>GGA     | 59.4                             | 219                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8240879   | Ca8                                     | 8240879                       | TC/TCC                                                        | GTCGCCGCTACGAGAT<br>AAAC      | TTGTGCTGATGGTGA<br>TGGT     | 59.9                             | 729                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8272896   | Ca8                                     | 8272896                       | TAAA/TAA                                                      | TGGCACAGAACTTCG<br>ATTG       | TTACCGCTCTTCCTTT<br>TCA     | 59.8                             | 727                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8298480   | Ca8                                     | 8298480                       | CTATATATATATATAT/CTATATAT<br>ATATATAT                         | GTTTTTCCTTTGACCAT<br>GCC      | AACCAACTTTCTTAATT<br>CTCGCA | 59.4                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8306925   | Ca8                                     | 8306925                       | ATATC/A                                                       | TTGTAAAATTTGCATTT<br>TCATCG   | TCCTCATACACCCACTT<br>GTTTG  | 59.1                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8312325   | Ca8                                     | 8312325                       | AAATAGGAATGTTTA/AAATAGGAAT<br>GTTTAATAGGAATGTTTA              | CGGCGATCATTAAAGGA<br>GAAA     | ATTTTGAACAAGCGGA<br>CCTG    | 60.2                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8383020   | Ca8                                     | 8383020                       | T/TGATA                                                       | CCCAAACTTTCAAATC<br>GATGA     | TTGTAACCCGTACAGT<br>CGCA    | 59.9                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8427820   | Ca8                                     | 8427820                       | TCCC/TCC                                                      | CCTACAATGCCTGCCG<br>TATT      | CACCGTGCAAAGTTTC<br>TCAA    | 60.0                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                             |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_8623323   | Ca8                                     | 8623323                       | ATTTTTTTT/ATTTTTTTT                                                         | GGGGTGATTATGGAGC<br>AAGA    | GGTCACGTGTGTCCA<br>AGAA    | 59.9                             | 963                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8624257   | Ca8                                     | 8624257                       | ATTAAGC/ATTAAGCTCAACTT<br>TAAAGC                                            | CTTTGATTGGGGTTTT<br>GGAA    | TGGTGACAATTATTTTT<br>CCCGT | 59.8                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8624418   | Ca8                                     | 8624418                       | CAAAAATTTAGAAAAAT/CAAAAATT<br>TAGAAAAATTTAGAAAAAT                           | TCCTTTCAATGGACTG<br>GTGA    | GTCCCGAGCATGACGT<br>TTAT   | 59.1                             | 888                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8624597   | Ca8                                     | 8624597                       | TAAAAAAAAA/TAAAAAAAAA                                                       | CAATTCTGCATCCTAA<br>CCAAA   | GTCCCGAGCATGACGT<br>TTAT   | 59.1                             | 384                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8636114   | Ca8                                     | 8636114                       | ATTTTTT/ATTTTTT                                                             | TTGAATTGGTTTCAAT<br>TGGG    | ACTCTCTTTCCTCCCC<br>TCA    | 59.7                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8665470   | Ca8                                     | 8665470                       | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATA<br>T                 | GGGCAGAAACCCTAGA<br>ATCC    | TTGGAAGACGATTCT<br>CAACC   | 59.9                             | 876                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8701927   | Ca8                                     | 8701927                       | AATATATATATATATATATATATAT<br>ATATATATAT/AATATATATATATATA<br>TATATATATATATAT | GTGGAGTGCAAAGTTG<br>GTGA    | GCCTGAATATGCACAC<br>ACAAA  | 59.7                             | 795                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8803212   | Ca8                                     | 8803212                       | GAAAAAAAA/GAAAAAAAA                                                         | TTGCCTCTAGGGGAAA<br>TATATGA | AATCCTCGTTTCAATGT<br>GCC   | 59.0                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8836838   | Ca8                                     | 8836838                       | C/CG                                                                        | TGAAGTGCGAGAAGGA<br>TTCA    | AGCCGCCTCTCTCTTC<br>TCTT   | 59.5                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8852324   | Ca8                                     | 8852324                       | CTT/CTTT                                                                    | AAAACGCCACGCTAAC<br>AAAT    | AATCGGTTGTGAGGGA<br>AAGTT  | 59.7                             | 688                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_8852641   | Ca8                                     | 8852641                       | GTCAAAATCA/GTCAAAATCAAATC<br>A                                | CCTTGCTCCAAGGACT<br>CTAGTT | GTTTATGGGTGAAGGC<br>CAAA    | 59.1                             | 786                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8858477   | Ca8                                     | 8858477                       | GTTTATCCT/GT                                                  | GTGTGCCCATGTTGTG<br>TCTC   | AAATGCGGATGGTCCA<br>ATAA    | 60.0                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8860098   | Ca8                                     | 8860098                       | GAAAA/GAAAAA                                                  | ATGCATCCACTCCCAG<br>AAAC   | TGTTTTGGTTGTGTCC<br>CAGA    | 59.9                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8860891   | Ca8                                     | 8860891                       | GAAAAAA/GAAAAAA                                               | AGCCTCTCTACCCCA<br>AAAT    | TCAATGCCTGTGAAT<br>TAAGC    | 60.1                             | 424                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8861164   | Ca8                                     | 8861164                       | TG/TGTATTACAG                                                 | GGAGCTTAATTCACAG<br>GCCA   | TGAATAAAAGGGCTTG<br>TGTTTCT | 60.2                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8868722   | Ca8                                     | 8868722                       | ATTTTT/ATTTTT                                                 | TGGTGGTTCAAAGGTA<br>AGGG   | CAATTTTCAAACATGT<br>GCAA    | 59.8                             | 317                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8869164   | Ca8                                     | 8869164                       | TAAAAAA/TAAAAA                                                | TGAGATGCTCTCCATC<br>TCCAT  | AAAACGACGGTGTGAC<br>ATATTTT | 59.8                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8869239   | Ca8                                     | 8869239                       | TT/TTGT                                                       | TTTTTATTATTCACGG<br>AATTGG | GGTAGCGCAATTCTCA<br>AAATG   | 57.3                             | 702                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8879287   | Ca8                                     | 8879287                       | GT/GTTTT                                                      | CGGATGTCTCGATGAT<br>TTGA   | ACTTGAAGGCTTTGGG<br>CTTT    | 59.6                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8880565   | Ca8                                     | 8880565                       | ATTTTT/ATTTT                                                  | TTTCGACCCTTGAGCT<br>TTGT   | TTGCTCCCTTGACTCT<br>ACCA    | 59.9                             | 736                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_8881428   | Ca8                                     | 8881428                       | CA/CAA                                                        | CCAAAGTCAACTGGTC<br>AAAGG   | TCGTGAAC TTGCTGAA<br>TTGG   | 59.6                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_888937    | Ca8                                     | 888937                        | CATATATATATATATATATATAT/CAT<br>ATATATATATATATATATATAT         | ATTTGGCCGAGTCATA<br>TCCA    | TGGAAAGTCAAAAATTC<br>GCC    | 60.3                             | 815                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8906932   | Ca8                                     | 8906932                       | ATTTTTTTTT/ATTTTTTTTTTT                                       | ATTCTTCGTCCAACAT<br>GGC     | GATGCTAACCAATAACA<br>AGGGTC | 59.9                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8907678   | Ca8                                     | 8907678                       | CAAA/CAAAA                                                    | TACCAAAGTTTTCCCC<br>CTCC    | GCAATGCATGAGAGGA<br>CAAG    | 60.2                             | 122                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8938717   | Ca8                                     | 8938717                       | G/GATA                                                        | GGTGT TGAGGGTGCA<br>GATTT   | GCAAGACATTCACGTT<br>GCAC    | 60.0                             | 751                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8951408   | Ca8                                     | 8951408                       | ATTT/ATTTT                                                    | TGGAGACCAAACTGG<br>GAAG     | TGTTATGTACGCCGGA<br>TCAA    | 60.1                             | 726                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8953211   | Ca8                                     | 8953211                       | CA/CAGA                                                       | GAGATGGATAGTTGAT<br>TTGTCCG | ATTGCAGGTCTTTCCC<br>CTTT    | 59.8                             | 814                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8954725   | Ca8                                     | 8954725                       | GAAAAAAAA/GAAAAAAAA                                           | ATCCATCGAGCAAGTC<br>GTTC    | GGCTTAGGGATAACTG<br>CATCC   | 60.2                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8956224   | Ca8                                     | 8956224                       | TATGCCATGCCATGCCAT/TATGCC<br>ATGCCAT                          | TGTGGGACCTTCCAAA<br>ACAT    | CAACAACGTCTATCTT<br>CGGC    | 60.2                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8956561   | Ca8                                     | 8956561                       | TG/TGATCG                                                     | GCCATGCCATCCTTGA<br>TAAT    | ATGTCCAACATCTGCTT<br>CCC    | 59.8                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_8956637   | Ca8                                     | 8956637                       | CATAAT/C                                                      | GCCATGCCATCCTTGA<br>TAAT | ATGTCCAACATCTGCTT<br>CCC | 59.8                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8967774   | Ca8                                     | 8967774                       | TTTCTTCTTCTTCT/TTTCTTCTTCTT<br>CTTCT                          | CTGCTGTTTGTGCCAC<br>TGTT | TCATCCGAATGGTATG<br>CTCA | 59.9                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8967849   | Ca8                                     | 8967849                       | TAAAAAAAA/TAAAAAAAAA                                          | CTGCTGTTTGTGCCAC<br>TGTT | TCATCCGAATGGTATG<br>CTCA | 59.9                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8968316   | Ca8                                     | 8968316                       | GTTTTTTTT/GTTTTTTTTTT                                         | TGTTGAGCATACCATT<br>CGGA | TCGTGTCTCATGTTCT<br>GCCT | 60.1                             | 780                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8968364   | Ca8                                     | 8968364                       | GTT/GTTT                                                      | TGTTGAGCATACCATT<br>CGGA | TCGTGTCTCATGTTCT<br>GCCT | 60.1                             | 780                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8969277   | Ca8                                     | 8969277                       | TAAAAA/TAAAAAA                                                | GCAACATTGGCAAAA<br>GTGA  | CACATGGCCGTGGGTA<br>AAT  | 59.7                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8969339   | Ca8                                     | 8969339                       | GACACA/GACACACA                                               | GCAACATTGGCAAAA<br>GTGA  | CACATGGCCGTGGGTA<br>AAT  | 59.7                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8972356   | Ca8                                     | 8972356                       | TC/T                                                          | TCCCATGACATCACA<br>CAAG  | TGAGAAAATTTGGCAAA<br>GGG | 60.4                             | 592                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8973230   | Ca8                                     | 8973230                       | TTAC/T                                                        | ACCTTGTAGCCCATGT<br>CACC | GGCAAAAGTTGGATCG<br>AAAA | 59.9                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8973285   | Ca8                                     | 8973285                       | ATGG/A                                                        | TCAAGCACGATCAATG<br>GAAA | GGCAAAAGTTGGATCG<br>AAAA | 60.2                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_8974020   | Ca8                                     | 8974020                       | TAAAAA/TAAAAA                                                 | TATGTGGCTGCAATGA<br>GAGG     | TTTCCGATCAAACCTT<br>TTGT   | 59.8                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8974041   | Ca8                                     | 8974041                       | TAA/TA                                                        | TATGTGGCTGCAATGA<br>GAGG     | TTTCCGATCAAACCTT<br>TTGT   | 59.8                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8974661   | Ca8                                     | 8974661                       | AA/AACA                                                       | GACGAATCTTTCTGG<br>GCAA      | CGGGAAGTGACATTTT<br>CAGA   | 60.2                             | 274                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8981299   | Ca8                                     | 8981299                       | GAAAAA/GAAAAA                                                 | AAGTTAATGGACGCG<br>ATTCT     | ACCAGAGGCCGTTTCT<br>TTCT   | 59.0                             | 235                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8981367   | Ca8                                     | 8981367                       | ATTTTTTT/ATTTTTT                                              | AAGTTAATGGACGCG<br>ATTCT     | ACCAGAGGCCGTTTCT<br>TTCT   | 59.0                             | 235                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8994344   | Ca8                                     | 8994344                       | A/AGG                                                         | TTCACTTCAACGGTTG<br>TGGA     | CGAAAAATCAAATGAA<br>GGAACA | 60.1                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8996121   | Ca8                                     | 8996121                       | TAATTAAATTAATTAATTAAT/TA<br>ATTAAATTAATTAAT                   | TGAATCAACATTTCAAT<br>TTTTCAA | TTCTGTGTCACTCATG<br>CAA    | 58.6                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8996810   | Ca8                                     | 8996810                       | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATAT           | AGTTTATGCGGGCGAT<br>TATG     | TACCATATCCCATCCC<br>ACG    | 60.0                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8996867   | Ca8                                     | 8996867                       | AAATAA/AAA                                                    | AGTTTATGCGGGCGAT<br>TATG     | TACCATATCCCATCCC<br>ACG    | 60.0                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8997113   | Ca8                                     | 8997113                       | ACC/AC                                                        | AGTTTATGCGGGCGAT<br>TATG     | CCGTGAATGCAGTTAC<br>TTTTG  | 60.0                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_8997181   | Ca8                                     | 8997181                       | T/TA                                                          | GTATTGCGCGCAGCTT<br>TTAT     | CCGTGAATGCAGTTAC<br>TTTTG   | 60.4                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8998003   | Ca8                                     | 8998003                       | TTGT/TTGTGT                                                   | TTTGATGACTCGTAAG<br>CCCC     | TGTAAGATGGAGGATC<br>CAAAGTG | 60.1                             | 240                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_8998056   | Ca8                                     | 8998056                       | TG/T                                                          | TTTGATGACTCGTAAG<br>CCCC     | TGTAAGATGGAGGATC<br>CAAAGTG | 60.1                             | 240                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9000433   | Ca8                                     | 9000433                       | TAAAAA/TAAAAA                                                 | AAACACTCGAGCAATC<br>CACC     | AAAATGAAACCCCAAAC<br>ACTT   | 60.1                             | 408                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9001455   | Ca8                                     | 9001455                       | GAAAAAAAAA/GAAAAAAAAA                                         | GAAGGTGGCGAACACA<br>TTTT     | CAGATATGCACCCTTTT<br>TGACA  | 60.0                             | 830                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9003481   | Ca8                                     | 9003481                       | GAAAAA/GAAAAA                                                 | TTTTTGGGTACAAGCA<br>CTCCT    | GCATTTATGGGTCTTG<br>GCAT    | 58.8                             | 905                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9023763   | Ca8                                     | 9023763                       | TTATATATATATATATATATA/TTATA<br>TATATATATATATATATA             | TAAGCGCATGTTCCAT<br>GTTG     | TGACGATGTGCTAAGC<br>ATGA    | 60.7                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9025422   | Ca8                                     | 9025422                       | CGG/CG                                                        | GCTTTTGTAACACCCC<br>GTTT     | GCCCTCAGATGAGAGT<br>CAGG    | 59.0                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9078335   | Ca8                                     | 9078335                       | AATTAATTTTGAT/AAT                                             | TCTTGATCTTCAACTTA<br>GCAATGG | AAACAAAACCATGATG<br>GGGA    | 59.8                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9078389   | Ca8                                     | 9078389                       | TAA/TAAA                                                      | TCTTGATCTTCAACTTA<br>GCAATGG | AAACAAAACCATGATG<br>GGGA    | 59.8                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_9081856   | Ca8                                     | 9081856                       | ATT/AT                                                        | TGGCACCACTCATAT<br>TTCA    | CCTTTTCCACCTTGCA<br>TAT    | 59.9                             | 322                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9082042   | Ca8                                     | 9082042                       | ATTTT/ATTT                                                    | TGGCACCACTCATAT<br>TTCA    | CCTTTTCCACCTTGCA<br>TAT    | 59.9                             | 322                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9082457   | Ca8                                     | 9082457                       | GTACA/GTACATTACTCTTTACA                                       | CAAACCTTCAAAACC<br>GCTA    | TCCATATTCCATTGGCA<br>CAC   | 60.1                             | 223                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9086154   | Ca8                                     | 9086154                       | CTTTTT/CTTTTTTT                                               | GGGCCATTGAGACAAT<br>CTTC   | TTGGAGGGAAGCACTT<br>TTTG   | 59.5                             | 746                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9087628   | Ca8                                     | 9087628                       | ATATTATTATT/ATATTATTATTA<br>TTATT                             | TTGGACCCCATCTTAC<br>TTGG   | TGTAGCATCCCATTTTC<br>CACT  | 59.8                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9088156   | Ca8                                     | 9088156                       | TAAAAA/TAAAAA                                                 | AGTGGAAAATGGGATG<br>CTACA  | CACAAATTTCAACGACA<br>AATCG | 59.4                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9088516   | Ca8                                     | 9088516                       | CTTT/CTT                                                      | CGATTTGTCGTTGAAA<br>TTTGTG | CCATACAAAACACAAG<br>GTGTGC | 60.4                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9089194   | Ca8                                     | 9089194                       | TAATAAAATAAAATAAAATAAA/TAA<br>TAAATAAAATAAA                   | CGCGTTCCCAAATGTT<br>TAAT   | CCCTAATCTTCACCAAC<br>CGA   | 59.8                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9105331   | Ca8                                     | 9105331                       | T/TCA                                                         | CCATGCAATCAGATGA<br>AGGA   | GGCGAGTTCAATTTGTG<br>GTTT  | 59.6                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9109482   | Ca8                                     | 9109482                       | TAA/TA                                                        | TGGGGACCAAAACTGA<br>GAAG   | GAAAGTTGGGGAACGTG<br>ACCA  | 60.1                             | 871                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_9125035   | Ca8                                     | 9125035                       | GAAAAAAAAA/GAAAAAAAAA                                         | TTCCGATTCTTTGTT<br>GGTTT  | TCAATGCCTCATTGGA<br>CTTTT  | 59.9                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9125685   | Ca8                                     | 9125685                       | AC/A                                                          | CCTAAAAAGTCCAATG<br>AGGCA | ACCATTGGGCATGAC<br>ACTT    | 59.2                             | 240                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9126027   | Ca8                                     | 9126027                       | AAA/AAACAGAA                                                  | AAGTGTCATGCCCAA<br>TGGT   | TTTCATTGATGCCAAAC<br>ACAA  | 60.2                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9134546   | Ca8                                     | 9134546                       | GAAAAAAAAA/GAAAAAAAAA                                         | TAGCGTTGGCCTTCTC<br>CTTA  | TTGCCTATACCCGACA<br>AAGG   | 60.0                             | 798                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9136066   | Ca8                                     | 9136066                       | CTTTTTTT/CTTTTTTTT                                            | ACAGCTTTGAAATTACC<br>GGC  | CTGTACGTTGAGGAA<br>ACCC    | 59.2                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9149110   | Ca8                                     | 9149110                       | CTTTTTTT/CTTTTTTT                                             | GCAAAAAGTGAAGGAT<br>TCGC  | TGCATGCAGTAAAAAG<br>TATCCA | 59.8                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9149327   | Ca8                                     | 9149327                       | AATATATAT/AATATAT                                             | TTCCAATGCAGATTGCG<br>TTGA | CACATTTACTTGCAATG<br>CGG   | 60.2                             | 793                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9149395   | Ca8                                     | 9149395                       | TTA/TTAATA                                                    | TTCCAATGCAGATTGCG<br>TTGA | CACATTTACTTGCAATG<br>CGG   | 60.2                             | 793                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9149530   | Ca8                                     | 9149530                       | TT/TTGT                                                       | TTCCAATGCAGATTGCG<br>TTGA | CACATTTACTTGCAATG<br>CGG   | 60.2                             | 793                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9166250   | Ca8                                     | 9166250                       | CAT/CATAT                                                     | TCACCAAATTAGCCATT<br>GTGA | CTCGTTCATAAACCG<br>CACT    | 59.0                             | 394                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_9174938   | Ca8                                     | 9174938                       | ATTTT/ATTT                                                    | TGAGAACAGGCTTTT<br>CCTT   | TGAAATGGCTGTCGTG<br>GATA  | 58.9                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9184413   | Ca8                                     | 9184413                       | TAAAAA/TAAAAAA                                                | CTACGGGAAAACCTCG<br>TCCA  | GGTATGGGGTAAAATT<br>TTCGG | 60.1                             | 722                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9184889   | Ca8                                     | 9184889                       | AT/ATT                                                        | CCGAAAATTTTACCCC<br>ATACC | CGAATAAAGGCAGATT<br>CCCA  | 59.4                             | 585                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9199027   | Ca8                                     | 9199027                       | AGG/AGGG                                                      | AGCTCCAAGGACAGA<br>TTCA   | AGAGGGCCCTGTGAAA<br>AA    | 59.8                             | 216                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9199825   | Ca8                                     | 9199825                       | GTAT/GTATAT                                                   | CAGAAGCTACGCCAA<br>TCAT   | AAATCCTGATTATCGA<br>CGC   | 60.2                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9201647   | Ca8                                     | 9201647                       | CA/CAA                                                        | GTCTCGATCGCAAGTC<br>ACAA  | GATATATACGGCTGAC<br>GGCG  | 60.0                             | 300                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9201705   | Ca8                                     | 9201705                       | GATGTATTATGTAT/GATGTAT                                        | GTCTCGATCGCAAGTC<br>ACAA  | GATATATACGGCTGAC<br>GGCG  | 60.0                             | 300                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9206162   | Ca8                                     | 9206162                       | TTGTGTGT/TTGTGTGTGT                                           | CCAGTCGATTGCATC<br>ATAG   | ACAGGCCAATCCACAA<br>CACT  | 59.1                             | 709                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9207788   | Ca8                                     | 9207788                       | CTGGT/CTTTTAAATGTATGGT                                        | ATGAGCTGCCTCATTT<br>GCTT  | GTGGCCCAACTAATCC<br>AAAA  | 60.0                             | 760                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9207853   | Ca8                                     | 9207853                       | TA/TAA                                                        | ATGAGCTGCCTCATTT<br>GCTT  | GTGGCCCAACTAATCC<br>AAAA  | 60.0                             | 760                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_9207994   | Ca8                                     | 9207994                       | TTTGTGTGTGTG/TTTGTGTGTG                                       | ACTGAGCAGATGGGTG<br>TGAA   | GTGGCCCAACTAATCC<br>AAAA  | 59.3                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9208402   | Ca8                                     | 9208402                       | TAAAA/TAA                                                     | TTTTGGATTAGTTGGG<br>CCAC   | TGTCAACAATAGTGTTT<br>GCGG | 59.8                             | 647                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9215036   | Ca8                                     | 9215036                       | GTTTTTTT/GTTTTTTT                                             | CATCCTCTGGTTGGAC<br>GACT   | TTTTTCCCCGACACAT<br>AAG   | 60.1                             | 837                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9215235   | Ca8                                     | 9215235                       | CG/CTGTG                                                      | GCCATAAACACATTGC<br>ACCA   | TTTTTCCCCGACACAT<br>AAG   | 60.4                             | 357                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9216235   | Ca8                                     | 9216235                       | CAAAAAA/CAAAAAA                                               | GATCGCATGAGCATTG<br>ACGA   | TGTATTGGGCATTGGT<br>TCCT  | 59.8                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9217069   | Ca8                                     | 9217069                       | TAAAAAAA/TAAAAAAA                                             | ATCATGGGAGTTCACC<br>TTGG   | TTTCAACTTTTGGTC<br>GCA    | 59.8                             | 879                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9218033   | Ca8                                     | 9218033                       | ATTTT/ATTTT                                                   | CAAAATCAGGTGTTGG<br>CTGA   | CGGTGTCAAAGTCAGG<br>GAAT  | 59.7                             | 730                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9268525   | Ca8                                     | 9268525                       | TCTTAAATTAGC/TC                                               | CGTGAAGCCTTGAAGA<br>AAGG   | GCCACTGCTGCTCATT<br>CATA  | 60.0                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9323855   | Ca8                                     | 9323855                       | TG/T                                                          | CCAACCGTTTCAAGAA<br>ATTAAA | CAACAAAAAGCCGAAC<br>CCTA  | 58.2                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9364522   | Ca8                                     | 9364522                       | ATT/ATTT                                                      | TTGTGCGTGAGATTGT<br>GTGAA  | AAAGATTGTGATTTTGG<br>CGG  | 60.1                             | 802                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_9375798         | Ca8                                     | 9375798                       | ATTTTTTTT/AATTTTTTTTTT                                        | TGAGGGGTACAAAAGC<br>CAAC  | AAAATTCTGTTTGGGG<br>GACC   | 60.0                             | 333                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9397792         | Ca8                                     | 9397792                       | ATTTTTT/ATTTTTTT                                              | CCGCTCAAAATCATCG<br>TACA  | ACGGGCATCTAATGTT<br>GAGG   | 59.7                             | 244                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca8_P4_9950679         | Ca8                                     | 9950679                       | GT/G                                                          | AATTGGA AAAACACAT<br>GCCC | TGGCATAATGTCAGAC<br>GCAT   | 59.7                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold10_P4_69425    | scaffold10                              | 69425                         | AA/AATAATA                                                    | TCGTCACGTCTTCCAT<br>TCAT  | TTGCTTGAATTGCAAAT<br>GTTTT | 59.1                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1003_P4_41332  | scaffold1003                            | 41332                         | G/GAGCGGT                                                     | GGGATTTGAAGGTGCT<br>GAAA  | TAGTGGCCACAACCA<br>CTCA    | 60.1                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1003_P4_41354  | scaffold1003                            | 41354                         | TCA/T                                                         | GGGATTTGAAGGTGCT<br>GAAA  | TAGTGGCCACAACCA<br>CTCA    | 60.1                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1006_P4_109456 | scaffold1006                            | 109456                        | T/TC                                                          | TTGATTTAGCCCGAG<br>ATTC   | TTTACAAGCAGCGGGA<br>AAGT   | 60.0                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1006_P4_212542 | scaffold1006                            | 212542                        | AATATATATATATATATAT/AATATAT<br>ATATATATATATAT                 | TTTAAGGAGGAGCGA<br>GTTG   | TTCTATGTGCACCGCTT<br>AGG   | 59.4                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1006_P4_324715 | scaffold1006                            | 324715                        | CAATAAAAAA/CA                                                 | TTCCCGTCTTCAATCA<br>ATGT  | CGATTATCAACCACTT<br>GGAG   | 59.4                             | 427                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1006_P4_353608 | scaffold1006                            | 353608                        | TAAAAA/AAAAA                                                  | GGGACTTCTTTGCGA<br>TTCA   | TCCAGTTGCAATCCTTC<br>CAT   | 60.2                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1006_P4_363605 | scaffold1006                            | 363605                        | ATTTTTTTTT/ATTTTTTTTT                                         | TTTCTCTGAAAAGGG<br>AGGG   | TGCTTACGCTTCAAGC<br>CTTT | 60.5                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1006_P4_414835 | scaffold1006                            | 414835                        | T/TC                                                          | AAGACTACGGCGCAC<br>AACT   | CCATTGTCCTTTTAGAG<br>CGG | 59.9                             | 186                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1006_P4_455227 | scaffold1006                            | 455227                        | ATTTTT/ATTTTTTT                                               | TAATGGCCCATCCTCT<br>ATGC  | CATTGTTGATGCCATTG<br>GAC | 59.9                             | 708                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1006_P4_530345 | scaffold1006                            | 530345                        | AATATATATATATATAT/AATATAT<br>ATATATATATATAT                   | TTACCCACGCGCTTCT<br>CTAT  | GACAACAGCCACCTGT<br>GAAA | 59.9                             | 903                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1006_P4_559163 | scaffold1006                            | 559163                        | TTT/TTTATT                                                    | CCATGACAATGATTGG<br>TGTGA | AGTTCATCCATGTTG<br>CTCA  | 60.2                             | 171                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1006_P4_621524 | scaffold1006                            | 621524                        | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>A   | TGGGCCACCACTATT<br>GACT   | GTGATTTGCGCCATGA<br>TTAG | 60.4                             | 803                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1006_P4_84469  | scaffold1006                            | 84469                         | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATATA<br>TAT | TGGGCCTATATGTTGC<br>ATTG  | ATCCAATTTCAACCGA<br>TGG  | 59.4                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1008_P4_12678  | scaffold1008                            | 12678                         | TC/T                                                          | TCTTGTTGTAACCTT<br>GGC    | GGGCTGATGCCATAAA<br>CACT | 60.0                             | 727                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1008_P4_51387  | scaffold1008                            | 51387                         | CTTTTT/CTTTT                                                  | TCCAGCTAGAACTGG<br>TGCC   | TCAGGCTCATTGAGT<br>GCAC  | 60.4                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1010_P4_147047 | scaffold1010                            | 147047                        | AATATATATATATATATA/AATATA<br>TATATATATA                       | CCTTGAGTTCGACATT<br>CGGT  | CGCTATGCGACCATTT<br>TACA | 60.1                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold10103_P4_4446  | scaffold10103                           | 4446                          | A/AC                                                          | GGGTTCTCGTCAGAT<br>TTCA   | AATGGAATAAGGGTTT<br>CCCG | 60.1                             | 625                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1013_P4_26274  | scaffold1013                            | 26274                         | GAAAAAAA/GAAAAAA                                              | TCAACCCCTGATTTT<br>GAAG   | TGCTAACCAAGGCCA<br>AAAT  | 59.9                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1017_P4_12762  | scaffold1017                            | 12762                         | ACTCCTC/ACTC                                                  | CGATTCTGTACCACCC<br>GACT  | GAAAATTGCCGAAAA<br>GACA  | 60.0                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold10180_P4_748   | scaffold10180                           | 748                           | AT/ATT                                                        | GGTGAGTTTGTGTCGT<br>TGGA  | AGGGAGGACGAAGATG<br>ACCT | 59.6                             | 448                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold102_P4_104861  | scaffold102                             | 104861                        | CAAA/CAA                                                      | GGAGTGAAATATGAA<br>ATGCGA | TTGTGTTTGTACAGG<br>CCAT  | 59.1                             | 888                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1020_P4_209789 | scaffold1020                            | 209789                        | G/GGGAAACCATGTAAATCGC                                         | ATTCCATTTTGTGTGG<br>GGA   | TGTACATGGGAAATGC<br>CTCA | 60.0                             | 758                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1020_P4_69432  | scaffold1020                            | 69432                         | GTTTTT/GTTTT                                                  | GATTCCCCCTCCTTAA<br>CGTC  | AGTTGCGAGCGGAGAT<br>TTTA | 59.8                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold10227_P4_12119 | scaffold10227                           | 12119                         | ATTT/ATT                                                      | CAAGTCTCCCAACTTC<br>CCAA  | TGAGTCATCTCGTCGT<br>CGTC | 60.1                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold10244_P4_859   | scaffold10244                           | 859                           | TAAA/TAAAA                                                    | TTTGGGTGGTTACCG<br>ATGT   | GAACGATTGTTATCGC<br>CGTT | 60.1                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1027_P4_243426 | scaffold1027                            | 243426                        | GAAAAAAAA/GAAAAAAAAA                                          | TTTCCCAGTTGGTCC<br>TTTA   | TACATCCGCGATCCCT<br>TAAC | 59.5                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)        | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                      |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1027_P4_261223 | scaffold1027                            | 261223                        | C/A/C                                                                | CAAGAATTCATCTGCC<br>CCTC  | GCCTCAATGGCTTGAG<br>ATT   | 59.6                             | 328                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold10285_P4_994   | scaffold10285                           | 994                           | AAA/AAATTAGGAAATAA                                                   | CGAAAACCTCAGAAAGG<br>CGAC | GCCTTATGTGGAAAGA<br>CACCA | 60.0                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1036_P4_203824 | scaffold1036                            | 203824                        | TAAATAA/TAAATAATAAAATAA                                              | TCTGCTAACGGGTCGT<br>CTCT  | TCCGTGTGTTTGTATG<br>ATAGC | 60.0                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1036_P4_204693 | scaffold1036                            | 204693                        | C/A/C                                                                | TCACAACAATCATCCAC<br>ACAG | TACATAGTTACGGAGC<br>CGCC  | 57.9                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1036_P4_205006 | scaffold1036                            | 205006                        | ATTGGAATTGGACTTGAATTGGAC<br>TTGGAATTGGA/ATTGGAATTGGAC<br>TTGGAATTGGA | GCAAGCGACTATGGGT<br>AAGG  | TACATAGTTACGGAGC<br>CGCC  | 59.7                             | 273                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1036_P4_236459 | scaffold1036                            | 236459                        | ACCC/ACC                                                             | TTGGATGCACAACATT<br>GGTT  | AGGTCAATTCGTCCT<br>CCCT   | 59.8                             | 369                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1036_P4_75415  | scaffold1036                            | 75415                         | TAAAAAA/TAAAAAA                                                      | CATTGGATGCACAAGA<br>TTGG  | TTTTCGTCCTCCCTAG<br>GCTT  | 59.9                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1038_P4_2468   | scaffold1038                            | 2468                          | AGGG/AGG                                                             | TCCAGATGAAATCGAG<br>GACC  | TTTTCGGACTAGACGA<br>TGGG  | 60.0                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1038_P4_720    | scaffold1038                            | 720                           | TGG/TG                                                               | CGAAAATCGCCAGAA<br>AATA   | TCCTGGTCCTCGATT<br>CATC   | 60.0                             | 842                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1039_P4_32388  | scaffold1039                            | 32388                         | GAAAAAAAAAAAAA/GAAAAAAAAA                                            | TGTTAGGAGGATCTCA<br>CGGG  | TCTGCGAAGGATCTAG<br>GGAA  | 60.1                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                           |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1039_P4_32679 | scaffold1039                            | 32679                         | T/TG                                                                      | TTCCCTAGATCCTTCG<br>CAGA | TGGATGGTAATCCAAC<br>GTGA  | 59.9                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1039_P4_4419  | scaffold1039                            | 4419                          | GGTAATTT/G                                                                | TTGGTATTGAACTCGG<br>AGGC | GTTGGTCCCTAGCAC<br>CGTA   | 60.1                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1039_P4_48817 | scaffold1039                            | 48817                         | ATTTTTTTTTT/ATTTTTTTT                                                     | CGACATGCATGCCTTA<br>TTTG | CATGAGGAAACAATTG<br>TGCAG | 60.1                             | 571                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1039_P4_59288 | scaffold1039                            | 59288                         | CAAAAAAAAA/CAAAAAAAAA                                                     | GCAATCTCCTCAACTC<br>GGTC | TACTGTGCGCCATCT<br>ACTG   | 59.8                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold10412_P4_1146 | scaffold10412                           | 1146                          | GCTC/GC                                                                   | TGATTCCATTGGGGTT<br>TCAT | ATTGTTTCTCGAGGTT<br>GCG   | 60.0                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold10415_P4_1060 | scaffold10415                           | 1060                          | TTGTG/TTGTGTG                                                             | GAGGAAGATGCCACCA<br>GAAA | TTGTATCCCACAGAA<br>GCCT   | 60.2                             | 774                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold10419_P4_1064 | scaffold10419                           | 1064                          | TAAAAA/TAAAAA                                                             | TTTTGGCTGATGTGGA<br>TGAA | GTTTGGGTTTGCTTGT<br>TTGG  | 60.0                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1043_P4_1901  | scaffold1043                            | 1901                          | GTATATATATATATATATATATAT<br>ATATATATAT/GTATATATATATAT<br>ATATATATATATATAT | CGAAGCAAAGAAAGA<br>ACCG  | TGGATTACGGGTGAAA<br>TGGT  | 60.0                             | 321                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1046_P4_10422 | scaffold1046                            | 10422                         | TAAAAA/TAAAAA                                                             | CATTGGATGCACAAGA<br>TTGG | TGCGTTTGTGTCATTG<br>GATT  | 59.9                             | 696                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1046_P4_17706 | scaffold1046                            | 17706                         | ACC/AC                                                                    | CATTGGATGCACAAGA<br>TTGG | AGGTCATTTTCGTCTC<br>CCT   | 59.9                             | 871                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1046_P4_20332  | scaffold1046                            | 20332                         | TAAAAAAA/TAAAAAA                                              | GCGCAACAACTAT<br>GTGA    | TCAGGTCATTTTCGTCC<br>TCC | 59.7                             | 788                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1046_P4_21076  | scaffold1046                            | 21076                         | GAAA/GAAAA                                                    | GGAGGACGAAATGAC<br>CTGA  | ACCGATCTTGTGCATC<br>CAAT | 60.1                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1046_P4_31524  | scaffold1046                            | 31524                         | AGGGGGGGG/AGGGGGG                                             | AGGGAGGACGAAATG<br>ACCT  | TTGTTGGCCAATTAGG<br>GTTT | 59.9                             | 395                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1047_P4_109934 | scaffold1047                            | 109934                        | TAAAAAAA/TAAAAAAA                                             | AAAGCAGTCCACCAT<br>TTTG  | CTAAGCGAAATCAATC<br>CCCA | 60.0                             | 829                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1047_P4_159189 | scaffold1047                            | 159189                        | CTTTTTTTTT/CTTTTTTTTT                                         | TTGGTGGGTGGTGGTA<br>GATT | TTACCCCTTCCTTTTC<br>GTG  | 60.1                             | 795                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1047_P4_169514 | scaffold1047                            | 169514                        | TTATATATATATATATA/TTATATA<br>TATATATATATATATA                 | CGACAATCAACTGTGC<br>CATC | AAGTTGGCCCAATCCC<br>TAGT | 60.3                             | 771                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1047_P4_171957 | scaffold1047                            | 171957                        | CATATATATATATATATATATATA<br>TAT/CATATATATATATATATATAT<br>AT   | GTGCGGAACAACACA<br>AATG  | AAATAAAGGCCAACTC<br>GGG  | 60.0                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1047_P4_212621 | scaffold1047                            | 212621                        | TAATAAATAAATAAATAAATAA<br>ATAAA/TAATAAATAAATAAATAA<br>AATAAA  | TTTTGTTTTGGCATGAA<br>CCA | TTCCACCATCCATTTTG<br>TGA | 59.9                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1047_P4_280682 | scaffold1047                            | 280682                        | GTTTTTTTTT/GTTTTTTTTT                                         | TTCTGAAGGTATTGGG<br>CCAC | TGGGTTTTAAGACGAT<br>CGAA | 59.9                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1047_P4_301121 | scaffold1047                            | 301121                        | GAAAAAAA/GAAAAAAA                                             | CAAGCGATCGAATGTC<br>TTGT | TATTGGGTCGGTCCTC<br>GTTA | 58.9                             | 806                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1047_P4_318054 | scaffold1047                            | 318054                        | T/TA                                                                          | ATCCAAACGAGGGACA<br>AAAA | AAACGCAGCTGCTTCT<br>CATT  | 59.4                             | 689                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1047_P4_419626 | scaffold1047                            | 419626                        | C/CAACATG                                                                     | CCGATGAAAATTCACC<br>CATC | CCATTGATAAAGCGTG<br>TACGG | 60.1                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1047_P4_43894  | scaffold1047                            | 43894                         | ATAGTTTAAAACTAGTTTAAACTAG<br>TTT/ATAGTTTAAAACTAGTTTAAAA<br>CTAGTTTAAAACTAGTTT | AACGACCAAAACAAATT<br>GCC | CGTTTCGTGGGAGACA<br>ACTC  | 59.8                             | 481                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1047_P4_461378 | scaffold1047                            | 461378                        | TTATATATATATATATATA/TTATA<br>TATATATATATATATATATA                             | TATATGCTTGACGAG<br>GCTG  | ACTCCAAAAGCACCGA<br>CAAT  | 60.0                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1047_P4_465736 | scaffold1047                            | 465736                        | CTATATATATATATAT/CTATATAT<br>ATATATATATAT                                     | AGGCAATGAGAGGGG<br>AGTT  | GCATCGCGTGTGTCA<br>CTAT   | 60.1                             | 346                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1047_P4_564264 | scaffold1047                            | 564264                        | GATATATATATATATATATATATA<br>TA/GATATATATATATATATATATA<br>TA                   | GCATGCCTCCTTTTC<br>ATTG  | GGAATTGGTGCATGAT<br>CTGA  | 60.6                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1049_P4_293719 | scaffold1049                            | 293719                        | TCC/TCCC                                                                      | CGTTTTTCAAAGCGAG<br>GGTA | GCCCTCAGATGAGAGT<br>CAGG  | 60.2                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1049_P4_293745 | scaffold1049                            | 293745                        | AAAGAAG/AAAG                                                                  | CGTTTTTCAAAGCGAG<br>GGTA | GCCCTCAGATGAGAGT<br>CAGG  | 60.2                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1049_P4_44931  | scaffold1049                            | 44931                         | CAA/CAAA                                                                      | TCACACTTCGACAGAT<br>TGCC | TAAGGGCTCCTCCAA<br>ACTT   | 59.8                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1049_P4_75199  | scaffold1049                            | 75199                         | ACC/AC                                                                        | ACGTTCTGAGGGAAT<br>TGTG  | GTAAAGGGTCACCAAC<br>CGAA  | 60.0                             | 828                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                 |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1050_P4_108877 | scaffold1050                            | 108877                        | ATTTTTTTTT/ATTTTTTTTT                                           | TATGATTGGGTGGAA<br>GCAT   | TGCACCAACAATCCCT<br>GTTA    | 60.2                             | 369                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1050_P4_28310  | scaffold1050                            | 28310                         | CTATATATATATATATATATATAT/<br>CTATATATATATATATATATATAT<br>AT     | CATGCAAATTGATGAG<br>ACGG  | TTCAATACATGTGCATC<br>CTCG   | 60.1                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1050_P4_39025  | scaffold1050                            | 39025                         | CAAAAAAAAA/CAAAAAAAAA                                           | TTGGCCAATACCTTACT<br>TCCA | TCTCTTCGCACAACGA<br>TCAC    | 59.5                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1050_P4_39371  | scaffold1050                            | 39371                         | TGCGGCGGCGGCG/TGCGGCGGC<br>GGCGGCGGCG                           | GTGATCGTTGTGCGAA<br>GAGA  | CTGAACCGAACCAAC<br>CACT     | 60.0                             | 301                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1052_P4_107001 | scaffold1052                            | 107001                        | GTATATATATATATATATATATAT<br>A/GTATATATATATATATATATATA<br>TATATA | TGACGATAAGTCATCG<br>GGGT  | TTTTGCTTTCCCGTAAC<br>CAC    | 60.3                             | 545                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1052_P4_10999  | scaffold1052                            | 10999                         | TGGG/TGG                                                        | CCACATTGTAACCCCT<br>GCCT  | AATGATCGTCTTCGGA<br>TTGG    | 59.9                             | 717                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1052_P4_16426  | scaffold1052                            | 16426                         | T/TG                                                            | CCGTTGTTTCAACTTC<br>CACC  | GCAGCAGCCATTCATA<br>CAGA    | 60.4                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1052_P4_216097 | scaffold1052                            | 216097                        | TG/T                                                            | CACGGTAGTCCCGAC<br>CTTA   | GTAAGGGGTGGGATGA<br>GGTT    | 60.0                             | 668                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1052_P4_233350 | scaffold1052                            | 233350                        | TAA/TA                                                          | TAACAAAACGCAACCG<br>ACAC  | TGTCAAGAAAACACCAT<br>GAATTG | 59.6                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1052_P4_256000 | scaffold1052                            | 256000                        | TCCCCCCC/TCCCCCCC                                               | GGTGGTGTACGGTGG<br>AAGTT  | GTCAAGGCAGACCAGA<br>AAGC    | 59.7                             | 195                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome:<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')    | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                               |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1052_P4_261508 | scaffold1052                            | 261508                        | GAAA/GAA                                                      | TTCATTTCGGGGCTTAC<br>TACG     | AGGTTTGTCTAGACCCT<br>CCCT  | 60.1                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1052_P4_303329 | scaffold1052                            | 303329                        | CAAAAAAAAA/CAAAAAAAAA                                         | ACACGTAAAATCGCAT<br>AAAATCT   | CGAAATTCGGTCAAGG<br>AAAA   | 57.1                             | 336                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1052_P4_317685 | scaffold1052                            | 317685                        | ATTTTTTTTTTT/ATTTTTTTTTTT                                     | GCACGTCATACAAAGC<br>ATCC      | GATCTTGCCTTTTGGG<br>ATCA   | 59.2                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1052_P4_327540 | scaffold1052                            | 327540                        | GTTTTTTTTTTT/GTTTTTTTTTTT                                     | TTGTAGGGATTATTTTG<br>AATGTGAA | CAGCTCCCTTCCCTTTT<br>CTT   | 58.9                             | 279                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1055_P4_16436  | scaffold1055                            | 16436                         | GTTTTTTTTTTTT/GTTTTTTTTTTTT                                   | TCAAGCCTCAAAATTG<br>GTCC      | GAATCCTGAAGGTGTT<br>GGGA   | 60.1                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1055_P4_164619 | scaffold1055                            | 164619                        | TTATATATATATATATATATATATA/T<br>TATATATATATATATATATATATATA     | GTTTAGTCCCTGCCCG<br>TTTT      | GTTGTTGGGTTGCAAA<br>GGAT   | 60.4                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1055_P4_339319 | scaffold1055                            | 339319                        | ATTTTT/ATTT                                                   | TTTAAGGTGTGGGACC<br>AAGC      | GGAACAATAAACCGA<br>GGCA    | 60.0                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1055_P4_340051 | scaffold1055                            | 340051                        | GAAAAAAAA/GAAAAAAAAA                                          | TGTTGTTCGGCATACG<br>ACAT      | TGCACATACATAATGGA<br>CCACA | 60.0                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1055_P4_340342 | scaffold1055                            | 340342                        | ATTAT/A                                                       | TGTTTCGGCATACGACA<br>TCAA     | ACATACTCCCTCACTCC<br>CCC   | 61.1                             | 820                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1055_P4_340491 | scaffold1055                            | 340491                        | T/TATC                                                        | TGCAATAAAGCTTTTGA<br>AGTGG    | ACATACTCCCTCACTCC<br>CCC   | 59.4                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)                                                       | Forward primers (5'-3') | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------|-------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                                      |                         |                           |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| scaffold1061_P4_27664  | scaffold1061                            | 27664                         | CAAA/CAA                                                                                                             | GCCAGATCTTTCGATT CAGC   | GGAACATGGCCTCAGT TGAT     | 59.9                             | 302                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1061_P4_31501  | scaffold1061                            | 31501                         | ATTTTTTTT/ATTTTTTTT                                                                                                  | TCGTTATGCAGTCAAA CCTCA  | CGTGTTTGAAATATGG CACG     | 59.3                             | 618                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1061_P4_32882  | scaffold1061                            | 32882                         | T/TC                                                                                                                 | ACTAACCATCGTTTGG CCTG   | GCAATTTTCGTACCCCT TGA     | 60.0                             | 227                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1061_P4_33010  | scaffold1061                            | 33010                         | ATT/ATTT                                                                                                             | TGCCCGGAAAGTCTAG AAGA   | TGTATTTCCGACCACA CGA      | 59.9                             | 453                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1061_P4_49764  | scaffold1061                            | 49764                         | TAAA/TAA                                                                                                             | CCTTGTCACACAGTTG GCTG   | TCTTGGTTGTAACCCCTT GGC    | 60.3                             | 150                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1061_P4_76996  | scaffold1061                            | 76996                         | CGG/CG                                                                                                               | TATTTGGACCAGAGGA TGGC   | CCCCAACAGTAGGACC AGGA     | 59.9                             | 109                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1061_P4_77938  | scaffold1061                            | 77938                         | GTTT/GTT                                                                                                             | TCAACGAAATCGATTG GACA   | TTTGCCAATGGGCTAA ACTC     | 60.0                             | 502                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1065_P4_198373 | scaffold1065                            | 198373                        | AATATATATATATATATATATATATATATATATATATATATATATAT/AATATATA TATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT | TGTGTTGCGTTGTGGA TTCT   | AACAACACATAATAAAAA CTGGCG | 60.2                             | 593                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1065_P4_86816  | scaffold1065                            | 86816                         | TAAAAAAAAAAAA/TAAAAAAAAAAAA                                                                                          | GAATCCTCCTTGGAAGCC      | TGCAATGCAATGTCCA TTTT     | 60.0                             | 199                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1067_P4_1118   | scaffold1067                            | 1118                          | ATT/ATTTTTCTT                                                                                                        | ATAAACCGGTGACCAT TGA    | TTGGAACATGCAAAAT GGA      | 60.1                             | 123                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)              | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                            |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1067_P4_117291 | scaffold1067                            | 117291                        | AATATATATATATATATATATATATATATATATAT/AAATATATATATATATATATATATATATATATATATAT | TTGCGCCACATCCTCT<br>AAAT | CAAGTTTGTGCCCCCT<br>TTTA | 60.6                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1067_P4_214494 | scaffold1067                            | 214494                        | GAGGTA/G                                                                   | GATAGGAGCATTCGGT<br>GGAA | TGACCTTAGCCCTAGG<br>CAGA | 60.0                             | 803                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1067_P4_220891 | scaffold1067                            | 220891                        | GG/GGAGCTTACG                                                              | CCAATCCGATATCCAG<br>TGCT | CTCCACCCTGGTGAAC<br>TCAT | 59.9                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1067_P4_222485 | scaffold1067                            | 222485                        | C/CGACAGGGT                                                                | AAGCAACCCAACAAC<br>AAGG  | ACTCTTAGCGAATCCC<br>AGCA | 60.0                             | 207                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1067_P4_229129 | scaffold1067                            | 229129                        | CTTTT/CTTTT                                                                | ACATGGTTCGAAACG<br>TAGG  | TCCATGCAAGAAGAGC<br>TCAA | 59.9                             | 341                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1067_P4_238607 | scaffold1067                            | 238607                        | T/TCGAC                                                                    | AGCATGCGGTATGTTA<br>AGGG | CCAACCTCCGATAGCA<br>AAAA | 60.0                             | 197                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1067_P4_238677 | scaffold1067                            | 238677                        | C/CT                                                                       | AGCATGCGGTATGTTA<br>AGGG | CCAACCTCCGATAGCA<br>AAAA | 60.0                             | 197                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1067_P4_242965 | scaffold1067                            | 242965                        | CAT/CATAT                                                                  | TTTCTTCGCTAGCCGT<br>TGTT | TCTTGTGTTGGGTAA<br>GGGC  | 60.0                             | 941                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1067_P4_243237 | scaffold1067                            | 243237                        | AGGGG/AGGGGG                                                               | TTATTGTTGTGCTTGG<br>GCA  | TCTTGTGTTGGGTAA<br>GGGC  | 60.1                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1067_P4_243320 | scaffold1067                            | 243320                        | TATCCAAAT/TATCCAAATCCAAAT                                                  | TTATTGTTGTGCTTGG<br>GCA  | TCTTGTGTTGGGTAA<br>GGGC  | 60.1                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                             | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                                           |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1067_P4_243546 | scaffold1067                            | 243546                        | GGGCTAG/GG                                                                                                                | GCCCTTAACCCAACAC<br>AAGA  | CTCCCGTTGTGGAAC<br>TATT  | 60.0                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1067_P4_243805 | scaffold1067                            | 243805                        | CAAGCCT/CAAGCCTAAAGCCT                                                                                                    | GCCCTTAACCCAACAC<br>AAGA  | AGGCGACCCTATACCG<br>AAGT | 60.0                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1067_P4_244025 | scaffold1067                            | 244025                        | A/AT                                                                                                                      | ATTAGGACGCGGGCTA<br>TCTT  | AGGCGACCCTATACCG<br>AAGT | 60.1                             | 155                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1067_P4_249436 | scaffold1067                            | 249436                        | TTCC/TTCCGTCC                                                                                                             | GATAAAGCTTTTGCGC<br>TTGG  | AGCAGTCCAACCTCTC<br>TGGA | 60.0                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1067_P4_263503 | scaffold1067                            | 263503                        | A/AGCTAGTCAGC                                                                                                             | CAGTGAGTAGCAAGCA<br>AGCG  | CCCAGCCTAGTGACAT<br>CCAT | 60.0                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1067_P4_266043 | scaffold1067                            | 266043                        | CTTTTTTT/CTTTTTTT                                                                                                         | ATCCAGAATGGAGCAA<br>CTGG  | CGGAGAAATCCGTTTT<br>GCTA | 60.1                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1067_P4_46697  | scaffold1067                            | 46697                         | TCAA/TCAAAATTTCAA                                                                                                         | GATGCAGCTGAAACCC<br>ATTT  | TTCTTGCGCCTTCTTCA<br>TCT | 60.1                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1081_P4_120686 | scaffold1081                            | 120686                        | GATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAA/GATAATAATAATAATAA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAA | TCCTACGTATCCCAA<br>GTGC   | TTGTTACATACCATCG<br>CGT  | 60.0                             | 308                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1081_P4_39164  | scaffold1081                            | 39164                         | T/TC                                                                                                                      | TTCAAATTCACCACCAT<br>TTCA | GGCCGTTGTTACTGCA<br>AAAT | 58.9                             | 774                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1081_P4_86270  | scaffold1081                            | 86270                         | GAAAAAA/GTAAAAAAA                                                                                                         | TTATTCGGGCCTGTCA<br>AAAC  | CATGCGTTCCTTGTTG<br>TAGA | 59.9                             | 251                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                         |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1081_P4_88052  | scaffold1081                            | 88052                         | TT/TTGT                                                                 | TGAGCATGGCTAAGTT<br>GCAC  | AAGGGGAAGGGCATAA<br>TGTT  | 60.0                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1082_P4_19861  | scaffold1082                            | 19861                         | TCCTAAACCT/TCCTAAACCTAAA<br>ACCT                                        | TTTGGCACTTATTGGA<br>CGAA  | GCGTTTCGGGTTTATG<br>GTTA  | 59.2                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1082_P4_20939  | scaffold1082                            | 20939                         | CCGTTAACCT/CCGTTAACCTTAA<br>TCGTTAACCT                                  | TTGGACGAAGTCAAT<br>GAAT   | GTTTAGGGTTGGGGT<br>TTGG   | 59.1                             | 372                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1083_P4_122050 | scaffold1083                            | 122050                        | C/CT                                                                    | AAGCCTAGGGAGGACG<br>AAAA  | AACGAATCATGTGCAT<br>CCAA  | 60.2                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1083_P4_44694  | scaffold1083                            | 44694                         | TG/TGG                                                                  | CCATCATCGATATTCAT<br>GCG  | GCATCCACAACCAGAA<br>ACCT  | 59.9                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1083_P4_74707  | scaffold1083                            | 74707                         | AATATATATATATATATATATATAT<br>ATATATAT/AATATATATATATATATA<br>TATATATATAT | ATCTCGGGTGCTGAAA<br>ATTG  | GGTCCCTAGCACCAT<br>AGCA   | 60.1                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1087_P4_12603  | scaffold1087                            | 12603                         | T/TTAA                                                                  | GCTTAGGCAGCCACAA<br>AATC  | CGGTTATTTGATATCAC<br>GGGT | 59.9                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1087_P4_13529  | scaffold1087                            | 13529                         | TTTTATTTATTTATTTATT/TTTTATT<br>ATTTATT                                  | TTCCGCATAACACTAA<br>GTGGC | CCATGCTAATGGATGC<br>TGTG  | 60.1                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1087_P4_14399  | scaffold1087                            | 14399                         | CGAGAGA/CGAGA                                                           | TGGGTTGTACCGTTAA<br>TTGG  | ACCCCAAATATTGCCAT<br>GAA  | 58.3                             | 810                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1087_P4_14921  | scaffold1087                            | 14921                         | TAAAAAA/TAAAAA                                                          | TTCATGGCAATATTG<br>GGGT   | AACTTGATTCTGGCCA<br>ACG   | 60.0                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1087_P4_23029  | scaffold1087                            | 23029                         | CTTTTTTTTT/CTTTTTTTT                                          | TGCACCACGAGATCTT<br>GAAA  | CGTTGATACATAACAAA<br>AATACAAACA | 60.4                             | 597                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1087_P4_23220  | scaffold1087                            | 23220                         | T/TG                                                          | TGTGGGATATCAAGTT<br>TTGGA | AAAAATGCACGGGACA<br>AATA        | 57.9                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1089_P4_12635  | scaffold1089                            | 12635                         | ACCCATATC/AC                                                  | CTCGTCGGACCATCAT<br>TTTT  | ACTCTGATGCGCTTCC<br>TGAT        | 59.9                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1089_P4_236672 | scaffold1089                            | 236672                        | GTTTT/GTTTTT                                                  | TGGTCATGCAGAACT<br>CAGC   | CGTTTTTCAAAGCGAG<br>GGTA        | 60.0                             | 768                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1089_P4_44145  | scaffold1089                            | 44145                         | ATTTTTTTTT/ATTTTTTTTTT                                        | CCCTAAAATTTTGTGG<br>GCCT  | GACTTAAGGGAGGGGC<br>TCAG        | 60.2                             | 286                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1092_P4_121415 | scaffold1092                            | 121415                        | AT/A                                                          | AGGTCATTTTCGTCCT<br>CCCT  | AATCCAATGGCACAAA<br>CACA        | 59.9                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1092_P4_139231 | scaffold1092                            | 139231                        | GTTT/GTTTT                                                    | TCCTCGCCAGGCTTAT<br>TCTA  | ATCCAACGACACGAAG<br>GAAC        | 59.9                             | 281                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1092_P4_146775 | scaffold1092                            | 146775                        | GTTT/GTT                                                      | CTTCCTCCCTCGGCTT<br>ATTC  | AGGGAGGACGAAAATG<br>ACCT        | 60.2                             | 365                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1092_P4_65384  | scaffold1092                            | 65384                         | GTTTTTTTT/GTTTTTTT                                            | AACCAATCTTGTGCAT<br>CCAA  | AACCCTAGGGAGGACG<br>AAAA        | 59.0                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1092_P4_83003  | scaffold1092                            | 83003                         | GTTTTT/GTTTTT                                                 | TAACCAATCTTGTGCG<br>TCCA  | AATAGGCCTAGGGAGG<br>ACGA        | 60.1                             | 280                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)              | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                             |                           |                           |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| scaffold1101_P4_3795  | scaffold1101                            | 3795                          | TCC/TC                                                                      | TTGGCTCATGCTTGA<br>GTTG   | AGCCAAGGGAGGATGA<br>AAAT  | 60.0                             | 214                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1101_P4_660   | scaffold1101                            | 660                           | C/CTTG                                                                      | TAACCAATCTTGTCG<br>GTCA   | CCAAGGAAGGACGAAA<br>ATGA  | 60.1                             | 372                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1107_P4_3745  | scaffold1107                            | 3745                          | CATATATATATATATATATATATA<br>TATATATATAT/CATATATATATATAT<br>ATATATATATATATAT | CAGCACATAGTAAAC<br>TTGGCG | GGACATTGTCATGAT<br>TTTGAA | 59.8                             | 335                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1107_P4_5288  | scaffold1107                            | 5288                          | TAA/TAAAAATAAAAA                                                            | TTGAATCGACACTCAA<br>CCCA  | AGTTTGGAAGGAACCC<br>CACT  | 60.1                             | 407                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1109_P4_14028 | scaffold1109                            | 14028                         | ATTTTTTTTTTTTT/ATTTTTTTTT                                                   | TTTGAAAACCTCACCA<br>GGG   | TAAACTGTCAGGGCG<br>AAGA   | 59.9                             | 416                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1109_P4_14081 | scaffold1109                            | 14081                         | GTT/GTTAATT                                                                 | TTTGAAAACCTCACCA<br>GGG   | TATAAACTGTCAGGGG<br>CGAA  | 59.9                             | 418                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1109_P4_17585 | scaffold1109                            | 17585                         | CTATATATATATATATATATATAT<br>AT/CTATATATATATATATATATAT<br>AT                 | TTTGGGAGGAACACTG<br>CTCT  | TCTTCCCCTTGATGTT<br>CTG   | 59.8                             | 792                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1109_P4_54372 | scaffold1109                            | 54372                         | TAAAAAAAA/TAAAAAAAA                                                         | AAGAGCACACCAATCC<br>TCTCA | ATCATCTTTGGATGCAA<br>GCC  | 59.9                             | 583                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1109_P4_97926 | scaffold1109                            | 97926                         | G/GGGAAAGAGACAT                                                             | TGGGTAGACTTGCGAG<br>ATGA  | TCTCTTCCCCTTCCCAT<br>TCT  | 59.4                             | 247                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1115_P4_49928 | scaffold1115                            | 49928                         | TA/TAA                                                                      | TCGCGAAAACCTTGCA<br>ATTA  | CCACTGTCCCATTTCAT<br>CCTT | 59.5                             | 805                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')        | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|--------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                   |                                |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1116_P4_118274 | scaffold1116                            | 118274                        | AATAT/AAT                                                         | TGCAGTCAAACCTTTAAC<br>AAGAAGAT | TTTGACAACCTCAATTT<br>GTTCTATTT | 58.6                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1116_P4_42811  | scaffold1116                            | 42811                         | TC/TCC                                                            | GATGAAACCGAGGACC<br>AAGA       | GTGTTTTCGGACCAGA<br>CGAT       | 60.1                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1116_P4_94918  | scaffold1116                            | 94918                         | TATAATAATAATA/TATAATAATAATA<br>ATA                                | TCTTCGTTATGCAGTC<br>AAACCT     | ACCCAACAAAAATGGA<br>CCAA       | 58.9                             | 728                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1118_P4_29890  | scaffold1118                            | 29890                         | GCTTCTTCTTCTTCTTCTTCTTC<br>TTC/GCTTCTTCTTCTTCTTCTTC<br>CTTCTTCTTC | AACGTTCTCCGTTTGT<br>AGCG       | TTTGAGACCAATGGT<br>GACA        | 60.3                             | 752                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1118_P4_34583  | scaffold1118                            | 34583                         | AATTATTATTATTATTATTATT/A<br>ATTATTATTATTATTATTATT                 | CGGGTTGAGTTGTTGT<br>TCCT       | TTGGTTTCAAGAAGGA<br>TGCC       | 60.0                             | 721                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1120_P4_44664  | scaffold1120                            | 44664                         | TCC/TC                                                            | AACCAATCTTGTCAT<br>CCAA        | AGGGACAAGAAAATG<br>GCCT        | 59.0                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1128_P4_108693 | scaffold1128                            | 108693                        | ATTTTTTT/ATTTTTTTT                                                | GGTCCATGGAAAATTG<br>GTTG       | TTGCGAGGCTGAATCT<br>TCTT       | 60.0                             | 836                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1128_P4_163033 | scaffold1128                            | 163033                        | CTTTTTTTTTTT/CTTTTTTTTTTTT                                        | TTTGCACTTCAGACGC<br>AAAG       | TCTAAATGCAAGAGCG<br>GATG       | 60.2                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1128_P4_179315 | scaffold1128                            | 179315                        | CTTT/CTT                                                          | TTGGACAGTGGTTGCT<br>CAAG       | CCCATGGTCACTTCTC<br>ACCT       | 59.9                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1128_P4_240075 | scaffold1128                            | 240075                        | ANNNNNNNNN/AAAACCTCCTTCC<br>CTNNNNNNNNNN                          | CCTCAGTGCCAAGAAG<br>GGTA       | GGGGCATCCTATAAGG<br>GGTA       | 60.2                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                      | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                                                    |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1128_P4_252712 | scaffold1128                            | 252712                        | TA/TAA                                                                                                                             | AGTTTGTGCGAAAGTCC<br>CCCT | ATTGCAACCAACTCTCC<br>CAC    | 60.0                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1128_P4_261287 | scaffold1128                            | 261287                        | AG/A                                                                                                                               | CCACTGGTGCTTTTCC<br>TTTC  | TGGGATCTTGTACCCA<br>AACC    | 59.7                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1128_P4_307507 | scaffold1128                            | 307507                        | CTTTTTTTTTTTTT/CTTTTTTTTTTT<br>TT                                                                                                  | GCAAATGCTAACACGA<br>GCAA  | CGTGGTGGAGTGAGAC<br>TGAA    | 60.0                             | 799                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1128_P4_420723 | scaffold1128                            | 420723                        | ATT/ATTTTT                                                                                                                         | TTCCATTGCCTTCATC<br>TTC   | TGGGCTATTTGATTG<br>GATT     | 60.0                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1128_P4_4291   | scaffold1128                            | 4291                          | CAAAAAAAAA/CAAAAAAAAA<br>AAA                                                                                                       | AAATGGCCACCCCTCT<br>TCTT  | CGAATAAGTCGTTGCT<br>GCAA    | 59.9                             | 276                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1128_P4_441123 | scaffold1128                            | 441123                        | TAAAAAAAA/TAAAAAAAA                                                                                                                | CATGGCAAACTTGAA<br>GCAA   | TCAAGCGTCACAACT<br>CACA     | 59.8                             | 373                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1128_P4_45001  | scaffold1128                            | 45001                         | CAAAAAAAAA/CAAAAAAAAA<br>ATGC                                                                                                      | ATGGGAAGGAACA<br>ATGC     | CACAAAATTAACCCAA<br>ATTGACA | 59.8                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1131_P4_125249 | scaffold1131                            | 125249                        | GTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>A/GTTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTA | TGTAGGCAGGAAGCGC<br>TAAT  | AGGTGGGAATTCTTA<br>GGTG     | 60.0                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1131_P4_153716 | scaffold1131                            | 153716                        | CATATATATATATATATATAT/CATAT<br>ATATATATATATAT                                                                                      | TCATGTGTTTGATTG<br>CACAT  | GGCACGTTTAATCGAC<br>ATGA    | 60.0                             | 754                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1131_P4_30056  | scaffold1131                            | 30056                         | AG/AGG                                                                                                                             | AGTCGGTACAACCA<br>TCCC    | TGTGGTGTTCTTGGTG<br>GAGA    | 59.7                             | 701                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                     | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                   |                            |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1131_P4_39565 | scaffold1131                            | 39565                         | TT/TTTAAAT                                                                                        | TGTCAAGCAGAGATCA<br>ATGTCA | ATTAATTGGGTGCGCG<br>AATA      | 59.4                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1131_P4_39818 | scaffold1131                            | 39818                         | TTATATATATATATATATATATATA<br>TATA/TTATATATATATATATATAT<br>ATATATATATATATATATA                     | TACGTGTATATTCGCG<br>CACC   | CAGCAGCTGTCGTGTC<br>GTAT      | 59.6                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1134_P4_22100 | scaffold1134                            | 22100                         | TAAAAAAAAA/TAAAAAAAAA                                                                             | TTTACAGCGCTTTG<br>GACA     | TGGAGATGATTGCAA<br>TGGA       | 59.5                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1134_P4_30212 | scaffold1134                            | 30212                         | AAATAATAATAATAATAATAATA<br>ATAATAATAATGATAATAATAA/A<br>AATAATAATAATAATAATAATAA<br>TGATAATAATAATAA | AACTAACTACCCAAA<br>CGGG    | TTGAGAAGTGGGTTTC<br>TTTGC     | 59.0                             | 901                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1134_P4_7572  | scaffold1134                            | 7572                          | CTTTT/CTTTT                                                                                       | TTGCAGAGATTACGT<br>TGCG    | TTACCCTCAAACCTGG<br>GGTG      | 60.0                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1135_P4_47902 | scaffold1135                            | 47902                         | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATATAT                                             | TGCTTTGAACTATTTT<br>TGCG   | CATCCATTTTGACATGA<br>CCG      | 58.2                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1135_P4_67023 | scaffold1135                            | 67023                         | TAAAAAAAAA/TAAAAAAAAA                                                                             | TTTTGCCATGTGTATGA<br>ATTG  | TCAAGTATGAATCACG<br>GCTGA     | 57.0                             | 773                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1135_P4_68800 | scaffold1135                            | 68800                         | TTAAACCCTAAACCCTAAACCCTAA<br>ACCCTAAACCCTAA/TTAAACCCTAA<br>ACCCTAAACCCTAA                         | ACCCTTAACCATAACC<br>CCGA   | GGTTTAGGGTTTTCG<br>GTTC       | 60.4                             | 719                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1135_P4_72246 | scaffold1135                            | 72246                         | ACTT/ACTTCTT                                                                                      | AAACCGAAAACCGAAA<br>ACCT   | CAATGTAGTTTGCTAA<br>GAAGTGCAA | 59.9                             | 667                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1135_P4_74988 | scaffold1135                            | 74988                         | TCTAAACCCTAAACCCTAA/TCTAA<br>CCCTAAACCCTAAACCCTAA                                                 | ACCCAAACCCTTAACC<br>TTCC   | CGGTTCCGGTTTATGG<br>TTTA      | 59.2                             | 291                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1135_P4_9704  | scaffold1135                            | 9704                          | GTTTGTGCT/GT                                                  | TTTCGGTTGGGTTTGC<br>TTAC  | TACCCGTGCTCAACAT<br>CAAG  | 60.0                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1139_P4_1257  | scaffold1139                            | 1257                          | CT/CTTT                                                       | TCTCAAACGGAGCGGT<br>AATC  | AAACTCCACATGGATG<br>GGTC  | 60.2                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1139_P4_1393  | scaffold1139                            | 1393                          | CT/CTTT                                                       | TCATCCAGTGTGGGT<br>ACAA   | TTGTGTGTGTGGAGA<br>TGAGC  | 59.8                             | 313                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1139_P4_1605  | scaffold1139                            | 1605                          | TAACAACAA/TAACAACAACAA                                        | TCATCCAGTGTGGGT<br>ACAA   | TTTGAGAATTTGGGAT<br>GGAAA | 59.8                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1142_P4_4296  | scaffold1142                            | 4296                          | T/TGA                                                         | AGGTCATTTTCGTCCT<br>CCCT  | TTGCATGCACAAGATT<br>GGTT  | 59.9                             | 268                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1145_P4_15770 | scaffold1145                            | 15770                         | ATATTATTATTATTATTATTA/AT<br>ATTATTATTATTATTA                  | TGGCACAACATCATCA<br>TCATT | GCGCATTCTTCATCTTC<br>TCC  | 59.8                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1145_P4_16263 | scaffold1145                            | 16263                         | CAAA/CA                                                       | GAGAAGATGAAGAATG<br>CGCC  | GTTACACCGGTGGTAG<br>CGTT  | 59.9                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1145_P4_16689 | scaffold1145                            | 16689                         | AAAGTAAATAAGTAAAA/AAAGTAA<br>AATAAGTAAATAAGTAAAA              | GGCCAAATGCCAAATC<br>TCTA  | TAGGAAAAGGGAAACC<br>CACC  | 60.0                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1145_P4_2304  | scaffold1145                            | 2304                          | GACGTTT/G                                                     | ATTCCCTAAGGCCGTG<br>AACT  | AGGTCTCCAAGACATG<br>GTGG  | 60.0                             | 467                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1145_P4_2640  | scaffold1145                            | 2640                          | TGGGG/TGGGGG                                                  | TTGTGTTTGACGTTTG<br>CGAT  | TCTGGCCATTATGTGTT<br>TGC  | 60.2                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |



[illegible]

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                  | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1159_P4_27402  | scaffold1159                            | 27402                         | TG/TGG                                                                         | AGGGAGGACGAAATG<br>ACCT   | CCTTCCTGGCTTGT<br>CTTG    | 59.9                             | 345                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1161_P4_1009   | scaffold1161                            | 1009                          | TA/T                                                                           | CGTAAAGGATTCACCG<br>CACT  | TTGATTGGGATTTTGC<br>CTC   | 60.1                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1174_P4_23485  | scaffold1174                            | 23485                         | GTTTTTT/GTTTTTTT                                                               | TTGTGCCTCCAATAGG<br>TG TG | AGGGAGGACGAAATG<br>ACCT   | 59.6                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1177_P4_777    | scaffold1177                            | 777                           | A/AT                                                                           | GCATTTTGCCTTTCCA<br>GAAG  | CGCAGATTGATCTTGA<br>AGCA  | 59.8                             | 736                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold118_P4_102911  | scaffold118                             | 102911                        | AATAATTATAATTATAATTATAATTAT<br>AATTATA/AATAATTATAATTATAATT<br>ATAATTATA        | TAATGGACACACGCC<br>TGTA   | GTCGTGCCATAAATAG<br>CCGT  | 60.0                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold118_P4_129054  | scaffold118                             | 129054                        | CAAAAAAAAA/CAAAAAAAAA                                                          | AGGGAGGTGCGCTAG<br>ATGAT  | TGAGGACTGGACGTAG<br>CCTT  | 60.1                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold118_P4_173557  | scaffold118                             | 173557                        | TTATATATATATATATA/TTATATATA<br>TATATATATA                                      | TGTCATGCTAATATCC<br>GCCA  | TGGATGGATTCTAGTT<br>GCCTT | 60.1                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold118_P4_188968  | scaffold118                             | 188968                        | A/AC                                                                           | AATAGGGGTGCAACA<br>GTCG   | GGTGTGCAAGGGAT<br>CTGT    | 60.0                             | 731                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold118_P4_63279   | scaffold118                             | 63279                         | GAATAATAATAATAATAATAATA<br>ATAATAATAATAA/GAATAATAATAAT<br>AATAATAATAATAATAATAA | TTAAAGCAACCCAATG<br>AGCA  | TGAGTGGAGACCTGA<br>GGATG  | 59.3                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1180_P4_135497 | scaffold1180                            | 135497                        | GTTTTTTT/GTTTTTTTTT                                                            | TTGTGTGCGTTTGACT<br>GACA  | AAGCGGAGAAGTCGGA<br>GATT  | 59.9                             | 789                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1180_P4_157703 | scaffold1180                            | 157703                        | TTC/T                                                         | TGGGGTTTAGGGTGTG<br>ACAT    | TGGTTAAGGGTGAAAG<br>TCGAA  | 60.1                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1180_P4_18808  | scaffold1180                            | 18808                         | GTATATAT/GTATATATAT                                           | GCAACTTAGGACCACC<br>TATGG   | AAACTTTTACCCCTTC<br>TCCA   | 58.6                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1180_P4_206096 | scaffold1180                            | 206096                        | AATATATATATATATATA/AATATATA<br>TATATATATATA                   | CCATGTGGTTCCTTTG<br>CATTT   | AACTTCGCCATTTGTCA<br>TCC   | 59.9                             | 548                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1180_P4_208476 | scaffold1180                            | 208476                        | TA/T                                                          | TAAGAGGGGCTTGTTA<br>CCCC    | CCAACCTAATATTCATG<br>CCACA | 60.3                             | 216                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1180_P4_215411 | scaffold1180                            | 215411                        | TCAAAAACAAAAACAAAA/TCAAAA<br>ACAAAAACAAAAACAAAA               | GGGAGAAACCCCATTC<br>TGAT    | CAAAACACAACCGACA<br>CGAC   | 60.1                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1180_P4_215596 | scaffold1180                            | 215596                        | ATTTTTTT/ATTTTTTT                                             | TCGTGTCGGTTGTGTT<br>TTGT    | TCATGCTATGATCCCAA<br>AAGG  | 60.0                             | 390                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1180_P4_226315 | scaffold1180                            | 226315                        | GTCCATTC/GTC                                                  | TGGGGTTTAGGGTGTG<br>ACAT    | AACCGGCACGACTAAC<br>ATTC   | 60.1                             | 101                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1180_P4_226418 | scaffold1180                            | 226418                        | ATTTTT/ATTTTT                                                 | GAATGTTAGTCGTGCC<br>GGTT    | TTTTGGGGTTTAGGGT<br>GTCA   | 60.0                             | 255                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1180_P4_227912 | scaffold1180                            | 227912                        | ATATAT/ATATATTATAT                                            | TTGATGATATTGTGTT<br>GATTTCG | GTTTGGCGTTGGTTT<br>CACT    | 58.9                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1180_P4_2599   | scaffold1180                            | 2599                          | ATT/ATTTT                                                     | GAGAGGTCATGGCACC<br>CTTA    | GAGCAACACATTGCAT<br>GTCC   | 60.1                             | 166                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                    | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                                                                                  |                          |                              |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1180_P4_2913   | scaffold1180                            | 2913                          | A/AC                                                                                                                                                             | GAGAGGTCATGGCACC<br>CTTA | TCTTGCCCAACGTTTTA<br>CAT     | 60.1                             | 513                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1180_P4_3279   | scaffold1180                            | 3279                          | GAT/GATAT                                                                                                                                                        | ACACATGTAAACGTT<br>GGGC  | GTACATGCAAATGACC<br>GCAC     | 58.4                             | 573                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1180_P4_3744   | scaffold1180                            | 3744                          | GA/G                                                                                                                                                             | GTGCACGAAAGTGTGG<br>CTTA | ACTTACCATTGCCTTC<br>CCC      | 59.9                             | 766                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1180_P4_39031  | scaffold1180                            | 39031                         | TAAAAAAAAA/TAAAAAAAAA                                                                                                                                            | AGGGAACAAACCGAA<br>CTGA  | AATGTGCCCTTTTGATAA<br>AAACCT | 59.6                             | 459                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1181_P4_11225  | scaffold1181                            | 11225                         | CTT/CT                                                                                                                                                           | CCATAAACCTGAACCC<br>CAAA | AAGGGTTAAGGGTCTA<br>CGTCA    | 59.7                             | 381                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1181_P4_5941   | scaffold1181                            | 5941                          | TAACCCTAAACCCTAAACCCTAAAC<br>CCTAAACTCTATACCCTAAACCCTA<br>TACCCTAAACCCTAAACCCTAAA/TA<br>ACCCTAAACCCTAAACCCTAAACTC<br>TATACCCTAAACCCTATACCCTAAA<br>CCCTAAACCCTAAA | AAACCCTAAATCCCAAA<br>CCC | TTTAGGTCATTTTGGCC<br>TTTTT   | 59.0                             | 465                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1183_P4_109517 | scaffold1183                            | 109517                        | TAAAAAAAAA/TAAAAAAAAA                                                                                                                                            | TTCCATGGTGAGAACG<br>ATGA | CCCAAAAGCTCACAGC<br>TAGG     | 60.0                             | 450                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1183_P4_131590 | scaffold1183                            | 131590                        | AATATATATATATATATATATATAT<br>ATATAT/AATATATATATATATATA<br>TATATATATATATAT                                                                                        | GAAATGGGTTTCGCGT<br>AGAG | TTTGGCTCGAAGGCTT<br>TTTA     | 59.7                             | 428                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1183_P4_142757 | scaffold1183                            | 142757                        | TAAAAAAAAA/TAAAAAAAAA                                                                                                                                            | TCAAATCCATTGGTCC<br>CTTT | AAAGATGCATTTGCCA<br>GGAC     | 59.2                             | 916                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1183_P4_148521 | scaffold1183                            | 148521                        | CTTTTTTTT/CTTTTTTTTT                                                                                                                                             | CCGAGTTATGGCCACT<br>GTTT | CCATCTAAATCGCCTTT<br>CCA     | 60.0                             | 395                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1183_P4_151980 | scaffold1183                            | 151980                        | ATTTTTTTTT/ATTTTTTTTT                                         | TGCCCATTTAAACTTG<br>GGT     | ACAATTGTCATGCGG<br>TCCT   | 59.3                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1183_P4_67473  | scaffold1183                            | 67473                         | GTTTTTTTTT/GTTTTTTTTT                                         | GGAGAGCGTGGAGAT<br>CACTC    | CCATGTCACGTGCAAAAT<br>TCG | 60.0                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1183_P4_76123  | scaffold1183                            | 76123                         | ATTT/ATT                                                      | TCTCCCTCCTTCCTCC<br>ATT     | CTCATTCTCAACGCC<br>AGTT   | 60.0                             | 793                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1185_P4_134184 | scaffold1185                            | 134184                        | TAAA/TAA                                                      | CATCTCGTCGGTCATC<br>ATTG    | CAAAACATCCACACTTG<br>GCA  | 60.1                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1185_P4_39023  | scaffold1185                            | 39023                         | G/GA                                                          | GTTTTGGCGTTGGTT<br>CACT     | TGGAAACTAAATGGT<br>GTTTGG | 60.0                             | 292                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1185_P4_47365  | scaffold1185                            | 47365                         | AAATAATAATAATAATAATA<br>ATA/AAATAATAATAATAATA<br>ATA          | TTCTTATAGGCATGAT<br>TTCTTGA | TCGTTTTGGTGTTGGT<br>TTCA  | 59.2                             | 809                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1185_P4_6345   | scaffold1185                            | 6345                          | CAAAAA/CAAAAA                                                 | TGAATGCGAACCTAGT<br>GTGG    | TAAAGGACCAACTCGG<br>GAAA  | 59.7                             | 745                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1185_P4_67322  | scaffold1185                            | 67322                         | GATATATATATAT/GATATATATAT                                     | CAATTCCACAGGTAC<br>GCTT     | GACGCGAAACAACAT<br>TTCA   | 60.0                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1185_P4_67468  | scaffold1185                            | 67468                         | T/TAGGGTGA                                                    | CAATTCCACAGGTAC<br>GCTT     | GACGCGAAACAACAT<br>TTCA   | 60.0                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1185_P4_85313  | scaffold1185                            | 85313                         | TGG/TG                                                        | GAAATTCCTGGAAGCC<br>AACA    | GTCGAGGCCTAATGTG<br>GAAA  | 60.1                             | 956                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)                                    | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                          |                                  | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------|----------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                   |                            |                           |                                  |                                               | Sequence components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | Tfs |
| scaffold119_P4_18026   | scaffold119                             | 18026                         | ATTTTTTTTT/ATTTTTTTTTT                                                                            | AAATGACGCCTTCAT<br>TCAC    | ATGGAGTGATGCCTTT<br>ACCG  | 59.9                             | 677                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold119_P4_35751   | scaffold119                             | 35751                         | A/AG                                                                                              | ACTCATATGCCAAAATG<br>CCCC  | TTATGCTGGAGATGGG<br>AAGG  | 59.8                             | 444                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold119_P4_60762   | scaffold119                             | 60762                         | TTATATATATATATATATATATATA<br>TATATATAT/TTATATATATATATATA<br>TATATATATATATATATATATATATAT           | GTA AAAATGAAGCGCTT<br>TCGC | AATCGATTGGCTGAAA<br>TCCA  | 60.0                             | 611                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold1193_P4_153525 | scaffold1193                            | 153525                        | CATATATATATATATATATATATA<br>TATATAT/CATATATATATATATAT                                             | TATTTTGGATTTTGGCT<br>CGG   | GTTGGTCCCTAGCAC<br>CGTA   | 59.9                             | 661                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold1193_P4_241608 | scaffold1193                            | 241608                        | CAA/CA                                                                                            | AAAGAAAGGGAGTTGG<br>ACGG   | CACACGAATACGATT<br>CACG   | 60.5                             | 401                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold1193_P4_51363  | scaffold1193                            | 51363                         | CTATTATTATTATTATTATTATTATTA<br>TTATTATTA/CTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATTATT<br>ATTA | ATACACGCAAAATCGC<br>ATGA   | TGCCAAACTACCTTCC<br>CATC  | 60.1                             | 351                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold1193_P4_7288   | scaffold1193                            | 7288                          | TCAA/TCAATTTAAGCAA                                                                                | AATGCTTTCAGAAAA<br>CCGA    | TGATCTGATGGCTGAC<br>TTTCA | 59.7                             | 367                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold1195_P4_21554  | scaffold1195                            | 21554                         | CTTATTATTATTATTATTATTATTATT<br>/CTTATTATTATTATTATTATTATT                                          | AAGGGTGCAACCGTAT<br>TGAG   | GAAAGGCTCAAACGAC<br>CAAA  | 60.0                             | 594                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold1195_P4_35553  | scaffold1195                            | 35553                         | TAAAAAAAAA/TAAAAAAAAAAAAA<br>AAA                                                                  | CGATTGGGAAATCGAT<br>TGAA   | AGTCTGTACAATCCAA<br>ACGG  | 60.8                             | 972                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold1195_P4_63610  | scaffold1195                            | 63610                         | AG/A                                                                                              | CTACACAGGTGGGGGA<br>AAAA   | CCCAATTATCAGGCAA<br>GGAA  | 59.8                             | 586                                           | INTERGENIC                                     | --                               | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                         | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                       |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1196_P4_103885 | scaffold1196                            | 103885                        | GAAAAAA/GAAAAA                                                                        | CAACTTGTTTCACCG<br>ACCT   | GGATTGTGGACAAGG<br>GAGA  | 60.0                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1196_P4_112009 | scaffold1196                            | 112009                        | AGGGGGGG/AGGGGGG                                                                      | GTTCTCCCTTCCATCG<br>TTCA  | TGTTAGGTGTTTGGT<br>GGCA  | 60.1                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1196_P4_113608 | scaffold1196                            | 113608                        | TGGGGGGGG/TGGGGGGG                                                                    | AGATACCAGATGCTGG<br>TGGG  | GCCATGCCTCTAACT<br>CTGC  | 60.0                             | 358                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1196_P4_117323 | scaffold1196                            | 117323                        | ATTTTTTTTTT/ATTTTTTTTTT                                                               | TGGACTTTGCTTTCTG<br>TTTGG | GTGCCCAACAACACT<br>TGAA  | 60.3                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1196_P4_129715 | scaffold1196                            | 129715                        | AACT/A                                                                                | ACCTATGAATCCCCCT<br>CACC  | AATGTCACAACAAGGC<br>TCCC | 60.0                             | 752                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1196_P4_27427  | scaffold1196                            | 27427                         | AATATATATATATAT/AATATATATAT<br>ATATATAT                                               | ATGTTTTGGATTTTGG<br>CTCG  | GGGGGAGGAAGAAGAT<br>GAAG | 59.9                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1196_P4_70371  | scaffold1196                            | 70371                         | GAAAAAAAAA/GAAAAAAAAA                                                                 | TTCGCAACTCCACTCTT<br>CCT  | ACCGTTGTTATTCTGC<br>GGTC | 60.0                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1197_P4_10258  | scaffold1197                            | 10258                         | AC/A                                                                                  | CGTTCTTGATCGGGAT<br>TGAT  | GATATGGTTCGCCAG<br>AAAA  | 59.9                             | 390                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1197_P4_160011 | scaffold1197                            | 160011                        | ATTTT/ATT                                                                             | GCAGTTTTGGTCCCC<br>TATT   | GGTACAATTGTTGCAC<br>CACG | 60.2                             | 175                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1197_P4_185392 | scaffold1197                            | 185392                        | TTCTCTCTCTCTCTCTCTCTCTCTCT<br>TTCTCTCTCTCTC/TTCTCTCTCTCT<br>CTCTCTCTCTCTTTCTCTCTCTCTC | CGACCCTCATGAACCT<br>CAAT  | TTGAGACCGGGTTTAG<br>GATG | 59.9                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1197_P4_191244 | scaffold1197                            | 191244                        | TAT/TATGACTTGCATCAT                                           | GGCATCCCTATGCAAA<br>ACAT  | TCCTTCATCTCCTGG<br>GTTG   | 59.8                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1197_P4_244871 | scaffold1197                            | 244871                        | ATGTT/ATGTTGTT                                                | CAAAGTCAGTTTCATC<br>GCCA  | ACTGTGATCCGGTGAT<br>TTGA  | 59.8                             | 625                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1197_P4_244953 | scaffold1197                            | 244953                        | TAAAAAAA/TAAAAAAA                                             | CACTTTTTGTTTCATCG<br>CCA  | ACTGTGATCCGGTGAT<br>TTGA  | 59.7                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1197_P4_26213  | scaffold1197                            | 26213                         | TA/TAATTAA                                                    | AAATGGCGTCTCAATT<br>CCAC  | CCCACGTAAC TAGCG<br>TTACA | 59.9                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1197_P4_5120   | scaffold1197                            | 5120                          | GT/GTT                                                        | TCGCAGCTCAATTGGT<br>AGTG  | GAGAGCTACCGTGCAA<br>CACA  | 60.0                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1197_P4_540966 | scaffold1197                            | 540966                        | ACCC/ACC                                                      | TAAGTGGGCGTTAAGA<br>ACGG  | TTGAGGGACATATTTTG<br>GGC  | 60.1                             | 901                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1197_P4_58275  | scaffold1197                            | 58275                         | TCATGTAGACAT/TCAT                                             | TGAAATAATTATCCACC<br>GGCA | GGCAACATGGAAATGG<br>AGTT  | 60.2                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1197_P4_75749  | scaffold1197                            | 75749                         | TTTATTATTATTATTATTATTAT<br>AT/TTTATTATTATTATTATTAT            | TAACCCAAAAATCCAA<br>CCA   | TGGATCGCATAACTCC<br>ATGA  | 60.0                             | 396                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold12_P4_144965   | scaffold12                              | 144965                        | TTATATATATATATATATATATATA<br>/TTATATATATATATATATATATA         | TAAATTGGCTCAAAAG<br>GCCA  | TTCCCTCCTGACACTTC<br>TCG  | 60.6                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold12_P4_16589    | scaffold12                              | 16589                         | TTATATATAT/TTATATATATAT                                       | AGTTTTGCAATCACGT<br>GCAG  | GGTGCACAAAAC TGCT<br>CCTA | 59.9                             | 214                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold12_P4_16684   | scaffold12                              | 16684                         | AAATTGTTTTCAATTGTTTC/AAATT<br>GTTTTTC                         | AGTTTTGCAATCACGT<br>GCAG    | AAGCTGCATCTCAACC<br>TCGT   | 59.9                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold12_P4_185430  | scaffold12                              | 185430                        | CAC/CACAGAC                                                   | TCCAATCAAACCCTTC<br>TCG     | GCATTTTCATTGTACATG<br>GCG  | 60.0                             | 314                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold12_P4_279489  | scaffold12                              | 279489                        | ATTTTTTTTT/ATTTTTTTTTT                                        | AAGACGAAGCTGGACA<br>AGGA    | ATCTCCCCCTTTTTCGAC<br>GAT  | 60.0                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold12_P4_296676  | scaffold12                              | 296676                        | ATT/ATTT                                                      | GGAACCAAGACTTTGG<br>GTGA    | CCAATACTTGCCTGGG<br>AACT   | 59.9                             | 715                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold12_P4_58042   | scaffold12                              | 58042                         | TA/T                                                          | GTGAAAGCGCTGTAAA<br>AGGC    | TCTTGGAGGTGCCAAC<br>TTCT   | 60.0                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1202_P4_25847 | scaffold1202                            | 25847                         | CTTTTTCTTTTTTTTC/CTTTTTCTT<br>TTTTTTCTTTTTTTTTC               | TTGTCCACAGTGGCAT<br>ATTGA   | TGGCAGATATGGGGT<br>GTAT    | 60.0                             | 737                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1202_P4_54722 | scaffold1202                            | 54722                         | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATAT         | GCACCGTAGCAATGGT<br>ACAAA   | TGGCGGCTGAAAACCTC<br>TAAT  | 60.9                             | 298                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1202_P4_82238 | scaffold1202                            | 82238                         | AATATATATATATATA/AATATATATA<br>TATATATA                       | AACACATCCGGTTCC<br>ATTA     | TTTGATCCATTTGCCCT<br>AGC   | 60.1                             | 739                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1202_P4_83479 | scaffold1202                            | 83479                         | GTATATATATATATAT/GTATATAT<br>ATATATAT                         | ACGGTGTAGGCAAGAT<br>GGAC    | AGGATGCATGGGATGA<br>AAAG   | 60.0                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1210_P4_576   | scaffold1210                            | 576                           | GTTTTTTTTT/GTTTTTTTTT                                         | GAAGTGTCTGAGTCAT<br>TTACGGC | TTTAGTGCCTCGTTAAT<br>TTCAA | 60.2                             | 240                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)  | Forward primers (5'-3')      | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------|------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                |                              |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1215_P4_12684 | scaffold1215                            | 12684                         | TAAAAAAAAA/TAAAAAAAAAAAAA                                      | TCTCTCCGATTGGT<br>CATT       | TTTGCTCCTCTTCTCT<br>GGC       | 59.5                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1215_P4_13648 | scaffold1215                            | 13648                         | TAAAAAA/TAAAAA                                                 | TCGTGGGACTAAAAC<br>GAGGA     | CGCACATATGAATGAT<br>CCCA      | 59.7                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1215_P4_14063 | scaffold1215                            | 14063                         | GGGATCAT/G                                                     | AATTGAAGGAAGATGG<br>AAAACA   | ACAAACTGGAGGGCAA<br>CAAC      | 57.7                             | 822                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1215_P4_45663 | scaffold1215                            | 45663                         | ATT/ATTT                                                       | TGGCTTTTGATTTTCAG<br>AGTTGG  | AGTGGGACCATGATTT<br>TTGAA     | 60.5                             | 492                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1215_P4_45939 | scaffold1215                            | 45939                         | ATTTT/ATTT                                                     | TTTCAAAAATCATGGTC<br>CCAC    | GGGGTGGTGTCTATCT<br>TTGC      | 59.7                             | 337                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1216_P4_15555 | scaffold1216                            | 15555                         | TAAAAAAAAA/TAAAAAAAAA                                          | AGGGAGGACGAAAATG<br>ACCT     | ACCGATCTTGTGCATC<br>CAAT      | 59.9                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1219_P4_16394 | scaffold1219                            | 16394                         | ATTTTTTT/ATTTTTTTTT                                            | GGCCGAAAAGGTGATC<br>AGTA     | TGAAACTCAACATTGTG<br>GGAA     | 60.1                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1219_P4_23613 | scaffold1219                            | 23613                         | TTATATATATATATATATATATATAT<br>T/TTATATATATATATATATATATATA<br>T | CCCCGCTCTGATAGGT<br>GATA     | TGCCAAATTGATTTTCG<br>TAAT     | 60.1                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1219_P4_40006 | scaffold1219                            | 40006                         | GTATATATATATATATAT/GTATATAT<br>ATATATAT                        | TGGTTAATGTTGGCA<br>AATGG     | ATCCAGTTGGTGAGGA<br>AAAA      | 60.6                             | 317                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1219_P4_44692 | scaffold1219                            | 44692                         | ATTTTTTTTT/ATTTTTTTTT                                          | TGAAGCTGGGGTATTA<br>AACTTACC | AAACATTAGTCCCTCGT<br>GTTAAAAA | 59.8                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                       |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1219_P4_7175   | scaffold1219                            | 7175                          | AT/ATT                                                                | GGAAACCTCACCTAC<br>CACA  | TGGGTCGTTCTTTTG<br>GAGT  | 59.8                             | 925                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1224_P4_904    | scaffold1224                            | 904                           | TG/TGATCATTTAG                                                        | TGAGGTCATTTTCGTC<br>CTCC | GGACAACAATATGCCA<br>AGGG | 60.1                             | 828                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold123_P4_66916   | scaffold123                             | 66916                         | CAAA/CAAAA                                                            | AACGTACTGCCTATCA<br>CGGG | TTTGCGGTGTCCATATT<br>TGA | 60.0                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1231_P4_143354 | scaffold1231                            | 143354                        | AATATATATATATATATATATATAT<br>ATATATA/AATATATATATATATAT<br>ATATATATATA | GCAATTTCTGCCGAA<br>ATAA  | TGGATCCTCTCACCT<br>CTCA  | 60.0                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1231_P4_7352   | scaffold1231                            | 7352                          | CAA/CAAA                                                              | ACACCTCAATCACACA<br>GCGA | GGAGGGTTTTGGTTTG<br>GAAT | 60.3                             | 231                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1238_P4_167384 | scaffold1238                            | 167384                        | AATA/AA                                                               | TGCATGCAAGATTGTA<br>CCTC | GAAGAGGAGGTGGGTT<br>GTGA | 59.8                             | 332                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1238_P4_25147  | scaffold1238                            | 25147                         | CTTTTTTTTT/CTTTTTTTTT                                                 | CTGCATCTCCCTCTAG<br>CACC | TGGGACACAATGTTGC<br>TTGT | 60.0                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1238_P4_42907  | scaffold1238                            | 42907                         | AATATATATATATATA/AATATATA<br>TATATATATATA                             | TATTTTGATTTTGGCT<br>CGG  | AGGAAGAGTGGAGTTG<br>CGAA | 59.9                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1239_P4_4253   | scaffold1239                            | 4253                          | TC/TCC                                                                | TCGAGTGGTACGAAAA<br>TCCC | TCCAGTCCTCGATT<br>CATC   | 59.9                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1240_P4_105707 | scaffold1240                            | 105707                        | A/AG                                                                  | ACATGGAACCCATCCA<br>AAGA | GCCCTCAGATGAGAGT<br>CAGG | 60.2                             | 268                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                           | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                                         |                            |                          |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1240_P4_117266 | scaffold1240                            | 117266                        | GAAAAAAAA/GAAAAAAAAA                                                                                                    | TAATCGGCGTAAAT<br>CCTG     | CCTGCCATTGTAAGT<br>CTGA  | 59.9                             | 911                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1240_P4_34177  | scaffold1240                            | 34177                         | CAACTGAATTAGTA/CA                                                                                                       | TGAAGATTGTCTCT<br>GCCA     | ATGACAAAGGGGGCCT<br>TACT | 57.0                             | 595                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1240_P4_70748  | scaffold1240                            | 70748                         | CA/CAA                                                                                                                  | TTCTTCATCACCCCTT<br>ACG    | TTGAGGATATACACGG<br>GCAA | 59.9                             | 668                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1242_P4_2626   | scaffold1242                            | 2626                          | AATATATATATATATA/AATATATA<br>TATATATATATA                                                                               | TGGTGTTGGAGTCATG<br>TTTTTC | TTCTCAACTGACGCAT<br>GAGG | 59.9                             | 388                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1244_P4_3584   | scaffold1244                            | 3584                          | AGGGGGGG/AGGGGGG                                                                                                        | CCTACGGAGGACGAAA<br>ATGA   | TGCCTAATCGATTGCT<br>CAG  | 60.1                             | 556                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1246_P4_7947   | scaffold1246                            | 7947                          | TAAAA/TAAA                                                                                                              | TGGATGCACAAGATGG<br>GTTA   | TCAGGTCATTTTCGTCC<br>TCC | 59.9                             | 871                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1252_P4_88493  | scaffold1252                            | 88493                         | CTT/CT                                                                                                                  | TTGGAAGGAGCCCTTA<br>CCTT   | TCTCCCTCCTTCCTCCA<br>TTT | 60.1                             | 343                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1252_P4_88820  | scaffold1252                            | 88820                         | GTATATATATATATATATATATAT<br>ATATATATATATATATATATATAT/<br>GTATATATATATATATATATATAT<br>ATATATATATATATATATATATATA<br>TATAT | AATGGAGGAAGGAGG<br>GAGAA   | TCTATGGAGGACGAGG<br>ATGG | 60.0                             | 629                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1252_P4_98018  | scaffold1252                            | 98018                         | CA/CAA                                                                                                                  | TTTGCCAATCGATTATC<br>GTG   | TGCACAAGTCAGTAGC<br>ACCC | 59.5                             | 561                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1255_P4_15043  | scaffold1255                            | 15043                         | ATAT/ATATATATATTTAT                                                                                                     | TTCTATGCATTTGACCC<br>ATGTT | CTAATGGTCTTAGGCG<br>GCTG | 59.3                             | 554                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                      | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                    |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1256_P4_55374 | scaffold1256                            | 55374                         | ATTT/ATTTT                                                                                         | TGTAGCAGTGGCTCAT<br>CAGG  | TACCGTGGGAGAAGTC<br>CTTG   | 60.0                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1256_P4_617   | scaffold1256                            | 617                           | ATTTTTTTTTT/ATTTTTTTTTT                                                                            | TCCAACACCCTCACAA<br>ATCA  | TTGGACTACGGGTTAG<br>TGGG   | 59.9                             | 914                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1256_P4_6511  | scaffold1256                            | 6511                          | ATTTTTTTTTT/ATTTTTTTTTTTTTT                                                                        | TAAAGAGATTCGCAGC<br>GGTT  | AGCGTGAATGTGACGT<br>CTTG   | 60.0                             | 109                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1259_P4_8966  | scaffold1259                            | 8966                          | GTTATTATTATTATTATTATTATT<br>ATTATTATTATTAGTTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTA | TGGAATGGATCACCAA<br>CTGA  | CGCAACTGTTTGCTCC<br>TTTT   | 59.9                             | 868                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold127_P4_144443 | scaffold127                             | 144443                        | AGTGT/AGT                                                                                          | CCCGAAAAGTCCAGAT<br>GAAA  | CAAGGATCAGAGGGGA<br>TTCA   | 60.0                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold127_P4_20427  | scaffold127                             | 20427                         | TAATAAA/TAATAAAATAAA                                                                               | AAACCCAAAATCCTGA<br>ACCTT | CTGGACATTTTGGCGA<br>TTTT   | 58.9                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold127_P4_256849 | scaffold127                             | 256849                        | GTGAT/GT                                                                                           | CCTTGGTTTCCATTTTC<br>CAA  | ATTGGCAGACATCCAT<br>TTCC   | 59.8                             | 144                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold127_P4_276167 | scaffold127                             | 276167                        | TA/TAA                                                                                             | GGCGATTTTCGTACCA<br>CCTA  | TAGCCCGAAAAGTCCA<br>AATG   | 60.0                             | 330                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold127_P4_54036  | scaffold127                             | 54036                         | TG/T                                                                                               | AAAAATGGGTGGTCAA<br>ATCAA | TGGCATTAAAGTTCTG<br>TGTTCA | 59.2                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold127_P4_5686   | scaffold127                             | 5686                          | CGGG/CGG                                                                                           | TGAGTTTCGTGTTCTG<br>CGTC  | CTTTTCGGCCGATTTTC<br>ATA   | 60.0                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                  |                           |                           |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1272_P4_20195 | scaffold1272                            | 20195                         | AT/AATCGATT                                                      | TCCAGTCAGACATTCC<br>CCTC  | GGAGGGTTTTGGTTTG<br>GAAT  | 60.0                             | 897                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1274_P4_6685  | scaffold1274                            | 6685                          | T/TGTG                                                           | TCATTTTCGTCCTTCCT<br>TGG  | ACACACCTATTGGACG<br>CACA  | 60.0                             | 272                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1275_P4_6195  | scaffold1275                            | 6195                          | CAA/CAAGAGATAA                                                   | TGTTGCCTCGTAATTC<br>AACG  | CAGGGACTAAACTGT<br>TTGCTG | 59.7                             | 556                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1276_P4_1671  | scaffold1276                            | 1671                          | TT/TTATAT                                                        | AAGCATGGGACCAAAG<br>TGAG  | TTTCCCAATCGATTTC<br>TTC   | 60.1                             | 942                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1276_P4_52730 | scaffold1276                            | 52730                         | AAGGGTTTAGGGTTTAGGGTTT/AA<br>GGGTTTAGGGTTTAGGGTTTAGGG<br>TTT     | CCTATTAGTGCAAAAG<br>TGCCA | AGACCTAGGCCCTTAA<br>ACCA  | 58.0                             | 491                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1278_P4_29851 | scaffold1278                            | 29851                         | TAAAAAAA/TAAAAAAA                                                | TGAAGAATAAAGGTTG<br>GCGG  | GTCGTTTTCTCGGTTTC<br>TGG  | 60.1                             | 893                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1278_P4_57695 | scaffold1278                            | 57695                         | CATTATTATTATTATTATTATTAT<br>TATTA/CATTATTATTATTATTAT<br>TATTATTA | ACCCGAATACCTCCAA<br>GGTC  | GCTATGTACGGCAGTA<br>GCCC  | 60.2                             | 720                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1278_P4_63103 | scaffold1278                            | 63103                         | GAAAAA/GAAAA                                                     | ACGAAGGGGTGTAGGAC<br>GATG | ATTGTGTTGCCGATCG<br>CTAC  | 60.0                             | 611                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1278_P4_63247 | scaffold1278                            | 63247                         | TAAAAAAA/TAAAAAAA                                                | ACGAAGGGGTGTAGGAC<br>GATG | ATTGTGTTGCCGATCG<br>CTAC  | 60.0                             | 611                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1278_P4_63301 | scaffold1278                            | 63301                         | ATT/ATTT                                                         | ACGAAGGGGTGTAGGAC<br>GATG | ATTGTGTTGCCGATCG<br>CTAC  | 60.0                             | 611                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                 |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1278_P4_65072 | scaffold1278                            | 65072                         | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>TTATTATTATTATTATTATTATT | TGGGTAGCAGTAATAA<br>TGGA   | TGAGCAAGATGTGTTTT<br>GTGG | 58.2                             | 341                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold128_P4_129082 | scaffold128                             | 129082                        | CAAAAA/CAAAAA                                                                   | TTTAGCACCCGACATTAA<br>AGCA | TTCTTGTAAGTGTG<br>GCAA    | 58.5                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold128_P4_222053 | scaffold128                             | 222053                        | C/CCGGA                                                                         | GCACTTGGGGATACGT<br>AGGA   | AGGAGTCGCCACCAAT<br>TTTA  | 60.0                             | 316                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold128_P4_232084 | scaffold128                             | 232084                        | CTTTTT/CTTTTT                                                                   | CAGTGCCCTGACTGTT<br>CTCA   | CTTCACGACGTATGGT<br>CCCT  | 60.0                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold128_P4_256571 | scaffold128                             | 256571                        | ATT/ATTT                                                                        | GCCAATCGATTACCCT<br>CAAA   | CACTTATGCAAAAAGG<br>GGGA  | 59.9                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold128_P4_27122  | scaffold128                             | 27122                         | CAATAAATAAATA/CAATAAATAAATA<br>AATA                                             | ATCGCTTCTCAACGCA<br>TCTT   | GGGAGGCAACCAATT<br>TTAT   | 60.0                             | 160                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold128_P4_304570 | scaffold128                             | 304570                        | TAAAAAAAAA/TAAAAAAAAA                                                           | GACATGCCTTTTGAGC<br>CAAT   | TAAAGGCACGTGACAA<br>AGCA  | 60.1                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold128_P4_547816 | scaffold128                             | 547816                        | CAAA/CAA                                                                        | CAACGCAACATAACAC<br>CCAG   | GGAAAGTTGCTCACCA<br>CCAT  | 60.0                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold128_P4_588046 | scaffold128                             | 588046                        | TAA/TAAA                                                                        | AGTACTGAGCCCCCTG<br>GTTT   | ATGATGTTGTAGCGATT<br>GCG  | 60.0                             | 308                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold128_P4_732668 | scaffold128                             | 732668                        | A/ATAAAC                                                                        | GCTCAAAGCACATGAC<br>AGGA   | CATTTTGAACCAAGCA<br>GCA   | 60.0                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                    | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                                                                                  |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold128_P4_747253  | scaffold128                             | 747253                        | G/GT                                                                                                                                                             | GGTGTGTTTGACGT<br>TGGA    | GGAGGACGAAAATGAT<br>CGAA  | 60.5                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold128_P4_88977   | scaffold128                             | 88977                         | TTTATTATTATTATTATTATTATT<br>A/TTTATTATTATTATTATTATTATTA                                                                                                          | ACAATGGCATAAGCGG<br>TAGG  | TCGATTTCGCTAGTTTTC<br>CAC | 60.0                             | 905                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1281_P4_1507   | scaffold1281                            | 1507                          | TAAAAAAAAA/TAAAAAAAAA                                                                                                                                            | CGATTTCCTCGAA<br>ATGT     | TTTTGGTTCTTTTGGG<br>TTTTT | 59.9                             | 786                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1281_P4_171001 | scaffold1281                            | 171001                        | ATTTTTT/ATTTT                                                                                                                                                    | TGAGGCGACCAATACT<br>ACCTG | GAAATTTTCAGTCTAC<br>AGCGA | 60.1                             | 197                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1281_P4_321536 | scaffold1281                            | 321536                        | TTATATATATATATATATAT/TTATAT<br>ATATATATATAT                                                                                                                      | CTCTGGATGCGTGAGA<br>GGTT  | TTGAGAGAATGGCAGG<br>TGTTG | 60.4                             | 508                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1281_P4_358084 | scaffold1281                            | 358084                        | TTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAA/TTAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATAA<br>AATAATAATAATAATAATAA | ATCAAGCCACTGGAGA<br>CACC  | TAAGCCAGAAGTGGGG<br>AATG  | 60.1                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1281_P4_360564 | scaffold1281                            | 360564                        | ATTTTTTTTTTT/ATTTTTTTTTTT<br>TT                                                                                                                                  | TTTGATTGCAACACCAA<br>AGC  | CTGAGAGACGTGTGAA<br>CGGA  | 59.7                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1281_P4_376337 | scaffold1281                            | 376337                        | GTTTTTTTTT/GTTTTTTTTT                                                                                                                                            | TGTTTAGGCGCTAGTT<br>TGCC  | TCGATTATGCGTAGGG<br>AAGG  | 60.4                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1281_P4_405119 | scaffold1281                            | 405119                        | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTA/TTTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTA                            | GACCAAAACCCTACCGA<br>CTCA | ACGGCTATGTTTGCCA<br>CTTC  | 60.0                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1281_P4_446683 | scaffold1281                            | 446683                        | CACAGAACCCAAAACAGAACCCAAA<br>ACAGAACCCAAAACAGAACCCAAA<br>CAGAA/CACAGAACCCAAAACAGAA<br>CCCAAAACAGAACCCAAAACAGAA                                                   | GGGATAGGCAACAACA<br>CCAT  | CTTCACTCTTCCTGCG<br>AACC  | 59.7                             | 629                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                     |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1281_P4_469460 | scaffold1281                            | 469460                        | GAAAAAAAAA/GAAAAAAAAA                                               | TCTCTGGCAACCGTTC<br>TTCT   | ACCTCGTTGAGACAG<br>CTTT     | 60.0                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1281_P4_471713 | scaffold1281                            | 471713                        | AATATATATATATA/AATATATATATA<br>TATA                                 | GAGCATTGTGACAAA<br>TTGAGC  | CGGGAATTCTTGATGA<br>ATCG    | 59.8                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1281_P4_472602 | scaffold1281                            | 472602                        | CATA/CATATATA                                                       | CAATGGAGGTTATTG<br>CATTG   | AGCAGTGCTTCAACTC<br>ATGC    | 58.0                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1281_P4_473339 | scaffold1281                            | 473339                        | GATATATATATATATATATA/GATA<br>TATATATATATATA                         | ACGCATGGATATTGCA<br>GTCA   | TCCGATTGTTGACCAG<br>TTTTT   | 60.1                             | 783                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1281_P4_492209 | scaffold1281                            | 492209                        | TAAAA/TAAAA                                                         | GGAATGGAAAACACAT<br>TCAACA | GAATGCTTGAGAACT<br>TTGGG    | 59.7                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1281_P4_492299 | scaffold1281                            | 492299                        | A/AACGTT                                                            | CCCAAAGTTTCTCAAG<br>CATTG  | TCTTTCGATTTCAATTA<br>ATGGCT | 58.8                             | 188                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1292_P4_2932   | scaffold1292                            | 2932                          | CATATATA/CATATATATA                                                 | GCCTTAAGGTTGACAG<br>GCAG   | GGCTCGCTATGTATGG<br>CAGT    | 60.0                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1292_P4_7985   | scaffold1292                            | 7985                          | CAAAAA/CAAAAA                                                       | TTGCTGTTACCCAATC<br>CTTG   | TTTGGGGATTAGGGT<br>GTCA     | 58.6                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1292_P4_8345   | scaffold1292                            | 8345                          | AATATATATATATATATATATATAT<br>ATATATA/AATATATATATATATATAT<br>ATATATA | TCACAATTGGACCGAG<br>ATGA   | GACTGGTTTGACCTTG<br>CGTT    | 60.0                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1293_P4_67835  | scaffold1293                            | 67835                         | AG/A                                                                | TCAGCTGGCTCATGTT<br>GTTC   | GGGCAAGAAATCTCC<br>ATGA     | 60.0                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                        | Forward primers (5'-3')      | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------|------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                      |                              |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1307_P4_6228  | scaffold1307                            | 6228                          | A/AG                                                                                 | ACACACCTATTGGACG<br>CACA     | AGGTCAATTCGTCCT<br>CCCT       | 60.0                             | 377                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1308_P4_16327 | scaffold1308                            | 16327                         | ACCC/ACC                                                                             | AGGGAGGACGAAAATG<br>ACCT     | CCAATTGGGGTTTTAA<br>CCA       | 59.9                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1308_P4_79242 | scaffold1308                            | 79242                         | TC/T                                                                                 | AATCCAATGACGCAAA<br>CACA     | GGTTTCGAGGAAATTG<br>GACA      | 60.0                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1308_P4_98092 | scaffold1308                            | 98092                         | ATCTCCCTC/ATC                                                                        | TCTTCACGAGCATCGA<br>TTTG     | AGTTGGAGGTGGTGAA<br>GGTG      | 59.9                             | 387                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1309_P4_26842 | scaffold1309                            | 26842                         | ATTT/ATTTT                                                                           | CGCCTTTCCAATTCCAT<br>CTA     | AAATGCCCCAAACATCT<br>GAC      | 60.0                             | 348                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1312_P4_58670 | scaffold1312                            | 58670                         | TAAAAAAAAA/TAAAAAAAA                                                                 | TTGCCTAAGATCTTTGA<br>AAATCAG | CGAGAAATTAATGCCT<br>GTTCCA    | 59.0                             | 835                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1312_P4_59370 | scaffold1312                            | 59370                         | GAAAAAAAAA/GAAAAAAAA                                                                 | GCATTAAATGTGGAAC<br>AAGCA    | CGACATAATTCGAGCG<br>AGGT      | 58.7                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1312_P4_65816 | scaffold1312                            | 65816                         | TCAATATTTGTAACAATATTT/TCAAT<br>ATTT                                                  | CGCGGGGACTTAGAGA<br>TGTA     | AAGCGAACATAATCCTT<br>TACTTTTG | 60.2                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1312_P4_70070 | scaffold1312                            | 70070                         | TTTTTGACCTTTGTTTTGACCTT/TT<br>TTTGACCTT                                              | ACTCCTCAAACCTTAGC<br>GGCA    | GCTCTAGAGTCCATGG<br>CAGG      | 60.0                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1312_P4_70265 | scaffold1312                            | 70265                         | AGCAACAACCTTGTGCAACAACCTGT<br>GCAAC/AGCAACAACCTTGTGCAACA<br>ACTTGTGCAACAACCTTGTGCAAC | ACTCCTCAAACCTTAGC<br>GGCA    | GCTCTAGAGTCCATGG<br>CAGG      | 60.0                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                 |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1312_P4_78648  | scaffold1312                            | 78648                         | TAAA/TAAAA                                                                      | GCATTAAATGTGGAAC<br>AAGCA   | TTACCTGTGTGGGACA<br>ACGA | 58.7                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1312_P4_78828  | scaffold1312                            | 78828                         | GAAAAA/GAAAAAA                                                                  | GCATTAAATGTGGAAC<br>AAGCA   | TTACCTGTGTGGGACA<br>ACGA | 58.7                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1312_P4_78884  | scaffold1312                            | 78884                         | TAAGAAGAAGAAGAAGAA/TAAGAA<br>GAAGAAGAA                                          | ATTTGACCTCGACACA<br>ACGG    | GCCGCTTGATCGTTAA<br>TTGT | 61.0                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1312_P4_78931  | scaffold1312                            | 78931                         | CG/C                                                                            | TCGACACAACGGACAA<br>GAGT    | GCCGCTTGATCGTTAA<br>TTGT | 59.3                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1312_P4_80554  | scaffold1312                            | 80554                         | ATTT/ATTTTTT                                                                    | GCCAAGGTAAGGGTGA<br>GACA    | ATGAATTGTCCCAATCT<br>CGG | 60.1                             | 322                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1312_P4_83212  | scaffold1312                            | 83212                         | T/TC                                                                            | TCTAGCGGATGCATGA<br>TGAG    | ATACTTGAACGGTTGG<br>CTGG | 59.9                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1312_P4_89696  | scaffold1312                            | 89696                         | ATTTTTTTTT/ATTTTTTTTT                                                           | TTCATTACGCCATTGAC<br>ACTTT  | ACAATGTGTGCCCAAC<br>AAAA | 59.5                             | 457                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1312_P4_89732  | scaffold1312                            | 89732                         | ATTTTTTT/ATTTTTTTTT                                                             | TTCATTACGCCATTGAC<br>ACTTT  | ACAATGTGTGCCCAAC<br>AAAA | 59.5                             | 457                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1313_P4_102973 | scaffold1313                            | 102973                        | GAAAAAAAA/GAAAAAAAAA                                                            | GTGTACAACGCATT<br>GGTG      | CGGCTTGGTCTCATGA<br>TTTT | 60.2                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1313_P4_133490 | scaffold1313                            | 133490                        | AATATATATATATATATATATATATAT<br>ATATAT/AATATATATATATATATATA<br>TATATATATATATATAT | TCGTGTCTCCATTCTTC<br>TACTCA | CACAACCGCTTACTGC<br>TTCA | 60.3                             | 146                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                              | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                            |                              |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1316_P4_4181  | scaffold1316                            | 4181                          | TA/TAA                                                                                                     | GTAAGGGTCACCAAC<br>CGAA      | TTGTCCGTGAGAGACT<br>GCAC   | 59.8                             | 813                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1317_P4_1107  | scaffold1317                            | 1107                          | GATCAA/GA                                                                                                  | GCATGAGAGTGTGCAA<br>GCAT     | CCGTCATTTTGTATGAT<br>GTGA  | 60.0                             | 830                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1317_P4_22112 | scaffold1317                            | 22112                         | TATAATAATAATAATA/TATAATAAT<br>AATAATAATAATAATA                                                             | TTTGATTCATGCTTCTT<br>TCTTTTC | TTTGATCGGGGAAGTT<br>TGAG   | 59.0                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1317_P4_22473 | scaffold1317                            | 22473                         | CAA/CA                                                                                                     | ATGCGATGGGATGAGA<br>AGAG     | TGTTTGATGAAGGGT<br>TTTGA   | 60.2                             | 213                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1317_P4_2766  | scaffold1317                            | 2766                          | ATTTT/ATT                                                                                                  | GGGAAGATAGAGGACC<br>TTCCTT   | GCCCTTAAATGGGTTT<br>GGAT   | 59.1                             | 332                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1317_P4_41791 | scaffold1317                            | 41791                         | AAATTCATTAAGAATATAATTCAT<br>TAAGAATATAATTCATTAAGAATAT<br>AATTC/AAATTCATTAAGAATATAA<br>TTCCATTAAGAATATAATTC | ACGGATCTGTCAACCT<br>CCAC     | CGATACAGTCTGCCTT<br>GCAC   | 60.0                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1317_P4_44894 | scaffold1317                            | 44894                         | AT/A                                                                                                       | GAGCAATGACAGCTCG<br>TTGA     | ATTGGATCGTTGGTTG<br>TGGT   | 60.1                             | 718                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1317_P4_45149 | scaffold1317                            | 45149                         | GA/GAA                                                                                                     | CGTTCTCACTCTCCTC<br>CACC     | TGTTGTGGTGTTC AAG<br>CCAT  | 59.8                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1317_P4_46249 | scaffold1317                            | 46249                         | AC/A                                                                                                       | CATGGGTGAAGACTGT<br>GGTG     | ACCAGTGTGCATGCC<br>TAAA    | 60.0                             | 134                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1317_P4_46362 | scaffold1317                            | 46362                         | AAATAAATAAAATTTTAATA/AAATA                                                                                 | CATGGGTGAAGACTGT<br>GGTG     | TTGGTTTGCTTCTTTTG<br>AATTG | 60.0                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1317_P4_46601  | scaffold1317                            | 46601                         | TAAAAAAAAA/TAAAAAAAAA                                         | CATGGGTGAAGACTGT<br>GGTG    | CAATTGCGAAAACATCT<br>CCA    | 60.0                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1317_P4_4720   | scaffold1317                            | 4720                          | GTATA/GTATAGGGTAAAAACATAT<br>A                                | CTTAGGGGCATATCCC<br>AAGC    | CCAATGGATTAACGCT<br>CGTC    | 60.8                             | 391                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1317_P4_5044   | scaffold1317                            | 5044                          | TAA/T                                                         | TGACGAGCGTTAATCC<br>ATTG    | GAATGACATAATCCAA<br>GTTGCG  | 59.7                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1317_P4_59870  | scaffold1317                            | 59870                         | AAAGAG/AAAGAGAAAGCAAGAG                                       | AAAATCAGCCAAATCC<br>AACG    | TTGGAAAATCTCATTAA<br>GCCAGA | 59.9                             | 930                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1317_P4_62216  | scaffold1317                            | 62216                         | CATATATATATATATATATATAT/C<br>ATATATATATATATATATAT             | TGATTTTGTTGTTTT<br>ACTCAACG | TCAAACAATGGAATGA<br>GATAGCA | 59.5                             | 250                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1317_P4_63018  | scaffold1317                            | 63018                         | GGTT/GT                                                       | AATCTCAGCCTATGCG<br>GTGT    | GCGCAACAATGTCAAT<br>TCAA    | 59.7                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1319_P4_1205   | scaffold1319                            | 1205                          | CA/C                                                          | AATTGTGTTTCAGGTT<br>CGC     | TCGACTTGTCAATCGC<br>TTTG    | 60.0                             | 771                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1323_P4_6638   | scaffold1323                            | 6638                          | ATTT/ATTTT                                                    | GGCCACTGACTTGCAG<br>TGTA    | TTGTGCATCCAATACGT<br>GTG    | 59.9                             | 717                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_227334 | scaffold1324                            | 227334                        | TG/T                                                          | TTGGTGACATTTAGCA<br>TTTCTCA | GTCCTTTGTGTCGTGG<br>GTCT    | 59.6                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_235091 | scaffold1324                            | 235091                        | CGTTGT/CGT                                                    | TCTTGTTGTAACCCCT<br>GGC     | TTTCGACAAAAGGTTCT<br>CCG    | 60.0                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1324_P4_256337 | scaffold1324                            | 256337                        | CAAAA/CAAA                                                    | TTCAACCATTGGGGTA<br>GCTC    | TTCACCTGAATATTTTG<br>TGGA    | 59.9                             | 474                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_266092 | scaffold1324                            | 266092                        | CAA/CAAA                                                      | GAGGGGGTCCGAAAA<br>TAAA     | TCAATTGAACTCAAAC<br>CCAT     | 60.1                             | 396                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_266713 | scaffold1324                            | 266713                        | AATCTATTATCTATTATCTATTAT/AA<br>TCTATTATCTATTAT                | TGTATGCATCAACAAT<br>GTCAAGA | TCAGAGGATGTGGCAT<br>AGAGG    | 59.1                             | 160                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_266796 | scaffold1324                            | 266796                        | CA/CAA                                                        | TCCTCTATGCCACATC<br>CTCTG   | CACAAATAGTTGTACAT<br>TGGTTGC | 60.2                             | 238                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_267973 | scaffold1324                            | 267973                        | A/AT                                                          | CCAAGGCACACAAAA<br>TGAA     | AGAGAATAACCCGCAC<br>GTTG     | 60.6                             | 344                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_268436 | scaffold1324                            | 268436                        | A/AGTTCTG                                                     | CAACGTGCGGGTTATT<br>CTCT    | GGCACGTGAAGTCCAC<br>TTTT     | 60.1                             | 358                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_270833 | scaffold1324                            | 270833                        | GTT/GT                                                        | ACAAAATCGGCCACTG<br>AATC    | TCCCGTTCTCTCTCTC<br>ACC      | 59.9                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_272072 | scaffold1324                            | 272072                        | ATTTTTTTT/ATTTTTT                                             | CAAATGTCGGGAGCTA<br>CCAT    | TGACACCCTAAATCCC<br>CAAA     | 60.0                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_272116 | scaffold1324                            | 272116                        | TGGGG/TGGG                                                    | CCCCGCTCTGATAGGT<br>GATA    | TGTTTGCATGCGAGC<br>ATTT      | 60.1                             | 767                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_272202 | scaffold1324                            | 272202                        | GTTTTTTT/GTTTTTTT                                             | CCCCGCTCTGATAGGT<br>GATA    | TGTTTGCATGCGAGC<br>ATTT      | 60.1                             | 767                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                    | Forward primers (5'-3')       | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------|-------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                                  |                               |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1324_P4_272539 | scaffold1324                            | 272539                        | TAAAAAAAAA/TAAAAAAAAA                                                                                            | TTTGGGGATTAGGTT<br>GTCA       | AAATTCTTGGGGACTTT<br>CGG       | 60.2                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_409829 | scaffold1324                            | 409829                        | AAGCAAGA/AA                                                                                                      | ACAATGAAGCCCAAAA<br>CTCG      | CCGTTGGACACACTTC<br>ACAA       | 60.1                             | 300                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_516063 | scaffold1324                            | 516063                        | ATTTTTTTTT/ATTTTTTTTT                                                                                            | AAAACACGCTAGGCTC<br>CAAT      | TGGTCATGTGTTTTT<br>GCAT        | 58.9                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_520260 | scaffold1324                            | 520260                        | AATTATTATTATTATTATTATT<br>TATTATTATT/AATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATT                            | TTCTTTTCGCTATTTTA<br>TTTTCGTG | TCTTACGTATCTCCG<br>GTGC        | 60.0                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_642408 | scaffold1324                            | 642408                        | ATTTTT/ATTTTTT                                                                                                   | CCTTGCCCTTTTATTT<br>GGT       | TCCTAGAACATGCATCA<br>CGC       | 60.3                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_642722 | scaffold1324                            | 642722                        | TA/TAA                                                                                                           | AGCCTATGGTAGCGTG<br>ATGC      | CAAGTCTCCCACTTC<br>CCAA        | 60.3                             | 747                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_652312 | scaffold1324                            | 652312                        | GATTTGAATT/GATTTGAATTGAAT<br>T                                                                                   | CAGTGTGTGCTTGACC<br>ATGA      | CCCATTTTGGTCGGA<br>AAAA        | 59.3                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_700658 | scaffold1324                            | 700658                        | CATATATATATATATATAT/CATAT<br>ATATATATATATAT                                                                      | ATCACACCAAGAATGG<br>CACA      | CACGTAAATAGTTATTT<br>GATTTTGTA | 60.0                             | 294                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_751048 | scaffold1324                            | 751048                        | C/CA                                                                                                             | GAACCACGGCCACTAC<br>CTAA      | TGCTGGACCCCTTCTT<br>TATG       | 60.0                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1324_P4_78551  | scaffold1324                            | 78551                         | CATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA/<br>CATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATA | TGGTCCCATTTTGTGG<br>TTTT      | TGCAAGCTCAAAGGAA<br>TGTA       | 60.1                             | 938                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                 | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                               |                              |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1332_P4_517   | scaffold1332                            | 517                           | CAAAAAAAAA/CAAAAAAAAAA                                                                        | CCAAAATTTGAAGTCG<br>GGAG     | ACACGGGTCGTACAAC<br>TTGA | 59.5                             | 443                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1332_P4_801   | scaffold1332                            | 801                           | ATTT/ATTTT                                                                                    | ACGACCCGTGTCTCAA<br>AAAC     | CAGTCACCGCTCACTT<br>GTGT | 60.0                             | 686                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1332_P4_8473  | scaffold1332                            | 8473                          | ATTTTTTT/ATTTTTTTT                                                                            | CACAATTTCTTTTCTAT<br>GTGTGGA | AACCCGTCACACAGGA<br>AGTC | 58.2                             | 894                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1337_P4_17738 | scaffold1337                            | 17738                         | GAAAA/GAAAAA                                                                                  | TCTTTGTCATGTATTG<br>TGCTTCA  | GGTCCTCGATTTCATCT<br>GGA | 59.7                             | 855                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1337_P4_46228 | scaffold1337                            | 46228                         | AAAACCTAAACCCTAAA/AAAACCC<br>TAAACCCCTAAACCCTAAA                                              | AAACCCCAAACCTTAA<br>CCC      | TTGGGACATTTCGTT<br>TTTG  | 59.1                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold134_P4_235744 | scaffold134                             | 235744                        | AATATATATATATATATATATATAT<br>ATATATATATATA/AATATATATATAT<br>ATATATATATATATATATATATATA         | TGTGAACAGAGGCAT<br>GTGA      | TTGGAGATGGTTTGGG<br>TCTC | 58.8                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold134_P4_353601 | scaffold134                             | 353601                        | AATATATATATATATATATATATAT<br>ATATATATATA/AATATATATATATAT<br>ATATATATATATATATATATATATA<br>TATA | TTTTTGACAGGAAGAATT<br>CCG    | GGAGAGATCGTGTGA<br>CGGT  | 60.2                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold134_P4_365115 | scaffold134                             | 365115                        | T/TG                                                                                          | TTTCCCATGCAGAGT<br>TAGG      | AATCGCTAGCCACTTA<br>GGCA | 60.1                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold134_P4_424697 | scaffold134                             | 424697                        | TTTATTATTATTATTATTATTATT<br>ATTA/TTTATTATTATTATTATTATA<br>TTATTA                              | CACCTAAATTTCTCCG<br>GCA      | TTACATCGAGCGTGAA<br>CGAG | 60.1                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold135_P4_10445  | scaffold135                             | 10445                         | TA/TAA                                                                                        | TCGGATTCAATCTCCTT<br>TGG     | CGTTGTATGATCTTGG<br>GGCT | 60.0                             | 864                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')       | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|-------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                             |                               |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold135_P4_113512  | scaffold135                             | 113512                        | A/AG                                                                        | GCTTATTGGGAGAAGC<br>GTTG      | GCCCTCAGATGAGAGT<br>CAGG     | 59.8                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold135_P4_3946    | scaffold135                             | 3946                          | AATATATATATATATATATATATAT/ATATATATATATATATATATATATAT                        | CACCGTAGTGTGGTGG<br>TGAG      | ATCCTTACGGGGGTTA<br>TTGC     | 60.1                             | 855                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold135_P4_96093   | scaffold135                             | 96093                         | TAA/TAAA                                                                    | CAAGTTGTACTACATG<br>GTGGTTTTG | TCGATTATGCGTAGGG<br>AAGG     | 59.8                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1351_P4_109818 | scaffold1351                            | 109818                        | AATATATATATATATATATATATATAT/ATATATATATATATATATATATATATAT                    | AAACGATATCAGACGC<br>GACA      | GGTTTTGTTTGAATTT<br>TTGATGA  | 59.3                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1351_P4_110605 | scaffold1351                            | 110605                        | CATATATATATATATATATATATATATATATATATAT/CATATATATATATATATATATATATATATATATATAT | TGAGCATTGAGTTAT<br>GCATTTG    | TCTGTCAAATAACCAT<br>TAGCATCA | 60.1                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1351_P4_67128  | scaffold1351                            | 67128                         | CAAAA/CAAAA                                                                 | AGCTTCTGAATCGCCA<br>AGAG      | TTGATAGGCGATCCAT<br>CACA     | 59.7                             | 792                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1358_P4_778    | scaffold1358                            | 778                           | AC/A                                                                        | TCCACAAGAAACCTC<br>CATTG      | AGTGAAACCAACGCCA<br>AAAC     | 60.0                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1360_P4_2778   | scaffold1360                            | 2778                          | GAAAAAAAA/GAAAAAAAAAAAA                                                     | GCGTTCACCTGTTGGG<br>TTTT      | TGTGGTGAGGTCATG<br>AGAA      | 60.0                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1360_P4_3736   | scaffold1360                            | 3736                          | TA/TAA                                                                      | TGCAGATGGATTGGTG<br>AAAA      | ATCTGCACGTAAGAAC<br>GCCT     | 60.0                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1365_P4_59505  | scaffold1365                            | 59505                         | G/GTTTGAAACAAGGAT                                                           | ACGTGGTGAAATTCTT<br>TCGG      | ATTTTCACCAACATCC<br>CCA      | 60.0                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                           |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1365_P4_74314  | scaffold1365                            | 74314                         | T/TGA                                                                     | TATTGTGAAGAGGCGT<br>GTGC  | TGTTGGGATTGGTTG<br>TGAA    | 59.9                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1365_P4_74375  | scaffold1365                            | 74375                         | CATG/CATGATG                                                              | TATTGTGAAGAGGCGT<br>GTGC  | TGTTGGGATTGGTTG<br>TGAA    | 59.9                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1369_P4_145181 | scaffold1369                            | 145181                        | TTCTCTCTCTCTCTCTCTCTCT/T<br>TCTCTCTCTCTCTCTCTCTCT                         | AAAGGGTGACGACGAT<br>TTCA  | TGGCTTTAAGAAACAT<br>GGACAA | 60.5                             | 858                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1369_P4_197295 | scaffold1369                            | 197295                        | ATT/ATTT                                                                  | GGAAATATCTCGCAGA<br>CCCA  | TCACCAAGCAAACCCA<br>CATA   | 60.0                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1369_P4_54533  | scaffold1369                            | 54533                         | AATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATATA<br>TATATATATATAT | CCAATTACACACGGGT<br>TTCC  | ATTTGGCCACTGATTCA<br>ACG   | 60.1                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1369_P4_80991  | scaffold1369                            | 80991                         | TAAAA/TAAAAA                                                              | CGTATTTCTGGGGAAGA<br>GTCA | GGCAGTAGTGAATCT<br>GGGA    | 60.1                             | 425                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1370_P4_86329  | scaffold1370                            | 86329                         | AGGG/AGGGG                                                                | TGAGGGGAAGGACATA<br>ATGG  | ATGAGTCTATCCAAGG<br>GGCA   | 59.7                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1376_P4_69558  | scaffold1376                            | 69558                         | AG/A                                                                      | AACCCCTCCAAAGAAC<br>GACT  | CCATCATTTTCTTCGCA<br>CCT   | 60.0                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1380_P4_5644   | scaffold1380                            | 5644                          | ATTTTTTTT/ATTTTTTTTT                                                      | TTTtagCGGATGTCGT<br>AGGG  | TCACAAGGGGGACTCT<br>ATGG   | 60.1                             | 719                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1382_P4_225615 | scaffold1382                            | 225615                        | GTTTTT/GTTTTTT                                                            | AGGTCATTTTCGTCCT<br>CCCT  | CCCCCTAGGGTGTAAG<br>TGCT   | 59.9                             | 805                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3') | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                             |                         |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| scaffold1382_P4_265244 | scaffold1382                            | 265244                        | AAACACGA/AA                                                   | CAAAGCCTTACCCAAG GACA       | CAACCACCTCCAACGG CTAT   | 60.1                             | 643                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1382_P4_27531  | scaffold1382                            | 27531                         | ATTTTTTTTT/ATTTTTTTTT                                         | GCATCCCACTTTTAGG GACA       | TCCCCAATTTGCTTTCT CAC   | 59.9                             | 350                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1382_P4_294316 | scaffold1382                            | 294316                        | CT/CTT                                                        | GCTCGTATTATCCTC CCAA        | ACACACCTATCGGATG CACA   | 60.0                             | 523                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1386_P4_13609  | scaffold1386                            | 13609                         | CAAAA/CAAAAA                                                  | TTTGTTGGTAATTTATGG TTGCTACA | TTTCGGTTTCCTTTGTT TGC   | 59.7                             | 424                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1386_P4_19488  | scaffold1386                            | 19488                         | T/TCAATTACGAGTAGGGAAA                                         | GCGCAAATGAATTGTT GAGA       | GTCTCTATTGCACCTG GGGA   | 59.8                             | 438                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1390_P4_38477  | scaffold1390                            | 38477                         | A/AAC                                                         | TCGATGCACCAGATTG GTTA       | AGTGTGTTTGTGGCAT TGGA   | 60.1                             | 787                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1393_P4_2098   | scaffold1393                            | 2098                          | T/TG                                                          | GGTCACTTTCGTGCTC CCTA       | TGGATGCACGAGATTG GTTA   | 60.3                             | 873                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold140_P4_2406    | scaffold140                             | 2406                          | CATATATATATATATATATATATA TATATAT/CATATATATATATATATAT ATATAT   | CTTGTAATACTCCGCT CGC        | TTGGTATTGAACTCGG AGGC   | 60.0                             | 665                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold140_P4_25774   | scaffold140                             | 25774                         | AATTT/A                                                       | TCCTAGAACATGCATC ACGC       | CTCAAGTCGACAAGCC TTCC   | 59.8                             | 666                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1401_P4_99725  | scaffold1401                            | 99725                         | CATATATATATATATATATAT/CATAT ATATATATATATATAT                  | CAGCTCTCGTAACAAT GGCA       | TCAAAATCAGAACCGG AGGA   | 60.0                             | 566                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1408_P4_103952 | scaffold1408                            | 103952                        | GC/G                                                          | CTTGGGCATCCAATAG<br>GTGT | AGGGAGGACGAAAATG<br>ACCT | 59.8                             | 264                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1408_P4_24952  | scaffold1408                            | 24952                         | GTTTTTT/GTTTTT                                                | TGTGCGTCCAATAGGT<br>GTGT | GACACGAATAAGCCAA<br>GGGA | 60.0                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1408_P4_29515  | scaffold1408                            | 29515                         | TC/T                                                          | TTGGATGAACATTGG<br>GTCA  | ATAAGCCTATGGGGGA<br>CGAA | 59.8                             | 341                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1408_P4_29853  | scaffold1408                            | 29853                         | AT/A                                                          | TGGGTCATTTTCGTCC<br>TCTC | TGGACGCACAAGATTG<br>GTTA | 60.1                             | 667                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1408_P4_53719  | scaffold1408                            | 53719                         | TCC/TCCC                                                      | TTCATTGGGTCATCG<br>GATT  | ATACGCCAATGGAGGA<br>CGTA | 60.1                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1408_P4_70937  | scaffold1408                            | 70937                         | AGG/AGGG                                                      | TTTTTCATCCTCCCATG<br>CTC | ACACACCTATCGGATG<br>CACA | 60.0                             | 273                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1408_P4_7794   | scaffold1408                            | 7794                          | ATTTT/ATTTT                                                   | AACCAATCTTGTGCAT<br>CCAA | AGGGCGGACGAAAATA<br>ACTT | 59.0                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1408_P4_92293  | scaffold1408                            | 92293                         | GTTTTT/GTTTTT                                                 | AGGTCATTTTCGTCCT<br>CCCT | TAATTGGCAAGAATG<br>AGCC  | 59.9                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1409_P4_12185  | scaffold1409                            | 12185                         | TCC/TCCC                                                      | TGTGCATTCAATAGGC<br>GTGT | CCAAGGGAGGATGAAA<br>ATGA | 60.1                             | 259                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1409_P4_9058   | scaffold1409                            | 9058                          | CG/C                                                          | TGCCAAACGATAGGTT<br>GTTG | CCAATGGGTTTAAGCA<br>TGTG | 59.6                             | 128                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')   | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|---------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                               |                           |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1409_P4_9222   | scaffold1409                            | 9222                          | AAATAATAATAATAAA/AAATAATA<br>ATAATAATAATAATAA                                 | GCTTAAACCCATTGGT<br>CCCT  | GGAAGATGTGACGATG<br>CCTT       | 60.2                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold141_P4_176046  | scaffold141                             | 176046                        | AATATATATATATATATATATAT/AAT<br>ATATATATATATATATATATATAT                       | GAAGAAAATGACGGTG<br>CTTGA | TCCGAGTTAACAGCAA<br>ACGA       | 60.2                             | 621                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold141_P4_68702   | scaffold141                             | 68702                         | AT/ATCT                                                                       | TGCCTTAACTGACAAA<br>GGGG  | TAATTGTGCCAGTCGT<br>CCAA       | 60.1                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1412_P4_3330   | scaffold1412                            | 3330                          | G/GGCGGAATATGT                                                                | TGAACGTAGAGTTTGC<br>ACCG  | GGGACTGATTCGTCT<br>TTCA        | 59.9                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1414_P4_38236  | scaffold1414                            | 38236                         | GTTATTATTAT/GTTATTAT                                                          | TGGTCCTAGATTTTCAT<br>CGGG | CGTTATTAAGTACAAC<br>ACAAAACGAA | 59.9                             | 871                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1417_P4_123825 | scaffold1417                            | 123825                        | ACC/ACCC                                                                      | CCCTCTGCAATGTCGG<br>TAAT  | ATTTGACAAACCTTTTG<br>CGG       | 60.0                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1417_P4_243147 | scaffold1417                            | 243147                        | A/AG                                                                          | AGGTAAGGGCTCCTTC<br>CAAA  | ACGATCCACACCAAAA<br>CACA       | 60.1                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1417_P4_39952  | scaffold1417                            | 39952                         | TAAAAAAAAA/TAAAAAAAAA                                                         | AAAAGGATTCCATTCG<br>CCTT  | GGACACATTATTTCTG<br>GGGG       | 59.9                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1417_P4_96851  | scaffold1417                            | 96851                         | GTATATATATATATATATATATAT<br>ATAT/GTATATATATATATATATAT<br>ATATATATATATATATATAT | GGTACTGCGGTTAATT<br>CCGA  | CAAAAAGTGGTTTGGG<br>AAGTG      | 60.0                             | 402                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1418_P4_117515 | scaffold1418                            | 117515                        | ATTT/ATT                                                                      | GCCCTCAGATGAGAGT<br>CAGG  | CAAGATTACGATGGAG<br>GCGT       | 59.9                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                       | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                     |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1418_P4_16114 | scaffold1418                            | 16114                         | TAAAAAAA/TAAAAA                                                                     | ATTTCCCTCCACCAATCC       | GTGGTGTCACGTGTGCAACT     | 60.0                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1418_P4_17845 | scaffold1418                            | 17845                         | TAAAAAAAAA/TAAAAAAAAA                                                               | GCATTGTATCCATCCC<br>CATC | TATTGGTGGCCATGTT<br>CTCA | 60.0                             | 216                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1418_P4_18174 | scaffold1418                            | 18174                         | AC/A                                                                                | GCATTGTATCCATCCC<br>CATC | ACCCACGTTTAAAGGT<br>TCCC | 60.0                             | 797                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1418_P4_18332 | scaffold1418                            | 18332                         | A/ATAT                                                                              | TGAGAACATGGCCACC<br>AATA | ACCCACGTTTAAAGGT<br>TCCC | 59.9                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1418_P4_44838 | scaffold1418                            | 44838                         | AATATATATATATATATATAT/AAATATATATATATATATATATAT                                      | TGGACATGAACAAACC<br>ATGC | TACTACGTTGGACTTG<br>GGGG | 60.4                             | 754                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1418_P4_49097 | scaffold1418                            | 49097                         | CTTTTTTTTT/CTTTTTTTTT                                                               | CCGCTGATACTGAATG<br>CAAA | AGCCGATTCGACAGTT<br>GTGT | 59.8                             | 354                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1418_P4_5209  | scaffold1418                            | 5209                          | TATAATAATAATAATAATAATAA<br>TAATAATAAAT/TATAATAATAA<br>ATAATAATAATAATAATAATAA<br>AAT | CACAATTTACGATTTT<br>CACG | CGGCTAGGTTGACCCT<br>TACA | 59.1                             | 819                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1419_P4_10604 | scaffold1419                            | 10604                         | ATTTTTTTTTTT/ATTTTTTTTT                                                             | CCTCTTGCTGCAACA<br>CAAA  | AACTTTTCCGCTGCTT<br>GAA  | 60.0                             | 294                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1419_P4_21351 | scaffold1419                            | 21351                         | TAAAA/TAAAAA                                                                        | AAAAACCTTTGGGAAA<br>TCGG | AATTCAAGTTCGAAATG<br>CCG | 60.2                             | 207                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1419_P4_21445 | scaffold1419                            | 21445                         | TATTA/TATTAATTA                                                                     | ATTCGAACTTGGGCT<br>TCCT  | TGATTGCCGACAATAC<br>CAAG | 60.1                             | 840                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1419_P4_21828 | scaffold1419                            | 21828                         | ACC/AC                                                        | GGAAGTCGCCATTCCA<br>AATA | TGATTGCCGACAATAC<br>CAAG | 59.9                             | 198                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1419_P4_30683 | scaffold1419                            | 30683                         | T/TG                                                          | TCCATCTCCAACAACAT<br>CCA | TAATTGCTCTTGCGGT<br>CCTT | 59.9                             | 306                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1420_P4_5307  | scaffold1420                            | 5307                          | CC/CCACGGAAACAAAC                                             | AACGTACTGCCTATCA<br>CGGG | GGTAAGGGCTCCTTCC<br>AAAC | 60.0                             | 737                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1426_P4_5551  | scaffold1426                            | 5551                          | GAAAA/GAAAAA                                                  | CCTCAGATGAGAGCCA<br>GGAC | ACACCCCGTTTTTCAA<br>GTG  | 59.9                             | 434                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1426_P4_5828  | scaffold1426                            | 5828                          | T/TTC                                                         | AACGGGGTGTTACAAT<br>GAGC | CTGGTTTGACAATGCG<br>TTTG | 59.9                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1426_P4_6734  | scaffold1426                            | 6734                          | TCATCAC/TCATCACCATCAC                                         | TTGATACTATGCCACC<br>ACGC | GCATTTTGCTTGTGGA<br>CTCA | 59.6                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1426_P4_7221  | scaffold1426                            | 7221                          | TAAAAA/TAAAAAA                                                | TGAGTCCACAAGCAAA<br>ATGC | GGTTCCTCTTGTTTT<br>GGGT  | 59.8                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold143_P4_167364 | scaffold143                             | 167364                        | T/TG                                                          | ACACCACCTCTTCAT<br>CGTC  | GAAGGAGCAGTTGGAG<br>AACG | 60.0                             | 737                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold143_P4_5981   | scaffold143                             | 5981                          | CTTGTAATGAGTT/CTTGTAATGA<br>GTTGTAATGAGTT                     | CGATGGAACCCAGAAA<br>AGAA | TTGCACAAGCGAAATT<br>GGTA | 60.0                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold143_P4_67526  | scaffold143                             | 67526                         | TA/TAA                                                        | GGATTGTTGGTTCATT<br>TGGG | TTAGGAAATCGATTGG<br>GGTG | 60.0                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1430_P4_1269  | scaffold1430                            | 1269                          | ATTTTT/ATTTT                                                  | TCATGTGCATTCTACC<br>ACCA   | TGATTTCGAGTCAAACC<br>ACCA    | 60.0                             | 315                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1430_P4_6745  | scaffold1430                            | 6745                          | A/ATTT                                                        | AAGGATGTCTTGACTC<br>TCCCAA | CGGTTAACACCTCCCT<br>GAAA     | 60.1                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1430_P4_8611  | scaffold1430                            | 8611                          | TTAT/TTATAT                                                   | TGTTCAATTCAACGAG<br>GCAG   | GGATTACGATCCGTGG<br>CTAA     | 59.8                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1432_P4_2456  | scaffold1432                            | 2456                          | TAAAAAAA/TAAAAAA                                              | CCATGACATGACCTTA<br>GGGG   | CAATGTAATTTGCATCA<br>TAAAGGC | 60.2                             | 234                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1432_P4_80490 | scaffold1432                            | 80490                         | CTTTTTTT/CTTTTTTT                                             | GCCACTACCAACAACA<br>TTTTCA | ATTTGTGTTTGTGGGG<br>GAAA     | 59.9                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1432_P4_80541 | scaffold1432                            | 80541                         | A/AT                                                          | GCCACTACCAACAACA<br>TTTTCA | ATTTGTGTTTGTGGGG<br>GAAA     | 59.9                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1433_P4_21153 | scaffold1433                            | 21153                         | A/AG                                                          | TTCCGGGTCAGATTTC<br>AAAC   | GGTCCTCGATTTCATCT<br>GGA     | 59.9                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1433_P4_21283 | scaffold1433                            | 21283                         | ATTTTT/ATTTT                                                  | TCCAGATGAAATCGAG<br>GACC   | GAGATTTTCGTACCAC<br>CCGA     | 60.0                             | 481                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1433_P4_21769 | scaffold1433                            | 21769                         | AGCATTATTTTC/A                                                | TCCAGATGAAATCGAG<br>GACC   | TCATATGTACGTTTCGG<br>GCA     | 60.0                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1433_P4_21950 | scaffold1433                            | 21950                         | TAAAAA/TAAAAA                                                 | GATGAAATGGAGGACC<br>GAGA   | TCATATGTACGTTTCGG<br>GCA     | 60.0                             | 332                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1433_P4_33630  | scaffold1433                            | 33630                         | CAAAA/CAAAA                                                   | AGGCGATTTTCGTACC<br>ACAC | CGTGTCAATTTATGTCG<br>GGTG | 60.0                             | 112                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1439_P4_153871 | scaffold1439                            | 153871                        | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATAT             | TGAAAACGGGAGAAAT<br>GAGG | CATCAGCAAGAACCGT<br>GAGA  | 60.0                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1439_P4_282042 | scaffold1439                            | 282042                        | TTATATATATATATATATATAT/TTAT<br>ATATATATATATATATATAT           | TGGCAAGAACAATCAT<br>GGAA | TTGTTCACCCATTTTG<br>ATG   | 60.0                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1446_P4_21277  | scaffold1446                            | 21277                         | TATATA/TATATACATATA                                           | GGCGTTGGAGTCATGT<br>TTTT | TTCTCAACTGACGCAT<br>GAGG  | 60.0                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1447_P4_20275  | scaffold1447                            | 20275                         | T/TTAG                                                        | CCATGAGTGTTTCGTG<br>GATG | TGTCTCATGGCAAATA<br>CCGA  | 60.0                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1448_P4_100734 | scaffold1448                            | 100734                        | TT/TTGTCT                                                     | CATGGCATTAAACATTT<br>CCC | TTCGAACCCGAGATAA<br>GACG  | 60.0                             | 294                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1448_P4_11427  | scaffold1448                            | 11427                         | CAAA/CAA                                                      | AATCCAATGACGCAAA<br>CACA | AGGTCATTTTCGTCCTC<br>CCT  | 60.0                             | 792                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1448_P4_133221 | scaffold1448                            | 133221                        | GTTTTTTTTTTTT/GTTTTTTTTTTT                                    | AACCCACCTCGAAAG<br>AGTT  | CGTCGGATATTGGAGG<br>AAAA  | 60.0                             | 170                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1448_P4_139586 | scaffold1448                            | 139586                        | GC/GCC                                                        | CAGCGGTGAATATGCT<br>GCTA | GAGTTGCCCTGAATC<br>AAAA   | 60.0                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1448_P4_144701 | scaffold1448                            | 144701                        | CAA/CAA                                                       | AGCGGTGGAGAGAACT<br>CTGA | CGTTCGTGCTGACACC<br>TTTA  | 60.1                             | 787                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                 |                               |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1448_P4_34501 | scaffold1448                            | 34501                         | TAAAAAAAAA/TAAAAAAAAA                                           | ACTCCTCGCCACAACA<br>TTTC      | GGTGGGGAGGATGT<br>AAGAA     | 60.1                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1448_P4_37449 | scaffold1448                            | 37449                         | GACACACACAC/GACACACACACAC                                       | ATTTTGCAGTGTGGGT<br>CTCC      | TTCAAACAGCAAAATT<br>GAAA    | 60.0                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1448_P4_39228 | scaffold1448                            | 39228                         | TG/T                                                            | CAACTGTTCACCTCTAA<br>AGTCCCTT | GGTTTGACGTTTTGTCT<br>CATTTT | 59.3                             | 216                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1449_P4_3971  | scaffold1449                            | 3971                          | AATATATATATATATATATATATAT<br>AT/AATATATATATATATATATATATA<br>TAT | AGGAAGAGTGGAGTTG<br>CGAA      | CTGTAAACTGAAGCGC<br>CCTC    | 60.0                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1452_P4_1227  | scaffold1452                            | 1227                          | GTATATATATATATATATATATAT/GT<br>ATATATATATATATATATATATAT         | CGAAATCTTTGGGTTTT<br>GGA      | ACCTAAATTGGGGAGC<br>TCGT    | 59.9                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1452_P4_30210 | scaffold1452                            | 30210                         | TAAA/TAAAA                                                      | TGCCCAATTACCACAA<br>TCAA      | ACCAACCCTTCATTCC<br>CTC     | 59.8                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1452_P4_30615 | scaffold1452                            | 30615                         | A/AAAAATCTT                                                     | TCCATTTTCATGAACCC<br>GATT     | TGTACATTGTTTCCGTC<br>CGA    | 60.1                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1452_P4_4003  | scaffold1452                            | 4003                          | TAA/TA                                                          | CAGCCACAAAATCAAC<br>CCTT      | ACCCGTTAACGATGAT<br>TTGC    | 60.0                             | 823                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1455_P4_12565 | scaffold1455                            | 12565                         | TCCTTCACCT/TCCT                                                 | TTATAGCCGTTGGAAG<br>TGGG      | TCAGGAAGGAAGAAGG<br>CAGA    | 60.0                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1455_P4_13166 | scaffold1455                            | 13166                         | TCCC/TCC                                                        | CGAAGGCTTTGTTGAG<br>AAGG      | CTTGCTTGTGCAGAT<br>TTGA     | 60.0                             | 220                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)  | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1457_P4_19983  | scaffold1457                            | 19983                         | G/GA                                                           | TGGCTTTCAAATCCAC<br>ACA   | GCGAGCAGAGATTTT<br>ACCG     | 60.1                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold146_P4_9980    | scaffold146                             | 9980                          | TC/T                                                           | CTTTCACATCGGCATT<br>CCT   | GTTTCGTACCTTTTCGAC<br>CCAA  | 60.1                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1462_P4_12076  | scaffold1462                            | 12076                         | G/GACCACCGAATGCC                                               | CTGGGTCCTAGTTCGC<br>TCAA  | TCAGCTTTTGGCTGAT<br>GTG     | 60.4                             | 129                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1464_P4_79010  | scaffold1464                            | 79010                         | AT/ATT                                                         | ATCGATTGATTGAGC<br>CAAG   | CGTTTTTCAAAGCGAG<br>GGTA    | 60.0                             | 809                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1465_P4_20135  | scaffold1465                            | 20135                         | TTA/TTAGATA                                                    | ATAGATCCCCTCAGCC<br>CAAC  | TTTCGGTAGTCCCCT<br>CATC     | 60.3                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1465_P4_22512  | scaffold1465                            | 22512                         | ATTT/ATTTT                                                     | TTGCTTTGTCTTGGCA<br>AGTG  | AACCTCCATCGAGAA<br>GGAT     | 60.0                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1465_P4_29157  | scaffold1465                            | 29157                         | CATATATATATATATATATATAT/C<br>ATATATATATATATATATATATATAT<br>TAT | AGAGGGGTTTGTGTTT<br>GACG  | TGAATTTTGTCTGAAG<br>GCT     | 60.0                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1465_P4_3149   | scaffold1465                            | 3149                          | AATATATATATATATATAT/AAAT<br>ATATATATATATATATAT                 | AAGGCTCAACCTTACG<br>TGGT  | TTTTTAGCAATGGCACA<br>ACATT  | 58.7                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1465_P4_5789   | scaffold1465                            | 5789                          | TAA/TAACAA                                                     | TTGCTAATTGGCGACA<br>CTTCT | AAAAAGGGGCTAAATA<br>TAGCGTG | 59.9                             | 700                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1466_P4_353114 | scaffold1466                            | 353114                        | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                  | GCAAGCCGGTATGTTT<br>CATT  | CAAAGCAGACACGAAG<br>GTGA    | 60.0                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                               | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                             |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1466_P4_62106  | scaffold1466                            | 62106                         | CTTTTTTTTT/CTTTTTTTTT                                                                                       | TGCTAGGCCATATCAC<br>TCAA  | CCGTCGCTAAACACAC<br>TCAA  | 59.3                             | 904                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1466_P4_71337  | scaffold1466                            | 71337                         | AAATAATAATAATAATAATAAA/AA<br>ATAATAATAATAATAATAA                                                            | ACCGCGTTTTTAGAAG<br>GGAT  | CCTCCTTGCTTCTTGT<br>GGC   | 60.0                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1467_P4_135942 | scaffold1467                            | 135942                        | TATAATAATAATAATAATAATAA<br>TAATAAT/TATAATAATAATAATA<br>ATAATAAT                                             | ACTTCTAGTTTCGAGG<br>CCGA  | TATGCATGCTTACGGG<br>TTTG  | 59.1                             | 904                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1467_P4_16133  | scaffold1467                            | 16133                         | GTC/GTCAATC                                                                                                 | ACTTTCAAACGGTCAAT<br>CCG  | ACATTATGTGAGGGCG<br>CTTC  | 60.0                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1475_P4_99221  | scaffold1475                            | 99221                         | AAA/AATAA                                                                                                   | CGTGAAGTAGAGCCCC<br>TCAG  | TGCGATAACCCGCTTA<br>ACTT  | 60.0                             | 795                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1475_P4_99318  | scaffold1475                            | 99318                         | CTTT/CTTTTT                                                                                                 | CGTGAAGTAGAGCCCC<br>TCAG  | TCGGTAGCTATTCACA<br>CCCC  | 60.0                             | 865                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1475_P4_99881  | scaffold1475                            | 99881                         | AGG/ACTACTTTGG                                                                                              | GGGGTGTGAATAGCTA<br>CCGA  | TATTGCAGGTCTTGCT<br>GCAC  | 60.0                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1483_P4_32879  | scaffold1483                            | 32879                         | CATAAATAAATAAATAAATAAA<br>TAAATAAATAAATAAATAAAT/C<br>ATAAATAAATAAATAAATAAAT<br>AAATAAATAAATAAATAAATAA<br>AT | GGGGCATAATTGTTAT<br>TGCG  | ACAAGTCACCACCATG<br>GACA  | 60.2                             | 863                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1483_P4_56446  | scaffold1483                            | 56446                         | CT/CTTGAT                                                                                                   | TCTTCACTCAATGCAG<br>AAACC | GGAGATGTTGCTTGTT<br>GGGT  | 57.9                             | 262                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1483_P4_6428   | scaffold1483                            | 6428                          | TAAAAAAAAAAAAA/TAAAAAAA                                                                                     | TAACCTGCATGCCATT<br>GTC   | CAAAAGACACACATATT<br>TGCA | 59.5                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1483_P4_6873   | scaffold1483                            | 6873                          | ATGT/ATGTGT                                                   | GCACCACGTGCGATAA<br>CA    | TGTGTGAGCGTTATTG<br>GTTTG | 60.3                             | 984                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1488_P4_625    | scaffold1488                            | 625                           | A/AG                                                          | ACTCAATGCCAAAACT<br>GGG   | GCAGACCTTACACAAT<br>GCGA  | 60.0                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1490_P4_1256   | scaffold1490                            | 1256                          | GAAAAA/GAAAAAA                                                | CAAACACACCTGTTGG<br>ATGG  | AGGTCATTTTCGTCCTC<br>CCT  | 59.8                             | 281                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1490_P4_74253  | scaffold1490                            | 74253                         | TAAAA/TAAAAA                                                  | GGCATCACTCAGGTCC<br>TGTT  | CACTGGAATGATTGCC<br>AAAA  | 60.1                             | 304                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1493_P4_34926  | scaffold1493                            | 34926                         | AA/AACAAAGTTGCA                                               | TCCGGCTCTTCAGATT<br>CACT  | CCTCAACGATTTTCTG<br>GGA   | 60.0                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1493_P4_65515  | scaffold1493                            | 65515                         | AC/A                                                          | AGGCAATTTGGGATTCT<br>CTCT | GGCTGCTTTGAGTTCC<br>TTTTT | 59.9                             | 372                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1493_P4_73057  | scaffold1493                            | 73057                         | GA/GAAGAACCA                                                  | ATCTTCAAAATCAGGG<br>GGCT  | TTCGAATGACTCGATG<br>TTGC  | 59.9                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1493_P4_75776  | scaffold1493                            | 75776                         | TGGGGG/TGGGGGG                                                | GGCAAAACAAATGGG<br>TCAT   | ATTCATTCCCTCACGCA<br>AAC  | 59.7                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1496_P4_123420 | scaffold1496                            | 123420                        | GTTT/GTT                                                      | CTTGCTCTCCAGTTCC<br>CAAG  | TTTTTGCCCGTAAAGAC<br>CAC  | 60.0                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1496_P4_125238 | scaffold1496                            | 125238                        | TAAAAAAA/TAAAAAAA                                             | GCCGCATTCTGACTCT<br>TGA   | ATCGACGAAAAGTCATT<br>GGG  | 60.0                             | 140                                           | INTERGENIC                                        | --                                  | --                    | --  |





| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1499_P4_40217 | scaffold1499                            | 40217                         | TAA/TAAA                                                      | TCTGATCAGCTCTATG<br>CCTCC   | GGATGGTTGTTGAGT<br>GGCT      | 59.5                             | 157                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1499_P4_40647 | scaffold1499                            | 40647                         | GTT/GTTT                                                      | GCCACTCAAACAACCA<br>TCCT    | TGTTGTTGTGGTTGTG<br>GTTG     | 60.0                             | 850                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1499_P4_48638 | scaffold1499                            | 48638                         | AAAATAAATAAATAAATAA/AAAATA<br>AATAAATAA                       | CCGGGTGTAAGGTTCC<br>ACTA    | TTTGCAAAACCAATGA<br>ATACTT   | 59.8                             | 284                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1499_P4_61021 | scaffold1499                            | 61021                         | CAAAAAAAAAA/CAAAAAAAAA<br>A                                   | TCTTGTCATCCCTAATT<br>TTGTCA | GCATGTGGTGCTCTTA<br>TTGC     | 59.9                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1499_P4_62260 | scaffold1499                            | 62260                         | AAAAATAAATAAATA/AAAAATAA<br>ATAAATAAATAAATA                   | ATGATTGGCTTGGTAG<br>TGCC    | TGTGACGATATTTGTC<br>GAATGA   | 60.0                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1499_P4_62316 | scaffold1499                            | 62316                         | ATTTT/ATTT                                                    | ATGATTGGCTTGGTAG<br>TGCC    | ATGCCCCAAGCTTCT<br>TATT      | 60.0                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1499_P4_65960 | scaffold1499                            | 65960                         | AGG/AGGG                                                      | TTTGACGCCACAAAAG<br>ACAG    | CCCTCACAAAGGAGGG<br>ATT      | 60.0                             | 151                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1499_P4_87098 | scaffold1499                            | 87098                         | AT/ATT                                                        | CGAGATTACAATGAG<br>ATTGTTGG | TTTGCCAATCGATTACC<br>CTC     | 59.9                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1499_P4_931   | scaffold1499                            | 931                           | TAAAA/TAAAA                                                   | TTCTTATTCACCTGGT<br>CCTTT   | TTGAAGGATACATTAC<br>GAGATTCA | 58.3                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold15_P4_131277  | scaffold15                              | 131277                        | CAAAAA/CAAAAA                                                 | CATTAGTTTCGTTTTGT<br>AGCCG  | TTTCTTTGACAGCTTAA<br>TTGTGT  | 58.9                             | 199                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)          | Forward primers (5'-3')      | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------|------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                                        |                              |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold15_P4_13860  | scaffold15                              | 13860                         | GAAAAA/GAAAAA                                                          | AGGGTCTCTCGGTCCT<br>TGAT     | TTTGTGAGGGGTACG<br>AAAC       | 60.1                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold15_P4_143714 | scaffold15                              | 143714                        | CATA/CATATA                                                            | TTCATCTGGACTTTTTG<br>GGC     | ATACCCCGATCCTCAA<br>ACCT      | 60.1                             | 318                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold15_P4_143845 | scaffold15                              | 143845                        | GGGTTTAAGGTTTAAGGTTTAGGGT<br>TTAAGGTTT/GGGTTTAAGGTTTAG<br>GGTTTAAGGTTT | TTCATCTGGACTTTTTG<br>GGC     | TGAAGCACAAAGTACAT<br>GACAAAGA | 60.1                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold15_P4_144204 | scaffold15                              | 144204                        | CAA/CAAA                                                               | AGGTTTGAGGATCGGG<br>GTAT     | CAAGATTGGGCAATC<br>TGCT       | 59.7                             | 757                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold15_P4_76409  | scaffold15                              | 76409                         | GTTTTTT/GTTTTTTT                                                       | GGTGTGATTAGGTTTG<br>GGGA     | CGACGCAAATTCCTG<br>ATTT       | 59.6                             | 694                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold15_P4_76639  | scaffold15                              | 76639                         | AC/A                                                                   | AAAAATTGAACAATCTT<br>AATGGGT | CGACGCAAATTCCTG<br>ATTT       | 57.2                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold15_P4_98165  | scaffold15                              | 98165                         | C/CTTTTTCATAAT                                                         | GGCAATCGATTCCAAC<br>AAGT     | CCCAAGAAAGTAGCCA<br>CCAG      | 59.9                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold150_P4_14614 | scaffold150                             | 14614                         | ATT/ATTT                                                               | ACACACCTATTGGACG<br>CACA     | AGGTCATTTTCGTCCTC<br>CCT      | 60.0                             | 179                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1502_P4_859  | scaffold1502                            | 859                           | TAAAAA/TAAAAA                                                          | AGCCTAGGGAGGACGA<br>AATC     | TCCAATCTTGTGCATT<br>CAA       | 59.7                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1504_P4_5005 | scaffold1504                            | 5005                          | G/GT                                                                   | TTGCAATTTTACCTTG<br>CCC      | CTCCGGGTTTTAGGAT<br>GTGA      | 59.9                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                 |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1506_P4_110236 | scaffold1506                            | 110236                        | CATATATATATATATATA/CATATATA<br>TATATATATATATA                                   | GCTTTTTCGCAAAACAG<br>AAGG | GGGTGCTGATGTGAG<br>TGAA   | 60.0                             | 269                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold151_P4_11544   | scaffold151                             | 11544                         | GAAAAAAAA/GAAAAAAAA                                                             | TTACAGCGCTTGATTC<br>CACA  | AAGTGCTTCAAGGAAG<br>GCAA  | 60.4                             | 705                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold151_P4_1278    | scaffold151                             | 1278                          | TAAAAAA/TAAAAAA                                                                 | AGGCTCAAAGTGGGAT<br>AGCA  | GAAGAGCTTCAAGGAA<br>GGCA  | 59.8                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold151_P4_137398  | scaffold151                             | 137398                        | TAAAAAAAAAAAA/TAAAAAAAAAAAA                                                     | GCCCAAAACCAACA<br>AAAA    | TTGTTCGTCTCTGC<br>CTCT    | 59.8                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold151_P4_18758   | scaffold151                             | 18758                         | CAAAAAA/CAAAAAA                                                                 | ATGATGATTTTCTCCCC<br>GTG  | AAGCGCTGTAAAAGT<br>GCAT   | 59.8                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold151_P4_1987    | scaffold151                             | 1987                          | GAAAA/GAAAA                                                                     | GGACATTTGTGAACAA<br>GGCA  | TTGGAGCTTATGTGT<br>CCTCAA | 59.5                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold151_P4_221306  | scaffold151                             | 221306                        | TCCCC/TCCCC                                                                     | TTCAAAGGAGATGGTT<br>TGCC  | ATGACAATTCCAATGCA<br>CCC  | 60.1                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold151_P4_249272  | scaffold151                             | 249272                        | TTTATTATTATTATTATTATTATT<br>ATTATTAT/TTTATTATTATTATTATT<br>ATTATTATTATTATTATTAT | TGCGGAGAGTCAAGAA<br>AGGT  | GATGCAACCAGCTGAA<br>GACA  | 60.0                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold151_P4_294117  | scaffold151                             | 294117                        | ATTTTTTTTT/ATTTTTTTTT                                                           | CATTCTTTTCTCGCG<br>CAT    | CCAAGTCCCCAGAGT<br>CAAA   | 60.3                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold151_P4_29573   | scaffold151                             | 29573                         | GTATATATATATATATATATATAT/<br>GTATATATATATATATATATATAT<br>ATATATATAT             | ATGGAGGGAACGTGTT<br>TCTG  | CTTGGGAAGTGGAGAG<br>CAAG  | 60.0                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                 |                          |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold151_P4_330311  | scaffold151                             | 330311                        | ACTCTCTCTCTCTCT/ACTCTCTCTC<br>TCTCTCT                                                           | AATCCACACCAGATG<br>AAGG  | TAATTGCGCACCATGT<br>GTTT     | 59.8                             | 871                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold151_P4_35903   | scaffold151                             | 35903                         | AAT/AATAT                                                                                       | ACACACGCATAACACA<br>CGAG | TTGGAGTGCATGTGAC<br>CATT     | 58.2                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold151_P4_4221    | scaffold151                             | 4221                          | AGG/AG                                                                                          | TATAAGCCGAAAATGG<br>CAGG | ATGGCGTTTGATTGA<br>TGAT      | 60.1                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold151_P4_42359   | scaffold151                             | 42359                         | TCCC/TCC                                                                                        | CCTGCCACTAAGGCAA<br>CTTC | GGCTTTTCCCCACACA<br>AATA     | 59.9                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold151_P4_68819   | scaffold151                             | 68819                         | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATT/ATATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATT | AAATGAATGGAAGACG<br>CGAT | AAAAATCTCTTGAATCC<br>CCATT   | 59.5                             | 851                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold151_P4_814     | scaffold151                             | 814                           | ATTTTTTTTT/ATTTTTTTTT                                                                           | GGAGACTCCCATACAT<br>TGCC | TGCTATCCCACTTTGA<br>GCCT     | 59.4                             | 332                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1511_P4_110106 | scaffold1511                            | 110106                        | TAA/TAAA                                                                                        | TTAATGCAGGGGTTTG<br>TGCT | ATTGAAGCCCACTATG<br>GCTG     | 60.5                             | 396                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1511_P4_151014 | scaffold1511                            | 151014                        | AA/AATTTAATA                                                                                    | CGACTCAACCAAAAGG<br>GTGT | TGAAGGAGTCAAAATC<br>CGCT     | 60.0                             | 753                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1511_P4_167354 | scaffold1511                            | 167354                        | T/TA                                                                                            | GGCCTGGCCTACTTAA<br>GGTC | GCATGTTCTTGCCCA<br>TTAT      | 60.1                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1511_P4_169925 | scaffold1511                            | 169925                        | AATATATATATAT/AATATATATATAT<br>ATATAT                                                           | TTGTTCCAATTCCTCAA<br>GGG | GGCGATTTTACGTGTA<br>TATGTGAG | 59.9                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1511_P4_173795 | scaffold1511                            | 173795                        | ATTTTTTTTTT/ATTTTTTTTT                                        | TGGGTAATGTAACACC<br>CCGT | AACTTTTCCGCTGCTT<br>GAA  | 60.0                             | 143                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1511_P4_178928 | scaffold1511                            | 178928                        | GTTTTTTTTT/GTTTTTTTTT                                         | AAGGCGCCACTTGAAA<br>ATTA | AGGCGGAAACTTAGC<br>CATT  | 59.7                             | 336                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1511_P4_179381 | scaffold1511                            | 179381                        | ATTTTTTTTT/ATTTTTTTTT                                         | AATGGCTAAGTTTTCC<br>GCCT | ACCCGAAGATAGCACA<br>CCAC | 60.1                             | 786                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1511_P4_61297  | scaffold1511                            | 61297                         | TAAAAAAA/TAAAAAAA                                             | TTCGAATTTGTTGGTG<br>GTGA | AACCTTTTTACGGCGC<br>TTTT | 59.9                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1511_P4_61385  | scaffold1511                            | 61385                         | TAAAAAAA/TAAAAAAA                                             | CGACACTACGCCAAAA<br>ATGA | TGTCCAAAAGCGCTGT<br>AAAA | 59.7                             | 250                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1511_P4_80497  | scaffold1511                            | 80497                         | AC/A                                                          | GACTCTTCCATAGCG<br>TGCC  | TATGCGAGCATCATAG<br>GCAG | 59.8                             | 132                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1511_P4_86316  | scaffold1511                            | 86316                         | TCCACC/TCCACCGCCACC                                           | GAACTCTTGATTCGCT<br>TGCC | CGGGTTGAGATTCCTC<br>AAAA | 60.0                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1515_P4_15616  | scaffold1515                            | 15616                         | TAAA/TAA                                                      | TTATTCGAAAGGTGG<br>GTGG  | CCATGTCCATGCTCCT<br>TCTT | 59.8                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1515_P4_30120  | scaffold1515                            | 30120                         | TA/TTTATAAA                                                   | GGAAAACTCACTGGTT<br>CCGA | TCTGTCACGCTTTGC<br>CAAC  | 60.1                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1516_P4_3101   | scaffold1516                            | 3101                          | ATTTTCGTCCTCTTTTCGTCCTC/AT<br>TTTCGTCCTC                      | AGGTCATTTTCGTCCT<br>CCCT | ACACCATTGGATGCAC<br>AAGA | 59.9                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1521_P4_13506 | scaffold1521                            | 13506                         | TG/T                                                          | TCAGATTTCAGACGCC<br>ACAA | TTGATTCTGGCTGCCT<br>CTCT      | 60.4                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1521_P4_15206 | scaffold1521                            | 15206                         | T/TTTGAAATAAATTAT                                             | GGGGTTAGGGCTCATA<br>CGAT | GTTGCAGCGTGTGTT<br>CTGT       | 60.2                             | 821                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1521_P4_15603 | scaffold1521                            | 15603                         | GAA/GAAA                                                      | TCGTGGTTCATAATT<br>GGCA  | CAAATAACGATTCGG<br>GCTC       | 59.9                             | 228                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1521_P4_15896 | scaffold1521                            | 15896                         | TAAAAAA/TAAAAAAA                                              | TCGTGGTTCATAATT<br>GGCA  | AAATTAGGCATACAGAA<br>ATGAAGGA | 59.9                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1521_P4_17957 | scaffold1521                            | 17957                         | ATT/AT                                                        | CTAAGGCTGGCAGGAA<br>ACTG | CAAGACATGCTCTGTC<br>GCAT      | 60.0                             | 811                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1521_P4_27144 | scaffold1521                            | 27144                         | TATTTGATGAATTTGATG/TATTTGA<br>TG                              | GCATATGCGGTCCCTT<br>AACT | CAATGCAACAAAACATG<br>CCT      | 59.1                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1523_P4_1764  | scaffold1523                            | 1764                          | GTTTT/GTTTT                                                   | AGGTCATTTTCGTCCT<br>CCCT | TAAATGTTTCATCCAACG<br>GCA     | 59.9                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold153_P4_81004  | scaffold153                             | 81004                         | TT/TTGGTCAAT                                                  | ACTACCAATCGTCTGG<br>TCCG | GGTCTCGATTCATCT<br>GGA        | 60.0                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_10045 | scaffold1530                            | 10045                         | TAAAA/TAAAA                                                   | TTCACACACCACCAT<br>CGTT  | CGTGAATCGTATTTCG<br>TGTG      | 59.9                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_14211 | scaffold1530                            | 14211                         | GAATA/GA                                                      | TGATAGATGCAAAAAG<br>GGGG | TTTAGCCATCAACTTTG<br>GGG      | 59.9                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1530_P4_16153 | scaffold1530                            | 16153                         | ACCCCC/ACCCCC                                                 | TCTCACGGTTGTGAGG<br>ACTG    | ACCGTTCTTGGTTTCT<br>GACC    | 59.9                             | 746                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_16923 | scaffold1530                            | 16923                         | GATATATATATATATATATA/GATATA<br>TATATATATATATATATATATA         | CATTGTGAGTGGTGTG<br>GACC    | TAGCTTTCCACGATCT<br>GGCT    | 59.8                             | 299                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_17844 | scaffold1530                            | 17844                         | GATAATAATAATAATAA/GATAATAAT<br>AATAATAATAA                    | TGGAGAAGGGTTCCAA<br>AGTG    | CGTTTATCTAGGGCAA<br>CCGA    | 60.1                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_18676 | scaffold1530                            | 18676                         | AG/AGG                                                        | CAGTTGTTACACCTTA<br>TGTTGC  | CAACAGATGAATGGC<br>GATG     | 59.6                             | 196                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_19506 | scaffold1530                            | 19506                         | GTTTTTTT/GTTTTTTT                                             | GATTCATGGAAGCAAG<br>TTCTG   | AGGGCCGATTTAACTT<br>TGCT    | 59.2                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_19876 | scaffold1530                            | 19876                         | TAAA/TAAAGCTTTTAGAAAA                                         | TCATTTTCCGCCTTATC<br>AAGA   | AGGGCCGATTTAACTT<br>TGCT    | 59.7                             | 205                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_20086 | scaffold1530                            | 20086                         | ATT/ATTT                                                      | AGCAAAGTTAAATCGG<br>CCCT    | AGGCCTACGAGGAGAG<br>AAAA    | 60.1                             | 203                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_20299 | scaffold1530                            | 20299                         | A/AG                                                          | AGCAAAGTTAAATCGG<br>CCCT    | CCCATATCCAAGAGTA<br>AAACCAA | 60.1                             | 429                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_20775 | scaffold1530                            | 20775                         | T/TATAA                                                       | TTGGTTTTACTCTTGGA<br>TATGGG | TTCAATCGCACTTGTT<br>TGA     | 59.3                             | 919                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_21107 | scaffold1530                            | 21107                         | TC/TCC                                                        | TCTAAAAGATTTTGAAC<br>CCCAA  | TCCAAGGGTGTTAGAA<br>ACGG    | 59.1                             | 812                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1530_P4_23128 | scaffold1530                            | 23128                         | AATATATATATATATATA/AATATA<br>TATATATATATATA                   | TCTCCATTGCACACCC<br>AATA    | GGTGCTGAAATCGGAA<br>AATC     | 59.9                             | 189                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_23299 | scaffold1530                            | 23299                         | A/ATTAAGCC                                                    | TCTCCATTGCACACCC<br>AATA    | GAGCTCTCAGTATCTT<br>CCACCAA  | 59.9                             | 297                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_23816 | scaffold1530                            | 23816                         | TAAA/TAAA                                                     | GCATACCCATGAAGTA<br>AGAATGC | TCACCATCGTGACATT<br>CTCC     | 59.9                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_24452 | scaffold1530                            | 24452                         | AC/A                                                          | AGAAGGAGAATGTCAC<br>GATGG   | GACGTGTGCTGAACTC<br>TCCA     | 59.2                             | 261                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_24697 | scaffold1530                            | 24697                         | CTTTTTTT/CTTTTTTTTT                                           | TGGAGAGTTCAGCACA<br>CGTC    | CCTCCGGTACCATAAA<br>CCCT     | 60.0                             | 249                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_25494 | scaffold1530                            | 25494                         | TAT/TATGTCAAAT                                                | CTTTTCCGTTTTTCAGC<br>CAC    | TTTACCCTCGGTAAAA<br>CCTC     | 59.7                             | 607                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_25850 | scaffold1530                            | 25850                         | TTTTTTATTTTTATTT/TTTTTTAT<br>TT                               | TCGATCTTGAGCGAAT<br>TTGA    | CAATACCAATTTACGTA<br>AAATTCA | 59.5                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_26371 | scaffold1530                            | 26371                         | CTTTTTTT/CTTTTTTTTT                                           | CAAAATTTTCAAAACAAA<br>ACCCA | AAAGCACCTTTACAAA<br>AGCA     | 58.9                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_26727 | scaffold1530                            | 26727                         | CT/CTT                                                        | TGCTTTTGTTAAAGGT<br>GCTT    | ATTGCGAAACCAAACCT<br>GAT     | 57.6                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_26900 | scaffold1530                            | 26900                         | AT/A                                                          | CCCATCATAACCTACAA<br>ATTCCA | ATTGCGAAACCAAACCT<br>GAT     | 60.0                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                                |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1530_P4_27041 | scaffold1530                            | 27041                         | AATAT/AATATAT                                                 | CGTTTTCGACATCAAG<br>ATGGTA     | TCGCAAACCAAACTCG<br>ATAA        | 60.0                             | 134                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_27186 | scaffold1530                            | 27186                         | CTTATTTAT/CTTAT                                               | TCGAGTTTGGTTTGCG<br>AATA       | CGATTGCTCATAAAATC<br>GCTC       | 59.3                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_27232 | scaffold1530                            | 27232                         | ATTTTTTT/ATTTTTTTT                                            | TCGAGTTTGGTTTGCG<br>AATA       | CGATTGCTCATAAAATC<br>GCTC       | 59.3                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_27815 | scaffold1530                            | 27815                         | ATTTTTTTT/ATTTTTTTT                                           | TTTGAGAGGGCCTTTG<br>GTAA       | TCGACAGGTTTGTTTG<br>TTCG        | 59.7                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_27996 | scaffold1530                            | 27996                         | CCTATGGTG/C                                                   | TTTGAGAGGGCCTTTG<br>GTAA       | TCGACAGGTTTGTTTG<br>TTCG        | 59.7                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_28016 | scaffold1530                            | 28016                         | TGGTGTTAA/T                                                   | GGCCCTATGGTGTTAT<br>GGTG       | TCGACAGGTTTGTTTG<br>TTCG        | 60.1                             | 174                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1530_P4_28367 | scaffold1530                            | 28367                         | CAATTAA/CAA                                                   | GGCCCTATGGTGTTAT<br>GGTG       | TTCGAAGCCATTATGTT<br>TGATG      | 60.1                             | 817                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1531_P4_23687 | scaffold1531                            | 23687                         | GT/GTAAATT                                                    | CAAAATTGAGTTGTAAA<br>GTTGTCAAA | TCCAAATGAGATCGAG<br>GACC        | 58.8                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1531_P4_24929 | scaffold1531                            | 24929                         | AT/ATTCT                                                      | TCAGGATTTTGGGTTT<br>AGGG       | TTTTGTAGTTGTACTCA<br>ATAACAAGGA | 58.9                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1531_P4_29443 | scaffold1531                            | 29443                         | AG/AGGG                                                       | TCCAGATGAAATCGAG<br>GACC       | GATTTTCGTTCCACCCT<br>TCA        | 60.0                             | 621                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1532_P4_68652  | scaffold1532                            | 68652                         | CTTTTTTTT/CTTTTTTTT                                           | CATTGCACTGCATGCT<br>CTTT  | TCTTTGCTCACACACA<br>GCC   | 60.0                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1533_P4_36802  | scaffold1533                            | 36802                         | ATTT/AATTATTTATTTT                                            | AGTAGCCGATTTTGTG<br>TGGG  | GGGAGAATTGTAACCC<br>CCAA  | 60.0                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1544_P4_14620  | scaffold1544                            | 14620                         | CTTT/CTT                                                      | CCACTGGATGAATCTC<br>GGTT  | TAGAAGGAACGGAGGG<br>GTTT  | 59.9                             | 794                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1545_P4_176075 | scaffold1545                            | 176075                        | TACACACACACA/TACACACACAC<br>A                                 | TTGTTTTCAAATGCTCC<br>CCT  | TAACACCAACAGCATC<br>CGAA  | 59.5                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1545_P4_178426 | scaffold1545                            | 178426                        | CATATATATATATATATA/CATATATA<br>TATATATATATATATATA             | ACGGCAAGACCCTAAA<br>ACCT  | ACCAGCATGATGACCA<br>GACA  | 60.0                             | 763                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1545_P4_81448  | scaffold1545                            | 81448                         | GCC/GC                                                        | TTGCATGCGATTTATG<br>CAAT  | TCGTGATCTGCTGAGA<br>GTGC  | 60.1                             | 814                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1545_P4_95527  | scaffold1545                            | 95527                         | ATCTACACATGT/AT                                               | AAGGTTCAACGTGTTT<br>TTGG  | CATCAAAAAGTTGCATCA<br>CCG | 59.9                             | 874                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1546_P4_124714 | scaffold1546                            | 124714                        | TAAAAA/TAAAAA                                                 | AATCCTATGGCGCAAA<br>ACAC  | GCCTGAAATATGCCGA<br>GGTA  | 60.0                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1546_P4_6541   | scaffold1546                            | 6541                          | AAT/AATTAT                                                    | GGAACAACAATTTGGT<br>TGGAA | CCAAACAACATGGCCA<br>CATA  | 59.7                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1548_P4_11049  | scaffold1548                            | 11049                         | GTTT/GTT                                                      | CAACTTTGTCCCAAT<br>GCTT   | CTGGTGCTAGTTTTC<br>CACA   | 60.0                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                             |                             |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1550_P4_16901 | scaffold1550                            | 16901                         | CA/C                                                                        | GATGAAATCGAGGACC<br>AGGA    | TTTCATCTGGACTTTTC<br>GGG      | 60.0                             | 429                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1550_P4_33611 | scaffold1550                            | 33611                         | ACCC/ACC                                                                    | CCTTTTGGGCGATTTT<br>TGTA    | ATCGAGGATGAGGAGA<br>CCCT      | 59.9                             | 152                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1550_P4_56017 | scaffold1550                            | 56017                         | TAAAA/TAAA                                                                  | AGGCGATTTTCGTACC<br>ACAC    | TCCAGATGAAATCGAG<br>GACC      | 60.0                             | 322                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1550_P4_58285 | scaffold1550                            | 58285                         | AAATA/AA                                                                    | TTTTGTTCAAACGAAG<br>ATGATAA | TTGTTATGAAATAAAC<br>ATAAACGAA | 57.9                             | 314                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1552_P4_1897  | scaffold1552                            | 1897                          | AGG/AGGG                                                                    | ACCAAGAATGTCCCTG<br>CAAC    | TCTTGTGAAGGAAGC<br>TCGT       | 60.0                             | 223                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1561_P4_17518 | scaffold1561                            | 17518                         | ATTTT/ATTTTT                                                                | TTAGGTCATTACCGT<br>CCGC     | GAAGCCAATGGAGGAT<br>GAAA      | 60.0                             | 330                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1561_P4_34214 | scaffold1561                            | 34214                         | AATATATATATATATATATATATAT<br>ATATATATATA/AATATATATATATAT<br>ATATATATATATATA | TGTGTTATGGGGGAAA<br>TGTT    | GTTGGTCCCTAGCAC<br>CGTA       | 59.9                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1562_P4_18085 | scaffold1562                            | 18085                         | TAAA/TAA                                                                    | GCCATTTTTCCCTCCTT<br>CTC    | GATTCCCCTCCTTAA<br>CGTC       | 60.0                             | 872                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1562_P4_42332 | scaffold1562                            | 42332                         | AGGGG/AGGG                                                                  | GGAGGAGAAGGAGGG<br>ATTG     | TATTTGGATTTTGCT<br>CGG        | 60.0                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1562_P4_44885 | scaffold1562                            | 44885                         | GTTTTTTTT/GTTTTTTTTT                                                        | TTTTCGCTTGACTGA<br>TGT      | TCCAACCTCCCTCCCTT<br>TTT      | 59.5                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')    | Reverse primers (5'-3') | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|----------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                 |                            |                         |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| scaffold1562_P4_62422 | scaffold1562                            | 62422                         | AATATATATATATATATATATATATATATATATATATATATATAT/AATATATATATATA<br>TATATATATATATAT | TATGTCCCAACTTGCAACA        | TCAACCTTTTGTTCTTCG      | 60.0                             | 875                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1566_P4_2139  | scaffold1566                            | 2139                          | GA/GGATCCAATA                                                                   | CCGATTGGATTGTCAGGACT       | CCAAGGAAGGACGAAAATGA    | 59.9                             | 439                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1569_P4_32526 | scaffold1569                            | 32526                         | ACC/ACCC                                                                        | CAGGGCCTTAACCATGAAA        | GTTTTGGGTTTGGA<br>TTTA  | 59.9                             | 601                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1569_P4_32547 | scaffold1569                            | 32547                         | GCCC/GCC                                                                        | CAGGGCCTTAACCATGAAA        | GTTTTGGGTTTGGA<br>TTTA  | 59.9                             | 601                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1569_P4_32980 | scaffold1569                            | 32980                         | TAA/TA                                                                          | ATAAACCGAACCGBAAACA        | GGTTTTATGGTTTAACGGCCT   | 60.4                             | 714                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1569_P4_33746 | scaffold1569                            | 33746                         | T/TC                                                                            | AAACCTTAACCTTAACCC         | ATGGTTTAAGGCCTTGGTA     | 58.2                             | 612                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold157_P4_119283 | scaffold157                             | 119283                        | T/TCCGTTTCTGCAG                                                                 | GAACGTCTTGTTTCCTGC         | TATTGCGGCTTCATCAACAA    | 59.7                             | 287                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold157_P4_139214 | scaffold157                             | 139214                        | ATTTTT/ATTTTTT                                                                  | ATGTTTCATGACGCGAGTG        | GCTCCATTTTGTTTTGGC      | 59.7                             | 675                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold157_P4_16947  | scaffold157                             | 16947                         | TTAATAATAATAATAATAATAATAATAA/TTAATAATAATAATAATAATAATAATAATAATAATAA              | TTCTTTAAATAATTGGTCGATGAAAA | CTCAAATCTGTTGGGGGA      | 59.4                             | 573                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold157_P4_246301 | scaffold157                             | 246301                        | GAAAAAA/GAAAAAA                                                                 | CGATGCTATTTGGTGTGA         | AATGGACCCAACTATTGCCA    | 59.5                             | 159                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold157_P4_248333 | scaffold157                             | 248333                        | CAA/CA                                                        | TTGTATTGCCTCCATCT<br>CAAAA  | TGGAAGTTGTGGATGC<br>AATG   | 59.6                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold157_P4_255926 | scaffold157                             | 255926                        | TA/T                                                          | TTTGGTCTTGCCCTTTG<br>ATGA   | TGCGGTTAAGGTTGGT<br>TCTC   | 59.2                             | 888                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold157_P4_257001 | scaffold157                             | 257001                        | ATTTTTTTTT/ATTTTTTTTT                                         | CACTTCATTGGATGAC<br>ACCG    | CCGTTCAAAAATCGAA<br>GGAA   | 60.0                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold157_P4_289273 | scaffold157                             | 289273                        | T/TATC                                                        | GCACATTCAGTGCCAA<br>GAGA    | ATTGAGGGCATTGTCA<br>CTCC   | 60.0                             | 492                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold157_P4_309691 | scaffold157                             | 309691                        | TAAAAAAAA/TAAAAA                                              | GCGGTGATCCGAAAGA<br>TAAA    | GCATTGGTTTTGGAGT<br>TTGG   | 60.0                             | 756                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold157_P4_311552 | scaffold157                             | 311552                        | TAAAAAAAA/TAAAAAA                                             | TGTGTCCTTGTGCAAA<br>ATCAA   | ACATCAGGATCTCGTT<br>GTGC   | 60.1                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold157_P4_345941 | scaffold157                             | 345941                        | TTT/TTTGTTGTGTGT                                              | GCAAAATGTAGCGCTG<br>TGTG    | CGCACAATGAAAGCTC<br>GTTA   | 60.5                             | 571                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold157_P4_348258 | scaffold157                             | 348258                        | A/AG                                                          | ATACGAGGTCACATCT<br>CGGG    | GCAACCATTTGCACGT<br>TTTT   | 60.0                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold157_P4_34896  | scaffold157                             | 34896                         | ATTTTTTTTT/ATTTTTTTTT                                         | CAACAAATTGGCACG<br>AAAA     | TGTTTTGGGATCATGG<br>GATAA  | 59.6                             | 733                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold157_P4_360517 | scaffold157                             | 360517                        | TA/TACA                                                       | ACGGGAGAAATATATG<br>TGATTGA | TTGGTGACAAACTTGA<br>ATTTTC | 57.5                             | 887                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')         | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|---------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                     |                                 |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold157_P4_361189  | scaffold157                             | 361189                        | TAA/TA                                                              | TGGGTGCATGATCTCT<br>CTTT        | CTCAGTGCCGTTAGCA<br>ACAA       | 58.2                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold157_P4_485175  | scaffold157                             | 485175                        | AAT/AATCTATATATAT                                                   | ATTTCCAGCATGCCAA<br>TTTC        | GGTGCTACAGTGTCGA<br>AGCA       | 59.9                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1575_P4_195052 | scaffold1575                            | 195052                        | CATATATATATATATA/CATATATATA<br>TATATATA                             | CTTGGTCTAACCCTCA<br>CCCA        | CCTGCATGCTTGGTTA<br>CTGA       | 60.0                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1578_P4_45374  | scaffold1578                            | 45374                         | TAAAAAAAAA/TAAAAAAAAA                                               | TGGACAAGAATAAGCC<br>TCGG        | AGGTCATTTTCGTCCTC<br>CCT       | 60.2                             | 232                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1578_P4_76566  | scaffold1578                            | 76566                         | CATATATATAT/CATATATATATAT                                           | TCATTGTTTGTGTTTGG<br>CGT        | CTTGTTTCTCCATGGT<br>CGC        | 60.0                             | 816                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1578_P4_76801  | scaffold1578                            | 76801                         | ATCTCT/ATCTCTCT                                                     | CTGATAGTGACACCGG<br>GTTG        | CTTGTTTCTCCATGGT<br>CGC        | 59.0                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1578_P4_77306  | scaffold1578                            | 77306                         | T/TG                                                                | GCGACCATGGAGAAAA<br>CAAG        | TTGGTTGAATCCACACA<br>CAAAT     | 60.6                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1578_P4_79414  | scaffold1578                            | 79414                         | GTATATATATATATATATATATAT<br>ATAT/GTATATATATATATATATAT<br>ATATATATAT | AAGATTTGCGCGATTT<br>TACA        | TTAACAATCAAACTCT<br>CATATTCAAA | 57.4                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1579_P4_18189  | scaffold1579                            | 18189                         | ATT/ATTT                                                            | TAGGCTTCAAGGAAGC<br>TGGA        | CCGACTAAAATGGACC<br>GAAA       | 60.1                             | 354                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1579_P4_35226  | scaffold1579                            | 35226                         | GAA/GAAA                                                            | CATTTTTAATTGACAAC<br>TCAATTTTCT | TGAAATAAAACCATAAA<br>ACGAAGA   | 58.3                             | 240                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')  | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|--------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                  |                          |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1579_P4_64472  | scaffold1579                            | 64472                         | A/AT                                                             | GAGCGAATTGAGAAAC<br>GAGG | TTTTCAAATAAGTAAC<br>ATTGACAACA | 60.0                             | 927                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1579_P4_7520   | scaffold1579                            | 7520                          | GTTTTT/GTTTT                                                     | GGTTCAGCTCATTGCC<br>AAAT | TCCAGCTTCCTTGAAG<br>CCTA       | 60.1                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold158_P4_121982  | scaffold158                             | 121982                        | CAAAAA/CAAAAA                                                    | ATTGCCCAAGATGTC<br>CAAG  | AGTCACCAGTCACCAG<br>TCCC       | 59.9                             | 777                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold158_P4_131962  | scaffold158                             | 131962                        | AAA/AAAAGCCACCACAA                                               | GTGACTGGGGACTGGT<br>GACT | ATATTTGTGTTGCCG<br>GCTC        | 60.0                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1580_P4_472188 | scaffold1580                            | 472188                        | ATTT/ATTTT                                                       | TGATGCAAGAAGCCAC<br>ATCT | CTTGAAAGCCATTGGA<br>GAGC       | 59.4                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1580_P4_472285 | scaffold1580                            | 472285                        | TC/T                                                             | TGATGCAAGAAGCCAC<br>ATCT | CTTGAAAGCCATTGGA<br>GAGC       | 59.4                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1580_P4_472375 | scaffold1580                            | 472375                        | CATA/CATATA                                                      | TTTTGGTCAGGGGAAG<br>GTTT | CTTGAAAGCCATTGGA<br>GAGC       | 60.7                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1580_P4_472426 | scaffold1580                            | 472426                        | CT/CTT                                                           | TTTTGGTCAGGGGAAG<br>GTTT | CTTGAAAGCCATTGGA<br>GAGC       | 60.7                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1580_P4_69955  | scaffold1580                            | 69955                         | ATTTTT/ATTTT                                                     | ATCACCAGCCACTTAG<br>GCAA | TCCCTTATGACAATTCA<br>TGGTG     | 60.7                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1585_P4_62915  | scaffold1585                            | 62915                         | CATATATATATATATATATATATAT<br>T/CATATATATATATATATATATAT<br>ATATAT | AGGAAGAGTGGAGTTG<br>CGAA | GTTTGAATTTTGCTC<br>GGA         | 60.0                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                   |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1586_P4_1838   | scaffold1586                            | 1838                          | AC/ACC                                                            | AGGGAGGACGAAATG<br>ACCT    | TGACCAATTTTGAGCAT<br>CCA  | 59.9                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1607_P4_116947 | scaffold1607                            | 116947                        | GAAATATATAAAAATATA/GAAAT<br>ATA                                   | TTCCATAAAACACATT<br>TCCTCC | CACCTACACGTGTGTT<br>CGTAA | 59.3                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1607_P4_123790 | scaffold1607                            | 123790                        | TAAAAAAAAA/TAAAAAAAAA                                             | AGCTGACAATTTGTGT<br>GGCTT  | ATAAACGTGCATGCACG<br>GGAC | 59.8                             | 135                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1607_P4_32654  | scaffold1607                            | 32654                         | CAAAAAA/CAAAAAA                                                   | TGTTGCGTAGGTCCGT<br>GATA   | CCTCAGATGAGAGCCA<br>GGAC  | 60.1                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1609_P4_2922   | scaffold1609                            | 2922                          | A/AAGTTCATTT                                                      | TGTGTGTTTGTGTCAT<br>CGGA   | ATCCTTGGGAGGACGA<br>AAAT  | 59.5                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1613_P4_106669 | scaffold1613                            | 106669                        | C/CGATATCATAGCCAAG                                                | ACAATTTACGCCACCG<br>AAAG   | AGAAGCGACCCCATAG<br>GTTT  | 60.0                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1613_P4_19873  | scaffold1613                            | 19873                         | CATATATATATATATATATATATA<br>T/CATATATATATATATATATATAT<br>ATATATAT | AGCATAGGCTCGATAC<br>CAAGA  | TGTCGATTTCCAATCAC<br>CAA  | 59.0                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1613_P4_98434  | scaffold1613                            | 98434                         | A/AG                                                              | AAGAAAGTTGCTCCTT<br>GCCA   | AGGAGCACTTACCTCC<br>GTTG  | 60.0                             | 133                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1614_P4_131511 | scaffold1614                            | 131511                        | AATATATATATAT/AATATATATAT<br>AT                                   | CCGCAGTAATTCCGA<br>TAAA    | ATCAGCCTAAGGGGGA<br>AGAA  | 60.1                             | 875                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1614_P4_14076  | scaffold1614                            | 14076                         | TC/TCC                                                            | TTTTGGTCCCTCTAG<br>GCTT    | AGGGAGGACGAAATG<br>ACCT   | 60.1                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                     | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                                   |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1614_P4_164436 | scaffold1614                            | 164436                        | CTCTGAT/CT                                                                                                        | AAAACCGCCAAAGAAA<br>TGTG   | ATGACATGTGTGAGCC<br>GTGT  | 60.0                             | 161                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1614_P4_8293   | scaffold1614                            | 8293                          | ATATATATATATATAT/ATATATATAT<br>ATATATGTATATATATATATAT                                                             | CTTCTGATGCCCGGAT<br>TAAA   | AAGATGGAGGAAATGC<br>GATG  | 60.0                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1615_P4_725    | scaffold1615                            | 725                           | ATT/ATTT                                                                                                          | GATGAAATCGAGGACC<br>AGGA   | TTTCATCTGGACTTTTC<br>GGG  | 60.0                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1623_P4_3571   | scaffold1623                            | 3571                          | ACACCA/ACA                                                                                                        | TCGGCTCTGAAAAGAT<br>TTGAA  | CAGCTGTTGTTGCAGT<br>TGCT  | 59.9                             | 214                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1626_P4_132024 | scaffold1626                            | 132024                        | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>TTATTATTATTATTATTATTATT<br>TTATTATTATTATTATTATTATT<br>TTA | TCTTCTGTGGCCGAC<br>TCTT    | TGTTGACACCTAATTT<br>GTCCG | 60.0                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1626_P4_133406 | scaffold1626                            | 133406                        | A/ATATAT                                                                                                          | TGTCACCGTCATATTCA<br>TTCAA | TGCGAGATCCATGACT<br>TCAA  | 58.9                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1630_P4_6306   | scaffold1630                            | 6306                          | T/TA                                                                                                              | GTACCACCCGACAAAA<br>ATGG   | TCCAGATGAAATCGAG<br>GACC  | 60.1                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1631_P4_32889  | scaffold1631                            | 32889                         | TGGTTTAAAA/T                                                                                                      | GTCCACTTCCGTTTCG<br>GTAA   | GTCGCTTCAAAAGTTG<br>GCTC  | 60.0                             | 625                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1635_P4_74246  | scaffold1635                            | 74246                         | TCCC/TCCCC                                                                                                        | GGTAAACGTGTGTTGC<br>ATGG   | GGAGTACCATAGGCCA<br>ACGA  | 59.9                             | 258                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1638_P4_80225  | scaffold1638                            | 80225                         | AGCCAA/AGCCAATCGATTGCCAA                                                                                          | CTCTCATCTGAGGGCA<br>AAGC   | TGGTCATGCAGAACT<br>CAGC   | 60.1                             | 331                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                         |                          |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1643_P4_156175 | scaffold1643                            | 156175                        | CTT/CTTT                                                                | ATTGTCCAACACCTCC<br>AAGC | CTCCCTTTCTTCGTT<br>TTC      | 60.0                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_15960  | scaffold1643                            | 15960                         | CTTTTTTT/CTTTTTT                                                        | AGGGAGAAATTCGGGT<br>TGTT | ATTTTGAATACAAGGT<br>TTTGATT | 59.8                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_163768 | scaffold1643                            | 163768                        | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATAT<br>ATATATATATATA | ATTTCCAGCATGCCAA<br>TTTC | CTTCCAGAACTAGCC<br>GCAC     | 59.9                             | 719                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_166873 | scaffold1643                            | 166873                        | CAAAAAAA/CAAAAAA                                                        | GCAACTAGGGGTGTT<br>AGGA  | ATGCACACTTGTTGCA<br>CCTT    | 60.1                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_166918 | scaffold1643                            | 166918                        | CTTTTTTTTTT/CTTTTTTTTTT                                                 | GCAACTAGGGGTGTT<br>AGGA  | ATGCACACTTGTTGCA<br>CCTT    | 60.1                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_167427 | scaffold1643                            | 167427                        | CAAAAAAAAAAAAA/CAAAAAA<br>AAAAA                                         | GGTGCAACAAGTGTGC<br>ATGA | AAGCAGCGCGTTTTTA<br>GAAG    | 61.8                             | 346                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_169454 | scaffold1643                            | 169454                        | CAAAAAAAAAA/CAAAAAA                                                     | GTCATTTTTGGCGTAG<br>TGGG | TTTCCGGTCAACACTC<br>ATCA    | 60.4                             | 133                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_171022 | scaffold1643                            | 171022                        | TTTA/TTTAATTA                                                           | TAACCCCATCAAATTTG<br>GGA | TCTTGAAGGAGCGGT<br>AGAA     | 60.0                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_171559 | scaffold1643                            | 171559                        | AGATCGAT/AGAT                                                           | TTCTACCGCTCCTTC<br>AAGA  | TTTCCTCCGGTGTTAC<br>AGG     | 59.9                             | 352                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_171751 | scaffold1643                            | 171751                        | TTTTTAAAA/TTTTTAAATAAATGTT<br>TTAAAA                                    | TTCTACCGCTCCTTC<br>AAGA  | TGTTGAGTTGCACCA<br>CCAT     | 59.9                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1643_P4_180974 | scaffold1643                            | 180974                        | ATGATGAATCTTGATGAATCTTGAT<br>GAAT/ATGATGAATCTTGATGAAT         | CCCACGCTTCTTTAGC<br>AGTC    | TTTCACTTTCCCGCTTC<br>TGT   | 60.0                             | 859                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_192850 | scaffold1643                            | 192850                        | TATAAATA/TATA                                                 | GAGGGGGAGAAAGCT<br>GAGAG    | TGCTGACATGATTGTT<br>GATGTG | 60.5                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_193039 | scaffold1643                            | 193039                        | ATTTTTTT/ATTTTTT                                              | GAGGGGGAGAAAGCT<br>GAGAG    | TAGCATGCTGAAATT<br>GCTG    | 60.5                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_210380 | scaffold1643                            | 210380                        | CTTT/CTTTT                                                    | AATACAGCGAAAAGC<br>TCGC     | TCGAAAAGAAATCGAG<br>ACCG   | 59.6                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_210540 | scaffold1643                            | 210540                        | ATTTTTTTT/ATTTTTTTTTT                                         | CACACAATCACAAATT<br>TTCTCAA | AAAGAAATCGAGACCG<br>TTGC   | 59.1                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_211018 | scaffold1643                            | 211018                        | TGTA/T                                                        | TTCTCTCACCGCTAA<br>CTCG     | ATGGTGGGGGTATGAA<br>TGAA   | 60.5                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_211096 | scaffold1643                            | 211096                        | TTCT/TT                                                       | ACGGTCTCGATTTCCTT<br>TCG    | ATGGTGGGGGTATGAA<br>TGAA   | 59.3                             | 585                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_211209 | scaffold1643                            | 211209                        | GAAAAA/GAAAAAA                                                | TTCAATCATACCCCA<br>CAT      | CTCTCAGCTTTCTCCC<br>CCTC   | 59.9                             | 222                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_213932 | scaffold1643                            | 213932                        | TA/TATAA                                                      | CGGATTTGCTCTCTG<br>AAGC     | CATTGGTGCAGTTGTT<br>CGTC   | 60.0                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1643_P4_4999   | scaffold1643                            | 4999                          | CAAAAAA/CAAAAAA                                               | CTCCCAGCCTCTTGTA<br>CTGG    | AGGCAAGCCATTGAAA<br>GAAA   | 59.9                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1643_P4_55973 | scaffold1643                            | 55973                         | GATATATATATAT/GATATATATAT                                     | CAATTCCACAGGTAC<br>GCTT    | GTCGCGGAGTAACAAA<br>GACC    | 60.0                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_11144 | scaffold1651                            | 11144                         | TCCC/TCC                                                      | TGACATGTTTGGCATC<br>GTTT   | CCACCACCCCAACTT<br>AGAA     | 60.0                             | 378                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_11506 | scaffold1651                            | 11506                         | GTTTTTTTTTTTT/GTTTTTTTTTT                                     | TGACATGTTTGGCATC<br>GTTT   | ATCATGCTCCAAGTT<br>GCTT     | 60.0                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_11966 | scaffold1651                            | 11966                         | ATTTTT/ATTTTTT                                                | AAATTGTTGCTTGGGG<br>ACAA   | GTCCGAATTTGTTTT<br>GGTG     | 60.3                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_12361 | scaffold1651                            | 12361                         | GTTTTTTT/GTTTTTTTT                                            | AAATTGTTGCTTGGGG<br>ACAA   | TGACGTCATGACCTGC<br>ATT     | 60.3                             | 882                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_13370 | scaffold1651                            | 13370                         | TATTAATTAATTAATT/TATTAATTA<br>TTAATTAATT                      | CCTTGAGTTCGACACT<br>CGGT   | TGGTGACCGTGAATT<br>GTTG     | 60.3                             | 337                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_13586 | scaffold1651                            | 13586                         | CAAAAAA/CAAAAAAA                                              | CCTTGAGTTCGACACT<br>CGGT   | CAGGATGTGAACCGTA<br>AATCTTC | 60.3                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_14250 | scaffold1651                            | 14250                         | ATATTTTAAGGTATTTTAAGGTAT/A<br>TATTTTAAGGTAT                   | AAAAATGGAGAGATCG<br>AAAGTG | TTGATGCTAGGGGGAT<br>TTTG    | 57.5                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_15028 | scaffold1651                            | 15028                         | AGG/AGGG                                                      | TGATCCAACCAAC<br>TGAA      | TTGGTCTTGGATTGG<br>AAGC     | 59.9                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_16483 | scaffold1651                            | 16483                         | AGG/AG                                                        | GGGAAGGGATGTAAA<br>GGGA    | TTTCGTCGTGTTTCCT<br>GTG     | 60.1                             | 135                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1651_P4_16500 | scaffold1651                            | 16500                         | CA/CAAA                                                       | GGGAAGGGATGTAAA<br>GGGA  | ACGTCGTGATTTGTGC<br>TTCA | 60.1                             | 231                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_16843 | scaffold1651                            | 16843                         | GACC/GACCACC                                                  | GGGAAGGGATGTAAA<br>GGGA  | AAATCTGGCCTGGAC<br>CTG   | 60.1                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_16897 | scaffold1651                            | 16897                         | TTA/T                                                         | TAAGGCATGGTATGGG<br>GAAA | CTAAGCCTGAGTTGG<br>CCTG  | 60.1                             | 921                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_17729 | scaffold1651                            | 17729                         | GATAT/GATATAT                                                 | TCTCTTGGGTGATTTT<br>CGG  | ACACCCAACTCTTGT<br>GGC   | 60.0                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_18006 | scaffold1651                            | 18006                         | A/AG                                                          | TGATTGGGGGCATACA<br>TTTT | ACACCCAACTCTTGT<br>GGC   | 60.0                             | 171                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_18574 | scaffold1651                            | 18574                         | CA/C                                                          | CTGGATTGGAATTGTC<br>AGCA | TCACGCACACTCCATC<br>TCTC | 59.6                             | 679                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_18823 | scaffold1651                            | 18823                         | AG/A                                                          | GAGAGATGGAGTGTGC<br>GTGA | AACCCAGAACTCGAGC<br>TGAA | 60.0                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_4908  | scaffold1651                            | 4908                          | CAAAAAA/CAAAAAA                                               | TCGAACTCAAGGATTG<br>CATT | GGGGCCACTTAGGGTT<br>GTAT | 59.7                             | 860                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_5134  | scaffold1651                            | 5134                          | GAAAAAA/GAAAAA                                                | ATGGCACAAGTCTCCC<br>AACT | GGGGCCACTTAGGGTT<br>GTAT | 59.6                             | 276                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1651_P4_7825  | scaffold1651                            | 7825                          | AC/A                                                          | TGCTGGTATGTGAGAG<br>GCTG | AGTCGATGGAATGAAC<br>TCGG | 60.0                             | 691                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                     |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1659_P4_125279 | scaffold1659                            | 125279                        | TTATATATATATATATATATA/TTATA<br>TATATATATATATATATA                   | CCTTCTCATTGCGAAC<br>CCTA   | CTTCGACACTGTAGCA<br>CCCA    | 60.2                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1659_P4_19972  | scaffold1659                            | 19972                         | CAAAAAAAAAAAAA/CAAAAAAAAA<br>AAAAA                                  | TTGGGGTTGCTAATGG<br>GATA   | TTTGAGAACTTTCGG<br>GTTG     | 60.1                             | 289                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1659_P4_269627 | scaffold1659                            | 269627                        | AATATATATATATATATAT/AAATAT<br>ATATATATATATATATAT                    | CACCGTAGTGTGGTGG<br>TGAG   | CGGTGAATCCTTTACG<br>GAGA    | 60.1                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1659_P4_31301  | scaffold1659                            | 31301                         | CCA/CCACA                                                           | CCGTTGGAATTTCTGG<br>CTTA   | TGATGGACACGCTCTT<br>TCAA    | 60.1                             | 761                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1659_P4_385436 | scaffold1659                            | 385436                        | AAAAAAAA/AAAAAAAAATAAAAAA                                           | GGAAAGAAACAGGGCA<br>AACA   | AAGATGCGTTGAGAAG<br>CGAT    | 60.1                             | 278                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1659_P4_437080 | scaffold1659                            | 437080                        | GT/G                                                                | CCCATACACAGACTCC<br>GTCC   | GGTAAGGGCTCCTTCC<br>AAAC    | 60.4                             | 842                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1659_P4_96268  | scaffold1659                            | 96268                         | GTTT/GTTTT                                                          | TTGCTCACTACCACGC<br>TACG   | CACCAAAGCACATCCA<br>TTCA    | 60.1                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold166_P4_199609  | scaffold166                             | 199609                        | CCACA/CCACACA                                                       | TGCATTTCTTTTGTA<br>TTCTTGA | TGGGGTGTTACATTC<br>TCCC     | 60.0                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold166_P4_227311  | scaffold166                             | 227311                        | TTATATATATATATATATATATA<br>TATA/TTATATATATATATATATAT<br>ATATATATATA | CATCTCGTCGGTCATC<br>ATTG   | TGATTCATGTAACACC<br>CAAA    | 60.1                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold166_P4_24696   | scaffold166                             | 24696                         | AATATATATATATATATATATA/<br>AATATATATATATATATATATAT<br>A             | GCATTCTACCGTCAAA<br>ATGAAA | TTTTCTGTTGCAAACTT<br>GTCTGA | 59.1                             | 696                                           | INTERGENIC                                        | --                                  | --                    | --  |





| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                       | Forward primers (5'-3')        | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------|--------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                     |                                |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold167_P4_66850   | scaffold167                             | 66850                         | TAAAAAAAA/TAAAAAAAAA                                                                                | AAGAGAGGTCACTTTG<br>GCGA       | CAATTCCCACAGGTAC<br>GCTT       | 60.0                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1679_P4_2481   | scaffold1679                            | 2481                          | CGGGTTTAGGGTTTAGGGTTTAGG<br>GTT/CGGGTTTAGGGTTTAGGGTT                                                | TTACGGTTTTGCGTTTA<br>GGG       | AACCAAAATCCGACAC<br>CCTT       | 60.0                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1681_P4_934    | scaffold1681                            | 934                           | ATTTT/ATTTT                                                                                         | GAGATTTTCGTACCAC<br>CCGA       | TCCAGATGAAATCGAG<br>GACC       | 59.9                             | 797                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1682_P4_8324   | scaffold1682                            | 8324                          | TTGTGT/TTGT                                                                                         | AGGTCGTTTTCGTCCT<br>TCCT       | CACCCAATGACACCA<br>TGAA        | 60.1                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1684_P4_62791  | scaffold1684                            | 62791                         | ATT/ATT                                                                                             | TTAAGTACAACACAAA<br>ACGAAGATGA | AGTGTGTCAATGTTAC<br>TTTATTTCAA | 57.8                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1684_P4_6435   | scaffold1684                            | 6435                          | TA/TAA                                                                                              | TATCGCGGGTCTTGTT<br>TTTC       | ACCAAAATCGATTGGCA<br>CTTC      | 60.1                             | 330                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1684_P4_69381  | scaffold1684                            | 69381                         | TAA/TA                                                                                              | CGGGTTGTACAAAAAT<br>CGCT       | CAGCGATGGCTAGTGT<br>TTGA       | 60.0                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1685_P4_110905 | scaffold1685                            | 110905                        | TTATAT/TTAT                                                                                         | AAAATTGGGTGCCAA<br>ATAA        | AAATGGACCGAAATCG<br>AGTG       | 57.1                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1685_P4_2214   | scaffold1685                            | 2214                          | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTAT/ATAT<br>TATTATTATTATTATTATTAT<br>TATTATTATTATTATTAT | TTATTTCAACGTCGTGT<br>CCA       | AGGTGTGTTTGGGT<br>CTGC         | 60.0                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1687_P4_100356 | scaffold1687                            | 100356                        | GAAAAAAAA/GAAAAAAAAA                                                                                | CCAGTCAAGCATTCCC<br>ATCT       | CCCAAGGGCTCAGTTA<br>TTCA       | 60.1                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1687_P4_165308 | scaffold1687                            | 165308                        | GTTATTTATTTATTTATTTATTTA/GT<br>TATTTATTTATTTATTTA             | ACAAAATACCCGCATT<br>GAGC   | ATTTGAACTCACGACAC<br>CCC     | 60.0                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1687_P4_74331  | scaffold1687                            | 74331                         | T/TTGAACCG                                                    | CTGCCGAACCCCAACT<br>ATAA   | CGTATTTGCAACAAGC<br>TGGA     | 60.0                             | 481                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1696_P4_4415   | scaffold1696                            | 4415                          | ATTTTTTTTT/ATTTTTTTTT                                         | ATAACCCGAACCTCAA<br>ACCC   | TGTTTGAATATGACGC<br>CGA      | 60.1                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1696_P4_5390   | scaffold1696                            | 5390                          | TGTTTCGGGTTTCGGGTTTCG/TGT<br>TTCGGGTTTCG                      | TTGAAGTACGAAAATC<br>GCCC   | TTCGTTATGCGGTCAA<br>ACCT     | 60.1                             | 813                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1696_P4_6881   | scaffold1696                            | 6881                          | GAAAAA/GAAAAAA                                                | TTTCATCTGGACTTTTC<br>GGG   | CGAGGACCAGGAGACC<br>ATTA     | 60.0                             | 961                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold17_P4_297467   | scaffold17                              | 297467                        | AG/AGG                                                        | ACACCTTCAGCGGCAT<br>ACTT   | TGAGGCATGAACCTCA<br>ACTCT    | 59.8                             | 852                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold17_P4_64357    | scaffold17                              | 64357                         | AATAAT/AATAATTATAAT                                           | CGCCAAGTTTTACTGT<br>GTGTTG | TCACCAATATCTTAACC<br>ACCAAAA | 60.6                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1701_P4_101096 | scaffold1701                            | 101096                        | TT/TTCT                                                       | AGGTCATTTTCGTCCT<br>CCCT   | GCCCTCAGATGAGAGT<br>CAGG     | 59.9                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1701_P4_122702 | scaffold1701                            | 122702                        | C/CAA                                                         | CGCTTCCTACTCAAGG<br>CATC   | AACTGCATTGAGGACT<br>CGCT     | 60.0                             | 913                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1701_P4_126269 | scaffold1701                            | 126269                        | T/TCAC                                                        | CAATGCCAATAAAAGA<br>ATGCAA | GGTTGCATGAATGACG<br>TTTG     | 60.0                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                               |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1703_P4_131019 | scaffold1703                            | 131019                        | TGAAGAAGAAGAAGAAGAAG/T<br>GAAGAAGAAGAAGAAGAAGAA<br>G          | CCAAAACGATTTCCCTT<br>CAA      | TTTCCAAAAGTGACCG<br>AACC      | 59.9                             | 234                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1703_P4_299119 | scaffold1703                            | 299119                        | TAAAAAAAAA/TAAAAAAAAA                                         | GGGCTCACCCACATAT<br>TTTC      | TTGCGATGCTTAGATT<br>CTCC      | 59.2                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1704_P4_11771  | scaffold1704                            | 11771                         | AATATA/AATATATA                                               | AACGATCAAGAGTCGC<br>AAAA      | ACCCTAAACCTAAAG<br>CCCA       | 58.5                             | 347                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1704_P4_32949  | scaffold1704                            | 32949                         | GT/GTTT                                                       | TTCGCAACTCCACTCTT<br>CCT      | GACACGCCAAATACAA<br>CGAA      | 60.0                             | 255                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1704_P4_9435   | scaffold1704                            | 9435                          | GAAAAAAA/GAAAAAAA                                             | TTTTGTGTGCTTGACT<br>GATGTT    | GAAATTTGGACGAAAA<br>CGGA      | 59.7                             | 715                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1706_P4_101986 | scaffold1706                            | 101986                        | GAAAAAAA/GAAAAAAA                                             | TGTTAGGAGGATCTCA<br>CGGG      | AACAAGATTCACGGG<br>CAAG       | 60.1                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1706_P4_118201 | scaffold1706                            | 118201                        | TAAAAAAA/TAAAAAAA                                             | CCGGTTGGATAACCAC<br>TTGT      | GCATTCCAGTTGTTCTT<br>CCC      | 59.7                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1708_P4_12799  | scaffold1708                            | 12799                         | TA/T                                                          | TCTGATGGTTAAAGTAT<br>TGGTGGA  | GAACATGTGAAGGAGA<br>CACAAATTC | 59.8                             | 409                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1708_P4_13060  | scaffold1708                            | 13060                         | ATTTTTT/ATTTTT                                                | GAATTGTGTCTCCTTC<br>ACATGTTTC | GCAGCAACGTCAAGAA<br>CTCA      | 59.9                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1708_P4_14932  | scaffold1708                            | 14932                         | GTTT/GT                                                       | GCCATTTGGGTGGTTG<br>ATAG      | CTGCTTGAGGACAAGC<br>AACA      | 60.2                             | 901                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1708_P4_29368 | scaffold1708                            | 29368                         | GAAAAAAAA/GAAAAAAAAAAAA                                       | ATCCTACCGTTCGTA<br>CCCT    | TGATCCAGATTGCAT<br>GGAG     | 59.7                             | 731                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1708_P4_34637 | scaffold1708                            | 34637                         | TAAAAAAAA/TAAAAAAAA                                           | TGGAAACTGTGTTTG<br>GAAGAA  | GTTTGGCGTTGGTTT<br>CACT     | 59.6                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1708_P4_40978 | scaffold1708                            | 40978                         | ATTTTTTTTT/ATTTTTTTTT                                         | GACACCCTAAACGCCA<br>AAAA   | GCGTTTGCGAATCGT<br>AGTT     | 60.0                             | 395                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1708_P4_61127 | scaffold1708                            | 61127                         | GAAAAAAAA/GAAAAAAAA                                           | AGTTGATGGCAGTGGC<br>TTTT   | AAACCATTTTAGGGTT<br>CATCA   | 59.7                             | 786                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1708_P4_7817  | scaffold1708                            | 7817                          | GCCCC/GCCCCC                                                  | AGTTTCACCACCCGT<br>CCTC    | CCCAAAATGAAAATCC<br>CCT     | 60.0                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1708_P4_82415 | scaffold1708                            | 82415                         | TT/TTTCCCT                                                    | GTAAGTCTTGCTTGGG<br>CTGC   | ACACATACTTTGTGGC<br>GTGC    | 60.0                             | 138                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold171_P4_107206 | scaffold171                             | 107206                        | ATT/ATTT                                                      | ATTTCCACATCACCC<br>AAAA    | AAATCATTATTACCA<br>TAAGTGGA | 60.0                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold171_P4_111668 | scaffold171                             | 111668                        | TAAAAAAAA/TAAAAAAAA                                           | AAATCCGAGATTTGAT<br>CCTTTT | CCGAGATGATTTCCAT<br>GCT     | 58.2                             | 882                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold171_P4_122262 | scaffold171                             | 122262                        | GTTTT/GTTTTT                                                  | GAAGTTGAGCGCAATG<br>TTGA   | ATAAAAGGGTGACGTG<br>GCAG    | 60.0                             | 297                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold171_P4_214990 | scaffold171                             | 214990                        | ATTTTTTTTT/ATTTTTTTT                                          | GTGGGAGGTGCATTCT<br>GATT   | AAGGAGTACCACCCCA<br>TTCC    | 59.9                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                       | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                     |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold171_P4_222521  | scaffold171                             | 222521                        | TAAAAAAAAA/TAAAAAAAAA                                                                               | TGGTGCAATGATTGTA<br>TTCTTCA | GGTGAACGTGGGTCAA<br>ACTT   | 60.4                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold171_P4_224792  | scaffold171                             | 224792                        | TAAA/TAAAA                                                                                          | AAATCGATCCCCTAT<br>CACAT    | TAGCAGCTGGAGGAAC<br>ATGA   | 57.4                             | 348                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold171_P4_715     | scaffold171                             | 715                           | TAAAA/TAAAAA                                                                                        | AGGGAGGACGAAATG<br>ACCT     | GCATCCAATTGGTGTG<br>TTTG   | 59.9                             | 756                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1710_P4_118191 | scaffold1710                            | 118191                        | TA/TAA                                                                                              | ATGGCAATTCCTGGAA<br>ACAA    | AACCAAGGTTGGACTC<br>GAAA   | 60.3                             | 266                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1710_P4_13152  | scaffold1710                            | 13152                         | CATTATTATTATTATTATTATTAT<br>TATTATT/CATTATTATTATTATT<br>ATTATTATTATTATTATT                          | GGTCGCATCCTTGTA<br>TGTG     | AACAACCTCCTCGGATT<br>TGG   | 59.2                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1710_P4_153888 | scaffold1710                            | 153888                        | TAAAAAAAAA/TAAAAAAAAA                                                                               | CAAAATCTTCATGTTGA<br>CCCC   | GCACATGATATGCACT<br>CCTAAA | 59.3                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1710_P4_8434   | scaffold1710                            | 8434                          | TA/TTCAATCAAGTTAA                                                                                   | CCCTGTGACAAACACA<br>ATCG    | TGTTAATCGACGTGCC<br>AATC   | 60.0                             | 155                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1710_P4_90486  | scaffold1710                            | 90486                         | TAAAAAAAAA/TAAAAAAAAA                                                                               | GTCCGTCTTGGTGCAG<br>TTTT    | TGTGGTGACGTGGTT<br>GTAGTTT | 60.2                             | 686                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1710_P4_92835  | scaffold1710                            | 92835                         | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATT/TTTATTAT<br>TATTATTATTATTATTATTATTAT<br>T            | TTAAGTTGGTTGGGC<br>TTGG     | TGAAGGAAATCAACCC<br>ATTTTC | 60.0                             | 167                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1718_P4_51267  | scaffold1718                            | 51267                         | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATA/AAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAA | GCGGAGAGAGACATTG<br>TGGT    | TGCCACCCCTTTTCTCT<br>TAT   | 60.3                             | 805                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1722_P4_124015 | scaffold1722                            | 124015                        | TA/TAATATAA                                                   | CGTCCTCGAACTAAG<br>AGGAAA | TGGAAGATGTGACGAT<br>CCTG | 59.9                             | 871                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1723_P4_1064   | scaffold1723                            | 1064                          | ACTCTC/ACTC                                                   | CCTCATAGGTTTCGACT<br>GGGA | GCGCCCTCACATAATG<br>TTTT | 60.1                             | 467                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1725_P4_28680  | scaffold1725                            | 28680                         | TTT/TTTATT                                                    | GATTCACTGGCCGATT<br>TTGT  | TTGACGAAAAAGGAG<br>GAAA  | 59.9                             | 917                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1730_P4_19188  | scaffold1730                            | 19188                         | ATTTTTTTTT/ATTTTTTTT                                          | ACGGTGAAGAATAACG<br>GTGC  | GCGAAACCTTTTGTAAA<br>CCA | 60.0                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1730_P4_26122  | scaffold1730                            | 26122                         | AATAT/AAT                                                     | CGAACGGAGATTTTAT<br>CGGA  | CGCCAGTTAACCTAA<br>ACGA  | 60.0                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1730_P4_28639  | scaffold1730                            | 28639                         | AAATA/AA                                                      | CTACGTGAGGAGGATC<br>TCGC  | ACCACATGTAACACC<br>CCGT  | 60.0                             | 396                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1730_P4_64331  | scaffold1730                            | 64331                         | ACATATGATTTTTCATAT/ACATAT                                     | TTGGATGTTTCGCTTA<br>CCA   | CAAGTTAGTGGTGAAC<br>CGGG | 59.2                             | 882                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1730_P4_70178  | scaffold1730                            | 70178                         | TGGGG/TGGGGG                                                  | TGCCGAGAATATACCA<br>AGGG  | GGAGGCATTGTTTCCT<br>CAAA | 59.9                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1730_P4_84197  | scaffold1730                            | 84197                         | TAAAAAAAAA/TAAAAAAAAA                                         | GCCTTTCTCAATTGG<br>GTCA   | TTGATGGAAACAACA<br>CCCA  | 60.1                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1731_P4_39857  | scaffold1731                            | 39857                         | AATATATATATATATATAT/AAATATATATATATATAT                        | ATGTTTGGATTTTGG<br>CTCG   | GCACCGTGAGTAAAT<br>CGGT  | 59.9                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1731_P4_53952 | scaffold1731                            | 53952                         | AATATATATATATAT/ATATATAT<br>ATATATATAT                        | TTTGGATATTGGTTCG<br>GAGG | AGGAGGTTTGTGTTTG<br>ACGG  | 59.8                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1731_P4_65474 | scaffold1731                            | 65474                         | TTTATTATTATTATTAT/TTTATT<br>ATTATTATTATTATTAT                 | TAATCGGGGACTCAAC<br>ATCC | CCCTTTGGATGCGAAA<br>TAAA  | 59.8                             | 279                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1734_P4_695   | scaffold1734                            | 695                           | A/AT                                                          | TGCTTGATTGCTTGAG<br>ATCC | CCCACAAAAATAGAC<br>CGAA   | 59.0                             | 429                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1736_P4_21426 | scaffold1736                            | 21426                         | GTTTTTTTTT/GTTTTTTTTT                                         | CTTTGCAGGGTGTG<br>GTTT   | TCTCGAGGCATCACAT<br>TCAG  | 60.0                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_103191 | scaffold174                             | 103191                        | ATTTTTTT/ATTTTTTTT                                            | ACGCTTGTTAAAGGCA<br>GAGG | GAAAATTTGCGAGAAT<br>CCCA  | 59.5                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_111161 | scaffold174                             | 111161                        | ATTTTTTTTTTT/ATTTTTTTTTT                                      | GTGTTTGGCACATGTA<br>ACGC | GCATGAATGATGTTTG<br>ATTGG | 60.0                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_11363  | scaffold174                             | 11363                         | CAAAAAAAAA/CAAAAAAAAA                                         | TTATGTCGTTCTTAG<br>GGGC  | TGTGTGCAATAGGGAT<br>GGAA  | 60.0                             | 744                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_128651 | scaffold174                             | 128651                        | CAAAAA/CAAAAAA                                                | GTTTTCACCACACCCC<br>ATGT | GGGGTGAGAGAGATG<br>GTGAA  | 60.5                             | 949                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_136798 | scaffold174                             | 136798                        | TG/T                                                          | GAAGGTAGCGTTGGG<br>GACA  | CTGTGGACGACCTTT<br>GGAT   | 60.0                             | 585                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_143696 | scaffold174                             | 143696                        | ATTTTTTTTTTT/ATTTTTTTTTT                                      | CCCCTTTTGAAGGC<br>TAAA   | CAACGGGTTAGCCAG<br>AAAA   | 59.6                             | 925                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold174_P4_154447 | scaffold174                             | 154447                        | GTTTTTTTTTTTT/GTTTTTTTTTT<br>T                                | CTCAATGCAACCCACC<br>TTTT   | GTCGCTTGATTCACCC<br>ATCT   | 60.0                             | 701                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_167666 | scaffold174                             | 167666                        | ATTTTTTTT/ATTTTTTTT                                           | ATTTGTCGTTTAGCCG<br>TGA    | TCACAGTTCGATGTTG<br>CAGA   | 60.5                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_174628 | scaffold174                             | 174628                        | TATTAT/TATTATGATTAT                                           | TGGGTAGAAAAATGTG<br>CAAGAA | TTGCGCTAGTAATATTT<br>GCGAT | 59.6                             | 817                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_185139 | scaffold174                             | 185139                        | CTT/CTTT                                                      | TTGAATTTTCCAAGCAA<br>GGG   | CACCGGAAGCAACGAT<br>AAAT   | 60.0                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_201342 | scaffold174                             | 201342                        | CTTT/CT                                                       | TTGCAATATTTCCATT<br>GCC    | CAGGGACATTGTCAAC<br>CCTT   | 58.5                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_201401 | scaffold174                             | 201401                        | TTTTTTT/TTTTTT                                                | TTGCAATATTTCCATT<br>GCC    | CAGGGACATTGTCAAC<br>CCTT   | 58.5                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_230745 | scaffold174                             | 230745                        | CTTTT/CTTTTT                                                  | GAGCTTCACGTGCAAA<br>GAAA   | CCTTGACATGGCTTGT<br>TCCT   | 59.2                             | 702                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_349945 | scaffold174                             | 349945                        | T/TCACGATTCCACC                                               | AACAATGAGTCGGCGA<br>AAAC   | AGGCAAGGGATCAACA<br>ACAC   | 60.1                             | 347                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_350080 | scaffold174                             | 350080                        | TGCCTCGCCTCGCCTCG/TGCCTCG<br>CCTCG                            | GTGTTGTTGATCCCTT<br>GCCT   | GCCATCATTCTAAAGCA<br>GCC   | 60.0                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_350136 | scaffold174                             | 350136                        | GAAAAGGTGTTTAAA/GAA                                           | GTGTTGTTGATCCCTT<br>GCCT   | GCCATCATTCTAAAGCA<br>GCC   | 60.0                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                  |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold174_P4_361125 | scaffold174                             | 361125                        | ACCCCC/ACCCCCC                                                   | TGAGGGAAGTGGATG<br>AGCC  | TCCAATTGAAGTGCA<br>AACA  | 60.1                             | 212                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_368925 | scaffold174                             | 368925                        | CATGCTTATTATATGCTTATTAT/CA<br>TGCTTATTAT                         | ATCCAAGGGCACATGT<br>TAGC | TCGACTGCGTTAATGTT<br>GGA | 60.0                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_397916 | scaffold174                             | 397916                        | GTTTTTTTTT/GTTTTTTTTT                                            | TGCAGCTTCAACCTTC<br>AGTT | TAGCTCGAGTTCTGGG<br>CTTC | 58.7                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_422115 | scaffold174                             | 422115                        | TAAAAAAAAA/TAAAAAAAAA                                            | GGGCAATCATATCCT<br>CCAA  | TGCATGCCACATTGTA<br>AACC | 59.7                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_424440 | scaffold174                             | 424440                        | CAACAAAACAAAACAAAACAAA<br>AACAAA/CAACAAAACAAAACAAA<br>AACAAA     | GGAGCTTTGATTCCCA<br>TGAA | GATGCATTTGGGAAAG<br>ATGG | 60.0                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_466002 | scaffold174                             | 466002                        | ATTTTTTTTTTT/ATTTTTTTTTTT                                        | TTTCGAAAGTTGGCA<br>TTGA  | CCGCATTATAATTCCG<br>CTGT | 59.3                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_481063 | scaffold174                             | 481063                        | GTTATTTATTTATTTATTTATTTATT/<br>GTTATTTATTTATTTATTTATTTATT<br>ATT | TTGCAACTGTTTGTGG<br>GGTA | TGTCATCGGTCCATCTT<br>CAA | 60.0                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_486953 | scaffold174                             | 486953                        | GTTTT/GTTT                                                       | CAATTTCGAATGTTTTG<br>CGA | GTCCGTTGTCCACCCA<br>TAAC | 59.7                             | 103                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_54864  | scaffold174                             | 54864                         | ATTTTTTTTT/ATTTTTTTTT                                            | GGGTAATTGGCTGGGT<br>AGGT | AAGGGGTTTCACGTTT<br>CACA | 60.1                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold174_P4_85476  | scaffold174                             | 85476                         | GTTTTTT/GTTTTTTT                                                 | TTGCGTCTACGCCTCA<br>GTAA | TCGGTCAATGATGACG<br>TTGT | 59.6                             | 847                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)          | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                        |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold174_P4_8927    | scaffold174                             | 8927                          | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA<br>AA                                    | TTACCACTTCCAGACC<br>CGAC | TTGGTTCCAACAATCTC<br>GCT | 60.0                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1740_P4_2698   | scaffold1740                            | 2698                          | TAA/TA                                                                 | CGATTGGCCATACAG<br>GAAT  | CCCATCTACATACCCAT<br>CCG | 59.8                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1750_P4_229441 | scaffold1750                            | 229441                        | TTCAAAAAATCAAAAAA/TTCAAAAA<br>ATCAAAAAATCAAAAAA                        | CATGCAATTATTCGTC<br>GTG  | TGTGGGATTAGTGGGC<br>CTAT | 60.0                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1751_P4_240108 | scaffold1751                            | 240108                        | GTTATTATTATTATTATTATTATT<br>AT/GTTATTATTATTATTATTATT<br>ATTATTATTATTAT | TCATGTTCTCCAGCT<br>GCTA  | GGCCAGACCATCTTTA<br>CCAA | 59.5                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1751_P4_293380 | scaffold1751                            | 293380                        | TAAAAAAAAA/TAAAAAAAAA                                                  | ACCGCCATTACATCAA<br>AAGC | GGCCAGACAACCTTTA<br>CCAA | 60.0                             | 731                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1751_P4_361951 | scaffold1751                            | 361951                        | ATTTT/ATTTT                                                            | TTGTGCTTGTGTAAG<br>TGGG  | AGCAGCACATCAAAAT<br>GCAG | 59.8                             | 219                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1751_P4_41242  | scaffold1751                            | 41242                         | GT/GTGCATCCAAT                                                         | AGGTCATCTTCGTCCT<br>CCCT | TGGAGGCACAACATTG<br>GTTA | 60.1                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1751_P4_433899 | scaffold1751                            | 433899                        | AGGGGGGGGGG/AGGGGGGGGGG                                                | CAACTGCATCCCATAT<br>GTCG | GGTGTGCAAGAGGACT<br>GGAT | 59.9                             | 391                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1751_P4_526988 | scaffold1751                            | 526988                        | GTTTTTTTTT/GTTTTTTTTT                                                  | ACATGCAAAAGGAGAA<br>TGGC | ATTTAGGCCCCCTCAA<br>GAGA | 60.1                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1755_P4_33561  | scaffold1755                            | 33561                         | CT/CTT                                                                 | CAGGTGCATTATCCCG<br>ATT  | CCAGGTTATGTCCCCA<br>AATG | 59.8                             | 404                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                     | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                   |                           |                          |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1755_P4_46481  | scaffold1755                            | 46481                         | CAATAATAATAATAATAATAATA<br>ATAATAATAATAATA/CAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATA      | TTTTTCCGAAGACAC<br>AATAA  | CGTTTGCCAACCTCTT<br>TCA  | 57.3                             | 668                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1756_P4_101789 | scaffold1756                            | 101789                        | TAAACCCAAAACCCAAAACCC/TAAA<br>CCCAAAACCC                                                          | CGATTAGAACCAAAT<br>GGGC   | GGGTATAGGGCTTTGG<br>GTTT | 59.4                             | 550                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1756_P4_3220   | scaffold1756                            | 3220                          | CTATATATATATATATATA/CTATATA<br>TATATATATATATATATATATA                                             | TCGTTTTTGAGTGGA<br>CCAA   | CGGTGTGCTAAGCATG<br>AAAA | 59.1                             | 493                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1756_P4_43727  | scaffold1756                            | 43727                         | CATATATATATATATATATATATA<br>T/CATATATATATATATATATATAT<br>ATATAT                                   | GTTGGTCCCTAGCAC<br>CGTA   | GGCTGTAGCCAGTT<br>TTTG   | 60.0                             | 658                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1756_P4_5242   | scaffold1756                            | 5242                          | CGGTA/C                                                                                           | GGTGAGTCTTTTGCC<br>TCAA   | TTGGATGAAGGCCATA<br>AAGG | 60.2                             | 665                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1756_P4_61886  | scaffold1756                            | 61886                         | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATATATATA<br>T                                       | TATTTTTGAGACGGCG<br>AAGG  | GAACGCTTCCGTTTTCT<br>CTG | 60.2                             | 624                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1756_P4_68155  | scaffold1756                            | 68155                         | CTTTTTTTTT/CTTTTTTTTT                                                                             | TCGGAATAATTAAGGG<br>CAAGA | TTGCAATGTGTCTATG<br>CGA  | 58.7                             | 791                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1756_P4_85932  | scaffold1756                            | 85932                         | T/TAGTA                                                                                           | ATTAGATTATGGCCG<br>CGA    | CCGATGCCACACCAAC<br>TTAT | 60.4                             | 499                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1757_P4_1167   | scaffold1757                            | 1167                          | CTT/CTTATT                                                                                        | AAGCGTACCTGTGGGA<br>ATTG  | TTAATAGGGGCTGAA<br>TTGG  | 60.0                             | 259                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1757_P4_128519 | scaffold1757                            | 128519                        | CATTATTATTATTATTATTATTATT<br>TATTATTATTATTATTATT/CATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATT | AACCAACCAAACTCA<br>ATAGGA | AATCCAGCAGGACAGA<br>CCTC | 59.7                             | 277                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')       | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|-------------------------------|---------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                   |                               |                                 |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1757_P4_3033   | scaffold1757                            | 3033                          | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATAT                 | TGCAGCCACTCTTGGT<br>TAAA      | CAAACGACGAAAACAC<br>AAACA       | 59.5                             | 156                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1757_P4_40939  | scaffold1757                            | 40939                         | GTTTTTTTTT/GTTTTTTTTT                                             | AGCGAGGGACTTTTCA<br>ATCA      | ATCAACCGTCCAGCAA<br>CATT        | 59.8                             | 623                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1757_P4_66546  | scaffold1757                            | 66546                         | GTATATATATATATATATATATAT<br>AT/GTATATATATATATATATATAT<br>ATATAT   | ACAATTTTGCCCTCA<br>CAAC       | TCATGGAGTTTGACAC<br>ATTGAA      | 59.8                             | 558                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1757_P4_86966  | scaffold1757                            | 86966                         | AATATATATATATATAT/AATATAT<br>ATATATATATATATAT                     | GTTTGGGGTGTGCTC<br>TTTA       | CACTTCACATGCGATT<br>CACAC       | 60.0                             | 577                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1761_P4_30766  | scaffold1761                            | 30766                         | TATAATAATAATAATAATAATAA<br>TAA/TATAATAATAATAATAATAA               | CCAGGCTTTGAAAGGC<br>ATAA      | AAAGGTTAGGCTCAGG<br>CCAT        | 60.2                             | 576                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1767_P4_28654  | scaffold1767                            | 28654                         | AATATATATATA/AATATATATATATA                                       | ATTTGCAATTCATTAG<br>CCG       | TGAATTTGCCTCTCTGC<br>CTT        | 59.9                             | 527                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1771_P4_91063  | scaffold1771                            | 91063                         | AATTTATAT/AAT                                                     | GCTTATATTTGGGGCC<br>CTCT      | AGTCGAATGTCACCAT<br>GAAGG       | 59.4                             | 491                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1773_P4_13836  | scaffold1773                            | 13836                         | TT/TTAATCGAGT                                                     | AATCCAATGACGCAAA<br>CACA      | GCCCAATTCGGGTTTT<br>TAAT        | 60.0                             | 655                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1776_P4_23561  | scaffold1776                            | 23561                         | CTTT/CTT                                                          | TCACAACTCAATTTTGC<br>TTTATGTT | TTCGTTTGGTAGTTGTA<br>TTTAATAACG | 59.2                             | 519                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1777_P4_141427 | scaffold1777                            | 141427                        | CTATATATATATATATATATATAT<br>ATA/CTATATATATATATATATATA<br>TATATATA | AGCAAAAGGAAGCAAC<br>GAAA      | GGAAGTGATGGGTGAA<br>ATGG        | 60.0                             | 228                                           | INTERGENIC                                           | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1783_P4_37981  | scaffold1783                            | 37981                         | CAA/CA                                                        | TTGAATTGTGAGGCTG<br>TTGG   | TGCAAAAACCACTTTCA<br>AGG   | 59.7                             | 915                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1795_P4_5623   | scaffold1795                            | 5623                          | A/AGCC                                                        | CAATGTCTGGGAGCTA<br>CCAT   | TCGTTTAATTTCTGGGAT<br>TGG  | 60.0                             | 456                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1804_P4_176118 | scaffold1804                            | 176118                        | AATATATATATATATATATATAT/A<br>ATATATATATATATATATATATATA<br>T   | AGCCCTGTTTGATTCC<br>CTTT   | TGAGCGTTCTAGTATC<br>CACCTC | 59.9                             | 765                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1804_P4_177014 | scaffold1804                            | 177014                        | TAAAAA/TAAAA                                                  | AGATGTGAATTGCACC<br>ACCA   | GTGATCAAAGCATTCC<br>CGTT   | 60.0                             | 602                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1804_P4_253551 | scaffold1804                            | 253551                        | TTAAT/TT                                                      | AACATGGTGCCAAAC<br>AAAT    | GAAGAACGTGTTGCCA<br>CTGA   | 60.1                             | 280                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1804_P4_257758 | scaffold1804                            | 257758                        | A/AAT                                                         | GTTGTGCGGAAGCCAT<br>TTAT   | CTGGAATGGCTCCAAA<br>TCAT   | 60.0                             | 549                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1804_P4_317982 | scaffold1804                            | 317982                        | G/GT                                                          | CAACATTTTCCTGTTGA<br>GTTGG | TCTTTCATGCATCCTCC<br>ACA   | 59.5                             | 267                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1804_P4_57835  | scaffold1804                            | 57835                         | CTGATT/C                                                      | CCTATTCTTTTCCCCC<br>AAA    | GCAGCTGACCGCGTAA<br>TAAT   | 60.1                             | 496                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1806_P4_3130   | scaffold1806                            | 3130                          | CAAAAA/CAAAAAAA                                               | TGGACTTCTCGAGCGA<br>TTTT   | TCCAGATGAAATCGAG<br>GACC   | 60.0                             | 656                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold1806_P4_6835   | scaffold1806                            | 6835                          | CAAAAA/CAAAA                                                  | TTTCATCTGGACTTTTC<br>GGG   | GATGAAATCGAGGACT<br>GGGA   | 60.0                             | 584                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)                                  | Forward primers (5'-3')     | Reverse primers (5'-3')         | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|-----------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                 |                             |                                 |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| scaffold181_P4_180803  | scaffold181                             | 180803                        | TTATATATATATATATATATATATA<br>T/TATATATATATATATATATATATA<br>TATAT                                | TTTCATTGCACTCACT<br>CCA     | ATAAGGGTGGAATAG<br>GCCA         | 60.2                             | 897                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold181_P4_76121   | scaffold181                             | 76121                         | CAAAAAAAAAAAAA/CAAAAAAAAAAA<br>A                                                                | AGAAAGCATGGGAAAC<br>AAGG    | ACGCGCAACTATGAGG<br>TTTT        | 59.2                             | 717                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1810_P4_103255 | scaffold1810                            | 103255                        | GC/GCC                                                                                          | TGCTAGTTGCTGATG<br>TGGC     | GGTGTCATCGGGAGTC<br>TGTT        | 60.0                             | 300                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1810_P4_103852 | scaffold1810                            | 103852                        | GAAA/GAAAAA                                                                                     | AACAGACTCCCGATGA<br>CACC    | AACATTTATGACGATAT<br>TTATGAGTGA | 60.0                             | 438                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1810_P4_32448  | scaffold1810                            | 32448                         | GTATTATTATTATTATTATTATTA<br>TTATTATTATTATT/GTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATT | TTCGCTTGAATTACAAA<br>TGTTTT | TCAATGATTGTTGACAA<br>GGGA       | 58.0                             | 469                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1815_P4_23915  | scaffold1815                            | 23915                         | AAAAATTGAAAAT/AAAAATTGAAAA<br>TTGAAAAT                                                          | CATCTGAGCTTCTTTG<br>GACG    | GCGGGTGCATTTTCAT<br>TTAT        | 58.6                             | 506                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1815_P4_24742  | scaffold1815                            | 24742                         | ATTTTTT/ATTTTTTTTT                                                                              | ATAAATGAAAATGCACC<br>CGC    | TAAATGCTGCGGTCCA<br>AAAA        | 59.8                             | 808                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1815_P4_5752   | scaffold1815                            | 5752                          | A/ATAC                                                                                          | TGTCCATCACAGGCTA<br>CATGA   | TGTGGGCAAATCTTG<br>TGGT         | 60.1                             | 434                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1816_P4_50409  | scaffold1816                            | 50409                         | A/AATAATAATAAAT                                                                                 | TGTCCGCATACCTACT<br>GAGAA   | CTTATCTCCGATCCG<br>TGAA         | 58.4                             | 624                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold1816_P4_53607  | scaffold1816                            | 53607                         | ATATATAATTTATATAATTTATATAAT<br>TT/ATATATAATTTATATAATTT                                          | TGGTGAGGAAATGAGC<br>AACA    | ACAAAATGAAGGTGCG<br>GAAG        | 60.2                             | 679                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1822_P4_17416  | scaffold1822                            | 17416                         | GTT/GTTT                                                      | AAGCACCAATTACCGA<br>GGTG | TTGTATTTGGCGTGTC<br>CGTA | 60.0                             | 720                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1822_P4_17500  | scaffold1822                            | 17500                         | GTT/GTTT                                                      | AAGCACCAATTACCGA<br>GGTG | TTGTATTTGGCGTGTC<br>CGTA | 60.0                             | 720                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1822_P4_18540  | scaffold1822                            | 18540                         | TA/TAAATACA                                                   | AGAAAGCGACGAAAC<br>GAAA  | ATTCCCCTCCTTGAAG<br>CAAT | 60.0                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1825_P4_148166 | scaffold1825                            | 148166                        | ATTTTTTTTT/ATTTTTTTTT                                         | GTTTTGGCGTTGGTTT<br>CACT | TACGTGTATATTCGCG<br>CACC | 60.0                             | 904                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1825_P4_15825  | scaffold1825                            | 15825                         | CATATATATATATATAT/CATATAT<br>ATATATATATATAT                   | GTTGGTTCCTAGCAC<br>CGTA  | CGGGATGGTGGCATAG<br>TATC | 60.0                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1825_P4_26286  | scaffold1825                            | 26286                         | CAAAGAAAAAGAAAA/CAAAGAAA<br>AA                                | TGGCAAATCGATTGAC<br>AGAA | AGTTTCCTCCCCGAAA<br>CCTA | 60.2                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1825_P4_53003  | scaffold1825                            | 53003                         | AGG/AGGG                                                      | CAGCAACAGGAAAACA<br>GCAA | TTCTGAGAGACTGCA<br>CAGG  | 60.0                             | 315                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1830_P4_4465   | scaffold1830                            | 4465                          | CTATA/CTA                                                     | CCAAGGGAAGACGAAA<br>ATGA | TGCATCCAACAGGTGT<br>GTTT | 60.0                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1835_P4_10086  | scaffold1835                            | 10086                         | GCC/GCCC                                                      | TGGTTAACCTTGCAAC<br>ACAA | GGATGCTTGAATTATG<br>CCGT | 60.0                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1835_P4_11243  | scaffold1835                            | 11243                         | GAACAACAAC/GAACAAC                                            | AAACGCATCCCGTAAA<br>TCAG | CGATTGCCCTAGAAAA<br>TGGA | 60.0                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                                |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1835_P4_8124   | scaffold1835                            | 8124                          | TCAACAACA/TCAACA                                              | TCATTGCTCCTTTGAGT<br>TGC       | ATTTGCCACAGATACC<br>GCTC       | 59.0                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1835_P4_8173   | scaffold1835                            | 8173                          | CAA/CA                                                        | TCATTGCTCCTTTGAGT<br>TGC       | ATTTGCCACAGATACC<br>GCTC       | 59.0                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1835_P4_8463   | scaffold1835                            | 8463                          | TAAAAAAAA/TAAAAAAAAA                                          | GAGCGGTATCTGTGGC<br>AAAT       | CGGTTTGTGGCTTTCC<br>TAAA       | 60.1                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1844_P4_120985 | scaffold1844                            | 120985                        | TCC/TC                                                        | GCCACTTCACACGTTT<br>CCTT       | TTTGAGTGATGCTGGG<br>TTGA       | 60.2                             | 126                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1844_P4_121436 | scaffold1844                            | 121436                        | GTTTTTTT/GTTTTTTTTT                                           | ACTTCCGTTACACGT<br>TTCC        | AAACCCAGCCCTTTCA<br>AACT       | 60.0                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1844_P4_2008   | scaffold1844                            | 2008                          | CTTTTTTTTTT/CTTTTTTTTTTT                                      | AACATGGGACGAGCTG<br>TTTC       | TTCAAAGAGAGATAAAT<br>TCAAAGGTC | 60.1                             | 903                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1844_P4_2095   | scaffold1844                            | 2095                          | AAA/AAAATAA                                                   | AACATGGGACGAGCTG<br>TTTC       | GGGATATTCAATAAGT<br>GAAATTCAAA | 60.1                             | 923                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1844_P4_2214   | scaffold1844                            | 2214                          | T/TC                                                          | TGCAATTATGATCATGC<br>TTTATATG  | GGGATATTCAATAAGT<br>GAAATTCAAA | 58.2                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1844_P4_22931  | scaffold1844                            | 22931                         | ACC/ACCC                                                      | TGCTTAACTTTTTGGG<br>CAGG       | AGTTGGCTTTGTACC<br>CCCT        | 60.2                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1844_P4_2526   | scaffold1844                            | 2526                          | CA/CAA                                                        | GACCTTTGAATTTATCT<br>CTCTTTGAA | TTACAACATGTCAGGC<br>CGAA       | 58.5                             | 373                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                   |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1844_P4_2737   | scaffold1844                            | 2737                          | TAGGCCAGGTCAGGCCAGG/TAGG<br>CCAGG                                                 | TGACTTGTAATAGGG<br>GTGGC    | TTACAACATGTCAGGC<br>CGAA | 59.0                             | 139                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1845_P4_11504  | scaffold1845                            | 11504                         | A/AAACGTGT                                                                        | TCCTTTTCATACCAAAG<br>CCAA   | GGACGGGTTTGAGTTC<br>AGAG | 59.6                             | 766                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1845_P4_7123   | scaffold1845                            | 7123                          | TTCATCTTCTTCATAACTCATCTTCT<br>TC/TTCATCTTCTTCATAACTCATCT<br>TCTTCATAACTCATCTTCTTC | ATCAACACCCCTCAAAT<br>TGC    | CAAAGACTCCGGGGTT<br>GATA | 59.8                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1845_P4_7423   | scaffold1845                            | 7423                          | AATATATATATAT/AATATATATATAT<br>ATATATATATAT                                       | ATCAACACCCCTCAAAT<br>TGC    | CGGCTCTTCCATTATT<br>CCA  | 59.8                             | 852                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1845_P4_79664  | scaffold1845                            | 79664                         | ANNNNNNNNN/ANNN                                                                   | CCTTGATATGCAATGC<br>TCACA   | ATCGAGCCTCTTGATAT<br>GGC | 59.7                             | 336                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1845_P4_83894  | scaffold1845                            | 83894                         | TAAAAA/TAAAAA                                                                     | AAGTGCATTTTGGCGT<br>ATCC    | CAACCTCTGTCTCATG<br>GCAA | 60.0                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1848_P4_3663   | scaffold1848                            | 3663                          | AAGGGTTT/AAGGGTTTGAGTTTA<br>GGGTTT                                                | GTCTCAGTTGCCAAAG<br>CACA    | ATCCCAAACCTTAAAT<br>CCG  | 60.0                             | 724                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1852_P4_101660 | scaffold1852                            | 101660                        | AC/ACCC                                                                           | CCCATAATTTTATGAAA<br>ATGCCA | TCTCCTGTACCGAGGC<br>TTGT | 59.9                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1852_P4_102659 | scaffold1852                            | 102659                        | TTATATATATATATATATATATATA<br>/TTATATATATATATATATATATATA<br>ATA                    | TCCGGAAGAGGCTTCT<br>GTAA    | TCGACACTCATTGGTC<br>CTCA | 59.9                             | 865                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1852_P4_102952 | scaffold1852                            | 102952                        | CAT/CATAT                                                                         | GGTCAGGGCCTCTAAG<br>GTCT    | TTGACACTCATTGCTCC<br>TCG | 59.7                             | 847                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                     | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                                                   |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1852_P4_103208 | scaffold1852                            | 103208                        | GATTT/GATTTATTT                                                                                                                   | TTGAGGACCAATGAGT<br>GTCG  | GTAAATTCGGGGTCG<br>AGGT     | 59.7                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1852_P4_103507 | scaffold1852                            | 103507                        | ATTTTTTT/ATTTTTTTT                                                                                                                | CGAGGAGCAATGAGTG<br>TCAA  | GTAAATTCGGGGTCG<br>AGGT     | 60.0                             | 253                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1852_P4_94250  | scaffold1852                            | 94250                         | TA/TATAAATAA                                                                                                                      | CATCCTCCTTCGCATC<br>CTTA  | ATTAGCGTCGATGTTG<br>GACC    | 60.2                             | 436                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1852_P4_94388  | scaffold1852                            | 94388                         | A/AAGCTTTACAT                                                                                                                     | GGTCCAACATCGACGC<br>TAAT  | CGAGCACACTCCATGG<br>TATC    | 60.0                             | 234                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1852_P4_94526  | scaffold1852                            | 94526                         | ATTTTTTT/ATTTTT                                                                                                                   | GGTCCAACATCGACGC<br>TAAT  | TCGGATGTTACACACC<br>TCACA   | 60.0                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1852_P4_94771  | scaffold1852                            | 94771                         | GGTGTGT/GGTGT                                                                                                                     | GGTCCAACATCGACGC<br>TAAT  | TTTCAGTCATTTGATT<br>CGGA    | 60.0                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1852_P4_94935  | scaffold1852                            | 94935                         | ATTGTT/ATT                                                                                                                        | TACCATGGAGTGTGCT<br>CGAA  | TTTCAGAACACAAATCT<br>GCATGT | 60.3                             | 765                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1852_P4_95478  | scaffold1852                            | 95478                         | TTT/TTTGGAGATGACCCTT                                                                                                              | TGCATGCTTATTTGCTC<br>TGTC | CCATCCTCGCAAAATC<br>ATCT    | 60.0                             | 492                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1852_P4_96237  | scaffold1852                            | 96237                         | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATT/ATATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATT | ACTATGAGGTGGCATG<br>GGAG  | CCTGACCGTCATCAAA<br>ACAA    | 60.0                             | 408                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold186_P4_112424  | scaffold186                             | 112424                        | C/CG                                                                                                                              | ATTCCTACGCGATTAC<br>CACG  | GCCTGTGATAGGCGGT<br>ACAT    | 60.0                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                       | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                     |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold186_P4_235870 | scaffold186                             | 235870                        | CATATATATATATATATATATATA<br>TATATATATATAT/CATATATATATAT<br>ATATATATATATATATATATATAT | ACTGTACCGCGATCAA<br>TTCC  | TTGTGAGTTTCATGCC<br>CAAA   | 60.0                             | 796                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold186_P4_252188 | scaffold186                             | 252188                        | AATATATATATATATA/AATATATATA<br>TATATATA                                             | TACTCCCAAATGGCGA<br>CTTC  | CATTTCGAACTTGGGTT<br>TGC   | 60.1                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold186_P4_51582  | scaffold186                             | 51582                         | GTATATATATATATATATATATAT<br>ATATAT/GTATATATATATATATAT<br>ATATATATATATAT             | TGTGTCCACCACCTGA<br>AAAA  | TGCACACAAAAATATCA<br>CCACT | 60.0                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold186_P4_77517  | scaffold186                             | 77517                         | AATATATATATATATATATAT/AAT<br>ATATATATATATATAT                                       | CGAGCCTTACCGACTA<br>TGGA  | GAAAAGCGGGTGTTTG<br>TGTT   | 60.2                             | 807                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1864_P4_14836 | scaffold1864                            | 14836                         | TAAAAAA/TAAAAAA                                                                     | CGCTCTGTTAAGTCGG<br>TTCA  | CATCCACGGAGCAAAA<br>ACTT   | 59.1                             | 251                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1864_P4_14934 | scaffold1864                            | 14934                         | GTGTGATAAGATAT/GTGTGATAAG<br>ATATGTGATAAGATAT                                       | AACTCGAACACGAAAC<br>CGAC  | CATCCACGGAGCAAAA<br>ACTT   | 60.2                             | 188                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1864_P4_20455 | scaffold1864                            | 20455                         | CATATATATATATATAT/CATATAT<br>ATATATATATATAT                                         | TCAATGCTCTCGCACG<br>TTAC  | GCAATTATCCGATGTC<br>CACC   | 60.0                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1864_P4_2902  | scaffold1864                            | 2902                          | GT/GTAGTAAT                                                                         | CGTGACAACCACCAAC<br>TCTTT | TCTGAAAGCCGTGAAA<br>GACC   | 60.1                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1864_P4_3660  | scaffold1864                            | 3660                          | TACCA/TA                                                                            | ATGTTGTGAAGATTGG<br>GGGG  | TGCATTGGGTCCCAT<br>AGA     | 59.6                             | 369                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1864_P4_4285  | scaffold1864                            | 4285                          | TCC/TC                                                                              | ATGGGACCCAAATGCA<br>ATAA  | ACGTAGCGTAGAAGTC<br>CCCA   | 60.0                             | 339                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                              |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1864_P4_4508   | scaffold1864                            | 4508                          | ATCCTGTTTACT/AT                                               | TTGGGGACTTCTACGC<br>TACG     | GCAACAGGGATGACTG<br>ACTG | 60.3                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1864_P4_4680   | scaffold1864                            | 4680                          | T/TC                                                          | TTGGGGACTTCTACGC<br>TACG     | TCGGTCAGAAGAAAAC<br>TGCC | 60.3                             | 883                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1864_P4_5094   | scaffold1864                            | 5094                          | TAAA/TAAAA                                                    | CAGTCAGTCATCCCTG<br>TTGC     | TCGGTCAGAAGAAAAC<br>TGCC | 59.3                             | 190                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1864_P4_5589   | scaffold1864                            | 5589                          | A/AT                                                          | TTCAGCGCTTAACGTG<br>AGAA     | TCGAGATGATGATGGA<br>TGGA | 59.8                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1864_P4_5884   | scaffold1864                            | 5884                          | CAAAAAA/CAAAAAA                                               | TTGCCCATTTCTCCAAG<br>TTTC    | CGGATATAAGCATGGC<br>ATCA | 60.1                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1864_P4_5957   | scaffold1864                            | 5957                          | AATG/AATGATG                                                  | TTGCCCATTTCTCCAAG<br>TTTC    | CGGATATAAGCATGGC<br>ATCA | 60.1                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1864_P4_5989   | scaffold1864                            | 5989                          | ATAGT/AT                                                      | TTGCCCATTTCTCCAAG<br>TTTC    | CGGATATAAGCATGGC<br>ATCA | 60.1                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1864_P4_6249   | scaffold1864                            | 6249                          | TCC/TC                                                        | AGTGACATGTGCTGCC<br>TTTG     | AAATTGGGGTCTCAAC<br>GAAA | 59.9                             | 295                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1866_P4_113475 | scaffold1866                            | 113475                        | AAATTATTTTACAATTATTT/AAATTA<br>TTT                            | TTAAACAGACCTCGC<br>CACC      | GAGGAGAAGTCCACGT<br>CAGC | 60.1                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1866_P4_116123 | scaffold1866                            | 116123                        | GAA/GAAA                                                      | TTCCAATTATGGTGAG<br>TAATGATG | GCGAGCATGAGAAGTT<br>GTTG | 58.1                             | 632                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                   |                           |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1866_P4_139647 | scaffold1866                            | 139647                        | TACACACACACACACACACACAC<br>ACACA/TACACACACACACACACAC<br>ACACACA                   | GCAAAATGCTCCCCTAA<br>TTGA | CAATTTTCTGCACTCTC<br>GCA      | 60.0                             | 296                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1866_P4_142765 | scaffold1866                            | 142765                        | TTATATATATATATATATATATATA<br>TATA/TTATATATATATATATATATAT<br>ATATATATATATATATATATA | CAAACAAGGTTGGTGT<br>GCTG  | CTTCCGATCCTCCTACT<br>CCC      | 60.2                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1866_P4_96337  | scaffold1866                            | 96337                         | ATTTTTTTTT/ATTTTTTTTTT                                                            | ACACAAAGGCCACCAA<br>TGAT  | GTCGACAGCAAAGCA<br>CAAA       | 60.2                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1867_P4_226694 | scaffold1867                            | 226694                        | ATTT/ATTTT                                                                        | ATCGATTTTGCCGTTT<br>TGC   | GGAGGGTTTTGTTTG<br>GAAT       | 59.9                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1867_P4_91419  | scaffold1867                            | 91419                         | TAAA/TAA                                                                          | AGGGAGGACGAAAATG<br>ACCT  | AACCAATCATGTGCATC<br>CAA      | 59.9                             | 171                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1869_P4_19075  | scaffold1869                            | 19075                         | AG/A                                                                              | CTCGATTTTCATCTGGC<br>CATT | CGAAAGTCGCTCCAAA<br>AGTC      | 60.0                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1869_P4_19531  | scaffold1869                            | 19531                         | GAAA/GAAA                                                                         | GACTTTTGAGCGACT<br>TTCG   | AACAATGTTTCAGGTTT<br>CGC      | 60.0                             | 273                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1869_P4_20055  | scaffold1869                            | 20055                         | CAA/CAAA                                                                          | TTTCAGGCGATTTTCG<br>TACC  | ATTGTGTTTCGGGTTTC<br>GAG      | 60.1                             | 825                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1870_P4_21211  | scaffold1870                            | 21211                         | TAAA/TAAA                                                                         | ATGGACTGAAATCGAG<br>TGGC  | CATATAACAAAATTGAG<br>TTGCAAAA | 60.1                             | 333                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1878_P4_25991  | scaffold1878                            | 25991                         | TATAATAATAATAATAA/TATAATAAT<br>AATAATAATAA                                        | CTAATGGGTTGATCCG<br>CTGT  | TTGACATGATTGGTTT<br>CGG       | 60.0                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1878_P4_45211 | scaffold1878                            | 45211                         | TAAAAAAAAA/TAAAAAAAAA                                         | GCCCTCAGATGAGAGT<br>CAGG   | GGAGGGTAGGCTTATT<br>TGGC        | 59.9                             | 780                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1878_P4_51803 | scaffold1878                            | 51803                         | T/TA                                                          | GATGCATATTTGCTTCT<br>TTCCA | CCAAAATTAGCCTTGTC<br>ACCA       | 59.2                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1878_P4_73568 | scaffold1878                            | 73568                         | AGG/AAATCATTTTTAGGG                                           | CATGTTCAATGCACCC<br>GTAG   | ATCATTGCCATTCAAG<br>AAGC        | 60.0                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1878_P4_8070  | scaffold1878                            | 8070                          | CAAAAAA/CAAAAAA                                               | TTGGTTTGAAAAAGGG<br>GTTG   | TACGTTGCAATCGTCC<br>AAAA        | 59.8                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1885_P4_40287 | scaffold1885                            | 40287                         | GATATATATATATAT/GATATATATAT<br>ATATATATATAT                   | CCATTGTGGTCGTTTA<br>GGCT   | CCCAATGACATCAAAA<br>CCC         | 60.0                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1885_P4_47510 | scaffold1885                            | 47510                         | A/AG                                                          | GTAGCTTCGGCTACAC<br>CGAC   | ATTCCGTTGTGCACTT<br>GATG        | 59.9                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1886_P4_17789 | scaffold1886                            | 17789                         | TA/T                                                          | GAGAGAGGCATTGCAC<br>AACA   | CGAAATTTCTTTAACGA<br>GGGG       | 60.0                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1886_P4_17993 | scaffold1886                            | 17993                         | TA/TAA                                                        | GAGAGAGGCATTGCAC<br>AACA   | CGAAATTTCTTTAACGA<br>GGGG       | 60.0                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1886_P4_24815 | scaffold1886                            | 24815                         | CGAAGAAGAAGAAG/CGAAGAAGAA<br>GAAGAAG                          | GCTTCTTGAAGGTTTC<br>GACG   | GGAAGAAAAATAGTAA<br>CAAGAAGACCA | 60.0                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1899_P4_33484 | scaffold1899                            | 33484                         | GAAAA/GAAAAA                                                  | GAATCCTGGGCTGAAA<br>TCAA   | TTGTCCGTGAGAGACT<br>GCAC        | 60.0                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                            |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1899_P4_37028  | scaffold1899                            | 37028                         | CATATATATATATATATATATATATATATATAT/CATATATATATATATATATATATAT   | AGGAAGAGTGGAGTTG<br>CGAA   | GAGGTTGTCGAGAGGT<br>TGGA      | 60.0                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1905_P4_1617   | scaffold1905                            | 1617                          | CT/CTCTGAT                                                    | ACTGATGTCAAGAGGG<br>CCAG   | AGAGGGTGGCAATGGT<br>AATG      | 60.3                             | 251                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1905_P4_16640  | scaffold1905                            | 16640                         | T/TAA                                                         | TCCAAGCTTACCCCAA<br>AGTG   | GCTCAACAAGAGACAT<br>GCCA      | 60.1                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1905_P4_21978  | scaffold1905                            | 21978                         | AATA/AA                                                       | CCTAGGGACGACGAAA<br>ATGA   | TGATGTCGAACCCCAA<br>TTTT      | 60.1                             | 295                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1910_P4_13931  | scaffold1910                            | 13931                         | CAATCGATTG/CAATCGATTGGCAA<br>ATCGATTG                         | AATGCACTCCAGGACC<br>AAAC   | CCAATCGATTATCGTG<br>GGTC      | 60.0                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1918_P4_213558 | scaffold1918                            | 213558                        | CTTAATTA/CTTA                                                 | TGACATGCCAAAATA<br>GTCAAAA | TGCAAAAATAACACATG<br>GACG     | 59.7                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1923_P4_10722  | scaffold1923                            | 10722                         | ATTTTTTTTT/ATTTTTTTTT                                         | GGCCCCCAATATTTTG<br>GTAA   | ATTATTGGCCCCAACT<br>CACA      | 60.7                             | 383                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1928_P4_108999 | scaffold1928                            | 108999                        | CT/C                                                          | ATTACCTGCGGAATTT<br>GCTG   | TTTACCTGCGGCATTA<br>CCT       | 60.1                             | 257                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1928_P4_109330 | scaffold1928                            | 109330                        | TTATATATATATATAT/TTATATATAT<br>ATATATAT                       | ATTACCTGCGGAATTT<br>GCTG   | TTTGTGGTGTACATATT<br>TTATGCAA | 60.1                             | 902                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1928_P4_15951  | scaffold1928                            | 15951                         | TG/T                                                          | ATCTACCCGGCAAACG<br>TCTA   | GCTGCAAAAGTCAACG<br>TCAA      | 59.6                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold193_P4_201902 | scaffold193                             | 201902                        | GTGTTAA/GTGTTAAAAATGTAA                                       | CCCGTGATAGGCAGTA<br>CGTT  | AGTACTGAGCCCCCTG<br>GTTT      | 60.0                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold193_P4_208565 | scaffold193                             | 208565                        | TTA/TTATA                                                     | CGTTCCTGAGGGAATT<br>GTGT  | AGTACTGAGCCCCCTG<br>GTTT      | 60.0                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold193_P4_329576 | scaffold193                             | 329576                        | TTATAAGTA/TTA                                                 | TCCATAAACCGTGTCC<br>CAAT  | TCAACCAAAATCCCCCA<br>ATA      | 60.1                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold193_P4_359988 | scaffold193                             | 359988                        | AATATATATATATATATAT/AATATAT<br>ATATATATAT                     | TTGGGTATGGGCAAGT<br>TAGC  | TGTATGTTTCCGAGAA<br>CGCA      | 60.0                             | 856                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold193_P4_394517 | scaffold193                             | 394517                        | ATAT/ATATTTAT                                                 | TTGGAAGGAGCCCTTA<br>CCTT  | ACCCAATTACTGGAGA<br>TGCG      | 60.1                             | 873                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold193_P4_79630  | scaffold193                             | 79630                         | TAAAAAAA/TAAAAAA                                              | AAAATAAATGCGCCGT<br>ATGC  | AGATCATGTGCAAAAA<br>GGGG      | 60.0                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold193_P4_79687  | scaffold193                             | 79687                         | TAATAA/TAATAATAAAATAA                                         | AAAATAAATGCGCCGT<br>ATGC  | AGATCATGTGCAAAAA<br>GGGG      | 60.0                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1930_P4_33808 | scaffold1930                            | 33808                         | TTATTAT/TT                                                    | CAACTGAATTTATTCG<br>TGCAA | CGTCATTAAGTACAAC<br>ATAAACGAA | 60.0                             | 142                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1930_P4_40318 | scaffold1930                            | 40318                         | GTTT/GTT                                                      | ATTAGCTCGAAAAGTG<br>CCGA  | GTTTGAAATCTGGCGA<br>GGAA      | 60.0                             | 265                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1930_P4_44785 | scaffold1930                            | 44785                         | CGG/CG                                                        | TATTTTGGGTTCCGCG<br>TTAG  | TCGGGAGATTTTCGTA<br>CCAC      | 60.0                             | 408                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1943_P4_104145 | scaffold1943                            | 104145                        | CTTTTTTTTT/CTTTTTTTTTT                                        | TAAAAACCGGTCGGT<br>TCAG     | AGTCTGAAATGACGT<br>GGGA     | 60.0                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1943_P4_121285 | scaffold1943                            | 121285                        | A/ATCTGAAT                                                    | TTGGATCAAATTGCTT<br>GGAAC   | TCGACTTGCAATCGC<br>TTTG     | 59.9                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1943_P4_193489 | scaffold1943                            | 193489                        | ATTTTTTTTTT/ATTTTTTTTTT                                       | TTGAAATCGACAATG<br>CACC     | TTTCCCGACTTGGTCC<br>TTTA    | 59.5                             | 429                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1943_P4_251763 | scaffold1943                            | 251763                        | TAAAAAAAAA/TAAAAAAAAA                                         | CCTTACCCCTCGCACT<br>ATGA    | TGGGTCATGGTTCCT<br>CATT     | 60.1                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1943_P4_2994   | scaffold1943                            | 2994                          | TAAAAAAAA/TAAAAA                                              | TTGTAGCCTGCTCG<br>ATT       | TCCATCGAGACTCATT<br>ATAAGCA | 59.8                             | 807                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1943_P4_340886 | scaffold1943                            | 340886                        | ATTTTTTTT/ATTTTTTTT                                           | GGAAAGAAGAAAACT<br>TTGTGGAA | AAAAACCAATATTGCCT<br>TCCTTA | 60.0                             | 210                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1943_P4_366143 | scaffold1943                            | 366143                        | GAAAAGAAATATAAAAGAAAT/GAAA<br>AGAAAT                          | TAATCCGCCTTGTGTG<br>TTCA    | CGTATGCAATTGTACG<br>GTGG    | 60.1                             | 923                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1943_P4_393620 | scaffold1943                            | 393620                        | ATC/ATCTTC                                                    | TGGTTCTCATGATACG<br>TGTTG   | GCGCAAAACACAAACAA<br>CAAA   | 59.4                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1945_P4_12188  | scaffold1945                            | 12188                         | CAAAGAGATA/C                                                  | TTCTCCCTCCTTCCTC<br>CATT    | GTTGGTTCCCTAGCAC<br>CGTA    | 60.0                             | 270                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1945_P4_31719  | scaffold1945                            | 31719                         | TAA/TAAA                                                      | CTCGTTGTAGGGCTCT<br>TGCT    | ATTAAAGGGAATGCGG<br>TGTTG   | 59.6                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                  |                              |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1945_P4_4916   | scaffold1945                            | 4916                          | GTTT/GTT                                                         | CGTCAAACACAAACCT<br>CCCT     | TGTTTTTCACGCCAAC<br>ATTA | 60.0                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1945_P4_705    | scaffold1945                            | 705                           | GACATA/GA                                                        | AGTCCTGACAATCCAA<br>ACGG     | GCGAGAAAAGCCAGCT<br>AGAA | 60.0                             | 238                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1946_P4_1226   | scaffold1946                            | 1226                          | TATATA/TATATAATATA                                               | ACATTAAATTCGGGG<br>GAGG      | CACACTCTCACCCGGC<br>TAAT | 60.0                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1954_P4_1118   | scaffold1954                            | 1118                          | GCCCC/GCCCCC                                                     | CCGCTATGGCAATTAC<br>TTTTG    | GTGGCATGGGAGTCTG<br>TTTT | 59.6                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1954_P4_1610   | scaffold1954                            | 1610                          | A/AG                                                             | AAAACAGACTCCCATG<br>CCAC     | TAGCGAAGTTTGTCGG<br>CTTT | 60.0                             | 506                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1954_P4_2359   | scaffold1954                            | 2359                          | ATTTT/ATTTTT                                                     | AAAGCCGACAACTTC<br>GCTA      | CGAGGAGCAATGAGTG<br>TCAA | 60.0                             | 752                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1956_P4_63893  | scaffold1956                            | 63893                         | ATATTATTATTATTATTATTATT/<br>ATATTATTATTATTATTATTATTA<br>TTATTATT | TTCTTTATGCAGTCAAA<br>TTTCTAA | AAAATGGACCAACGTC<br>CGTA | 58.1                             | 719                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1959_P4_121649 | scaffold1959                            | 121649                        | T/TCG                                                            | GACACCAGGAGGCATG<br>TTTT     | GGAAGGCTTGTCAGCT<br>TGAG | 60.0                             | 357                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1959_P4_67541  | scaffold1959                            | 67541                         | GT/G                                                             | CCTACGGATGACCTCT<br>CTCG     | TAACGGTGAGTTGACG<br>ACGA | 59.8                             | 400                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1959_P4_83297  | scaffold1959                            | 83297                         | CAAAA/CAAAA                                                      | TTCGGTGGCATAAATT<br>GTGA     | TTCAAAATGGTCGACAT<br>CCA | 59.9                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)      | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                    |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1962_P4_108825 | scaffold1962                            | 108825                        | ATTTTTTTTTTTT/ATTTTTTTTTTT                                         | TCAGTCCCGCAGAATA<br>GCTT | GAATGTTCTTCCCTCA<br>CCA  | 60.0                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1962_P4_159146 | scaffold1962                            | 159146                        | AAATATAAGCAGAAAATTAA/AAATA<br>TAAGCAGAAAATTAATATAAGCAGA<br>AAATTAA | CTTTTACAGCGCTTGT<br>GGG  | AAGCCGTGTAATCTGA<br>ACCG | 60.8                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1962_P4_170714 | scaffold1962                            | 170714                        | GTTTTTTTTT/GTTTTTTTTT                                              | TCAAGGACCCAAAGCA<br>CATT | TACTCCCCCTTTGAGC<br>TTGA | 60.5                             | 423                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1964_P4_172119 | scaffold1964                            | 172119                        | ATTGG/A                                                            | TTGTTTGTAGAAACG<br>CCG   | ACCCACATAGCGCAAG<br>ATTG | 58.9                             | 313                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1964_P4_172181 | scaffold1964                            | 172181                        | CG/CGG                                                             | ATAGCGCTTGATTGAT<br>TGGG | ACCCACATAGCGCAAG<br>ATTG | 60.1                             | 276                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1964_P4_20160  | scaffold1964                            | 20160                         | GAAA/GA                                                            | TGTTGTTTCCAACCACT<br>CCA | CAGTCCAACAAAACCA<br>ATGC | 60.0                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1964_P4_21448  | scaffold1964                            | 21448                         | CAAAATAAAATAA/CAAAATAA                                             | GGGTCAGTTCATCCCA<br>TGAC | TATGCATCTTTGTTGAC<br>GCC | 60.2                             | 292                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1964_P4_6786   | scaffold1964                            | 6786                          | GTTTTTT/GTTTTT                                                     | CCCTTGAAGAAAAAC<br>CACA  | TTGGGAAGGGAGATGT<br>CAAG | 59.9                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1964_P4_8928   | scaffold1964                            | 8928                          | ATTTTT/ATTTT                                                       | CCTCCACTGCTGAGTT<br>GTGA | AAGCCTAAGCTGCATT<br>GGAA | 60.0                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold198_P4_137468  | scaffold198                             | 137468                        | T/TC                                                               | TCATTGGAATCCGTGT<br>CTGA | ATCAAGCGTCCTTTGA<br>GCAT | 60.0                             | 867                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                      | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                    |                             |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold198_P4_263701 | scaffold198                             | 263701                        | ATTTTATAAGT/ATTTTATAAGTTTTA<br>TAAGT                                                                               | ATAAGTTGGTGTGGCA<br>TCGG    | CAACAACCTCTCATGCT<br>CGC     | 60.8                             | 921                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold198_P4_356714 | scaffold198                             | 356714                        | GA/GAA                                                                                                             | TGTTGGCAGTGCTCTG<br>TCTT    | CTCGGCAAGGAACAAA<br>TAGG     | 59.6                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold198_P4_366920 | scaffold198                             | 366920                        | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATA/AAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATA | GCGAGCTAGCTAGGTA<br>AGTGCT  | AAAGCGAATTGAGTGA<br>TGCC     | 59.5                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold198_P4_435699 | scaffold198                             | 435699                        | AATATATATATATATATATATAT<br>AT/AATATATATATATATATATATA<br>TAT                                                        | TTTTGAAATCAATCAA<br>ATCATGT | AATTTATTGCGCATGCT<br>CCT     | 57.6                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold198_P4_501505 | scaffold198                             | 501505                        | CA/CAA                                                                                                             | TTGCCAAGTCCCTGT<br>TTAC     | CGTTCCTGAGGGAATT<br>GTGT     | 60.0                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold198_P4_544150 | scaffold198                             | 544150                        | TAAAAAAAAA/TAAAAAAAAA                                                                                              | GGTGCATGTTTCTTGG<br>TCCT    | GCAAAAAGCGGTGTGG<br>TTAT     | 60.0                             | 185                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold198_P4_567421 | scaffold198                             | 567421                        | TTATATATATATATATATATATATA<br>TATATATATATA/TTATATATATATAT<br>ATATATATATATATATA                                      | TGCAATTTCTCCGACA<br>AGTG    | AAACAAATTCACAAAGC<br>GTATCAA | 59.8                             | 769                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold198_P4_60891  | scaffold198                             | 60891                         | TAAA/TAA                                                                                                           | ACAAGGATCAAAGGGT<br>GTGC    | CTCGATTGGTGGATG<br>AGTT      | 60.0                             | 391                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold198_P4_637738 | scaffold198                             | 637738                        | CTTAATTATATTTAATTA/CTTAATTA<br>TATTTAATTATATTTAATTA                                                                | TGACCGCAACCAGTTC<br>AATA    | CAATTGAAACTCTCACA<br>TTCAAAA | 60.1                             | 722                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold198_P4_70179  | scaffold198                             | 70179                         | ATTTTTTTTT/ATTTTTTTTT                                                                                              | TCAAAATCCCCCAATAA<br>CCA    | GCTGTGAGTTCCCAA<br>CAAT      | 60.0                             | 302                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                               |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold198_P4_95429   | scaffold198                             | 95429                         | ATTTTT/ATTTTT                                                 | ACTTTCATGAAGACAC<br>CGGG      | CTTCGAATCCAACCTT<br>GGTG      | 60.0                             | 845                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_116705 | scaffold1981                            | 116705                        | GATAATAATA/GATAATAATAATA                                      | TTGTTGATCGCAACTT<br>GAGG      | AATTGAACCAATAAAAC<br>ACGTTAAA | 59.8                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_117725 | scaffold1981                            | 117725                        | AT/A                                                          | TTCATTAATTGTCCAAT<br>TGCTAAGT | AGGTGCGATCACGTAA<br>AACC      | 58.3                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_118118 | scaffold1981                            | 118118                        | ACTCTCTC/ACTCTC                                               | GGTTTTACGTGATCGC<br>ACCT      | ATCGGAATTTTTGTGCC<br>TTG      | 60.0                             | 783                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_118182 | scaffold1981                            | 118182                        | TA/T                                                          | GGTTTTACGTGATCGC<br>ACCT      | ATCGGAATTTTTGTGCC<br>TTG      | 60.0                             | 783                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_118399 | scaffold1981                            | 118399                        | TAAAAAAAAA/TAAAAAAAAA                                         | AGCGAAAAGCACCATT<br>GAAC      | ATCGGAATTTTTGTGCC<br>TTG      | 60.3                             | 332                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_173749 | scaffold1981                            | 173749                        | AT/A                                                          | TTTAATTTGCACACTCG<br>ACAAA    | TGTGATTTTGATTAGC<br>TAGACTTG  | 58.4                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_229795 | scaffold1981                            | 229795                        | CTATATATATATATATATATATAT<br>ATAT/CTATATATATATATATATAT<br>ATAT | GCTTATTGCCAAAACG<br>CTGT      | ATGTGAATCCCACCAG<br>GAAA      | 60.3                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_233549 | scaffold1981                            | 233549                        | CTTTTTTTTT/CTTTTTTTTTTT                                       | CGTTTAGCCTCGTAGG<br>TTCG      | CAGCCATCTACTGCTC<br>CTCC      | 59.9                             | 756                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_234604 | scaffold1981                            | 234604                        | GTTTT/GTTTT                                                   | GCGCCATTTTACATC<br>GCT        | TGTGGTGTGGTGGTCT<br>ATGC      | 60.1                             | 756                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1981_P4_239519 | scaffold1981                            | 239519                        | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATAT<br>ATATATATATATATA     | AAATTTGCGTTTAAATA<br>ACGGG | TGGATCCTCCCTTTGT<br>ACG     | 59.3                             | 779                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_323872 | scaffold1981                            | 323872                        | TAATAAATAAATAAATAAATAAATA<br>ATAAATA/TAATAAATAAATAAATAA<br>TAAATAAATAAATAAATA | ACTTGGGAACCCGAAG<br>AAGT   | TGGGTACCCCTTTCTT<br>CCT     | 60.0                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_335599 | scaffold1981                            | 335599                        | T/TG                                                                          | TGCGCATTGAGTAATT<br>ATGGA  | TCGAGTCGATCACCAA<br>TTCA    | 59.2                             | 345                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_335897 | scaffold1981                            | 335897                        | TAAAAAAAA/TAAAAAAAA                                                           | GACTCGATCAAACCAT<br>TGGG   | AAATGGACCACTGGAG<br>TTGC    | 60.3                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_336889 | scaffold1981                            | 336889                        | ATTTT/ATTTT                                                                   | CTTGACGGTGGAGAGC<br>TAGG   | GCAAGGGTTTGAGATT<br>TTGG    | 60.0                             | 828                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_349007 | scaffold1981                            | 349007                        | CGG/CG                                                                        | GTGAGAAAGTGCTGGA<br>AGCC   | CCCATAAATTAACAT<br>AGTCGTGG | 60.0                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_349166 | scaffold1981                            | 349166                        | ATTTTT/ATTAATTTTTT                                                            | GTGAGAAAGTGCTGGA<br>AGCC   | GGACGGATTAAATTTG<br>TCGATT  | 60.0                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_351360 | scaffold1981                            | 351360                        | TAGACA/TA                                                                     | AGCTCCACCTCTGATC<br>TCCA   | TCACACAACGTGTGAGG<br>TCCTG  | 59.9                             | 308                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_351432 | scaffold1981                            | 351432                        | CAAAAAAAAA/CAAAAAAAAA                                                         | AGCTCCACCTCTGATC<br>TCCA   | TCACACAACGTGTGAGG<br>TCCTG  | 59.9                             | 308                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_355117 | scaffold1981                            | 355117                        | TCCC/TCCCC                                                                    | AAACCTCGAATTTTGT<br>GAATC  | GGGGCCTTTCAAAATA<br>TCGT    | 57.3                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1981_P4_355366 | scaffold1981                            | 355366                        | A/AC                                                          | ACGATATTTTGAAAGG<br>CCCC   | CGCGGATCCAATATCT<br>CACT  | 60.2                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_356890 | scaffold1981                            | 356890                        | AAATAAT/AAAT                                                  | GGACAAAAGGATGCCA<br>CACT   | GAGTGGAAAGTGGGGG<br>AATTT | 60.0                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_357708 | scaffold1981                            | 357708                        | AT/A                                                          | AGCCTTTTTGCAAATG<br>GTTG   | CCTTTTTGCAATTGGTT<br>GGT  | 60.1                             | 783                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_357939 | scaffold1981                            | 357939                        | TAAAAAAAAA/TAAAAAAAAA                                         | TCAAGTGTTCATTTTG<br>TTGGCA | CCTTTTTGCAATTGGTT<br>GGT  | 59.7                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_358146 | scaffold1981                            | 358146                        | TAAAAAAA/TAAAAA                                               | ACCAACCAATTGCAAA<br>AAGG   | TAACTTGTGTCCGG<br>AGGC    | 59.8                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_361189 | scaffold1981                            | 361189                        | TAAAAAAA/TAAAAA                                               | TCACACGCCTCAAGCA<br>TATC   | CGATCATGCTTCGACC<br>ACTA  | 59.8                             | 894                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_371669 | scaffold1981                            | 371669                        | CTATA/CTA                                                     | TTTCGTGGTCCTAAATT<br>GCC   | AACCCGAGTTCACCAT<br>TTTG  | 59.9                             | 989                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_378050 | scaffold1981                            | 378050                        | AAGAG/AAG                                                     | TGTGGGACTTTGATGT<br>TGGA   | TCCAAAGTTGGAAGCC<br>AAAC  | 59.9                             | 309                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_378498 | scaffold1981                            | 378498                        | AT/ATTT                                                       | GATGGTTGCCCAACAA<br>ACTT   | TCTACCCACGCGAGAG<br>TCTT  | 59.8                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_379339 | scaffold1981                            | 379339                        | GTTTTTTT/GTTTTTTT                                             | TTTAAACGGGCTTCT<br>CTGA    | GGATTGAAGATGGGG<br>GTTC   | 59.8                             | 855                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1981_P4_405853 | scaffold1981                            | 405853                        | TAA/TAAA                                                      | AAGAACGACCGGAACA<br>AAAA | CCATAGCCGTTTCAAG<br>TCCT  | 59.6                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_407023 | scaffold1981                            | 407023                        | ATTTTTTTT/ATTTTTTTTTT                                         | TGGATCCAAACGTGGA<br>AAA  | GTCGCATCCAACGACC<br>TATT  | 59.9                             | 333                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_407065 | scaffold1981                            | 407065                        | CTTTTTTTT/CTTTTTTTTTT                                         | TGGATCCAAACGTGGA<br>AAA  | GTCGCATCCAACGACC<br>TATT  | 59.9                             | 333                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_408460 | scaffold1981                            | 408460                        | TA/TAA                                                        | TAATGCGTCAAATGCC<br>TCAA | ATGCGCAAATTTCTGTG<br>ACTT | 60.2                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_408955 | scaffold1981                            | 408955                        | ATTTTT/ATTTTTT                                                | TGTGCAATGCAACAAT<br>TCAA | AATACTCGTGACCCGT<br>GGTT  | 59.7                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_413552 | scaffold1981                            | 413552                        | A/AT                                                          | TGTCATGATTGGCTAT<br>CGGA | TCGCAATTTGTAGTGG<br>ACGA  | 60.0                             | 668                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_415952 | scaffold1981                            | 415952                        | TAA/TA                                                        | GGCTCGCTACGTACGA<br>CATT | CGTTGCATGTTAGCTC<br>CTGA  | 60.3                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1981_P4_421011 | scaffold1981                            | 421011                        | GAT/GATAT                                                     | TTCGATTGGACCACTT<br>CACA | CGCGCATGTTTGTATC<br>TGTC  | 60.1                             | 228                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1983_P4_25976  | scaffold1983                            | 25976                         | CTTT/CTT                                                      | TCGCACTCCTGAGTCA<br>TGTT | TCAATTTCAACTGCAAA<br>CCAA | 59.4                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1983_P4_34254  | scaffold1983                            | 34254                         | G/GATAA                                                       | AGAAAGGCTCAAACGA<br>CCAA | CTCAAGTCGACAAGCC<br>TTCC  | 59.9                             | 301                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                      | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                                                    |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1983_P4_63035  | scaffold1983                            | 63035                         | TAAA/TA                                                                                                                            | GCGGGTGTAGTGACAT<br>GTTG   | TGTGGCCGTAAACATT<br>CAAA  | 60.0                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1984_P4_108680 | scaffold1984                            | 108680                        | TA/T                                                                                                                               | TTCCAACAACAAAATGC<br>AAA   | TCGCAAAAGTACGCTG<br>AAAA  | 57.7                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1984_P4_134237 | scaffold1984                            | 134237                        | CAATAAATAAATAAATAAATAA<br>ATA/CAATAAATAAATAAATAA<br>TAAATAAATA                                                                     | TGCACAGTGGCTATAC<br>CTGG   | GGGAGGCAACCCAATT<br>TTAT  | 59.7                             | 239                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1984_P4_135970 | scaffold1984                            | 135970                        | CAAAAA/CAAAAAA                                                                                                                     | CAAGTCTCCAAGTTC<br>CCAA    | TATGGCAGCGTGATGA<br>ATGT  | 60.1                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1984_P4_300039 | scaffold1984                            | 300039                        | TTTCTTCTTCTTCTTCTTCTTCT<br>TCTTCTTCTTCTTCTTCTTCTTCT<br>TTCT/TTTCTTCTTCTTCTTCTTCT<br>TTCTTCTTCTTCTTCTTCTTCTTCT<br>CTTCTTCTTCTTCTTCT | CGAAAAGCAGCAAAACA<br>TGAA  | GCTGACTGCCATTGAT<br>GCTA  | 60.0                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1988_P4_7769   | scaffold1988                            | 7769                          | TACACACAATCAAA/TACACACAAA<br>TCAAA                                                                                                 | ACCATACAAGTTCCTCCG<br>CATC | GAAGGAGCAGTAAGCC<br>ATCG  | 59.8                             | 725                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1991_P4_9498   | scaffold1991                            | 9498                          | AATATATATATATAT/AATATATATAT<br>ATATAT                                                                                              | TGCTCTCCTTCGTGAG<br>AGTTT  | CCAAGACCATCCTGCT<br>CAAT  | 59.2                             | 842                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1996_P4_1333   | scaffold1996                            | 1333                          | TG/TGG                                                                                                                             | CGGATGAATCATTGGG<br>AAAT   | AGTGAAACCAACGCCA<br>AAAC  | 59.6                             | 325                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1996_P4_5730   | scaffold1996                            | 5730                          | GAAAAAAA/GAAAAA                                                                                                                    | TGTTAGGAGGATCTCA<br>CGGG   | ATTGTTGGAAAAATTGG<br>CTGC | 60.1                             | 823                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1999_P4_27916  | scaffold1999                            | 27916                         | CAAA/CAAAA                                                                                                                         | AGGGAGGACGAAAATG<br>ACCT   | CTTGGGCATCCAATAG<br>GTGT  | 59.9                             | 763                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                              |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold1999_P4_29603 | scaffold1999                            | 29603                         | GACA/GACACA                                                                                  | AGGGAGGACGAAAATG<br>ACCT  | AACCAATCTTGTGCATC<br>CAA | 59.9                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold1999_P4_29835 | scaffold1999                            | 29835                         | TAAAAAAA/TAAAAA                                                                              | AATCCAACGACAACGG<br>AACT  | CCGATGTTGTGCATCC<br>AATA | 59.5                             | 541                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2_P4_36097    | scaffold2                               | 36097                         | CTTTCCTTCTTTCTTT/CTTTCCTT<br>TTTCTTTCTTTCTTT                                                 | TTGGAAGGAGCCCTTA<br>CCTT  | CGTTTGGGTTTGAAA<br>GAAA  | 60.1                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2_P4_387981   | scaffold2                               | 387981                        | TAAAAAAAAA/TAAAAAAAAA                                                                        | CACTTAGCCTTGTGT<br>GCCA   | TTGTTTCGAACAATTGC<br>ACC | 59.9                             | 337                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2_P4_503726   | scaffold2                               | 503726                        | TAAAAA/TAAAAA                                                                                | CAGGCATGTAAACAAT<br>GAGCA | ACACGAACCCAAAAG<br>AACG  | 59.7                             | 280                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2_P4_504035   | scaffold2                               | 504035                        | CAAA/CAAAA                                                                                   | CGTTCCTTTTGGGTTT<br>GTGT  | ATCCCATAGCCACATT<br>CCA  | 60.0                             | 265                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2_P4_69919    | scaffold2                               | 69919                         | GC/G                                                                                         | TTCGCAACTCCACTCTT<br>CCT  | CAACGCAACATAACAC<br>CCAG | 60.0                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold200_P4_67932  | scaffold200                             | 67932                         | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTAT/TTTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTAT | AGGGAGGACGAAAATG<br>ACCT  | AGAAAGGAGAAGGCAG<br>GGAG | 59.9                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2000_P4_1544  | scaffold2000                            | 1544                          | GAAAAAA/GAAAAAA                                                                              | GCCTAGGGATGACGAA<br>AATG  | TGTGTTTGCATCATTG<br>GATT | 59.5                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2003_P4_20377 | scaffold2003                            | 20377                         | TA/T                                                                                         | AAGCAAACACAAACCC<br>GAAC  | CTCCCTTGCCAGTTAA<br>TGC  | 60.0                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                          | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                        |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2005_P4_2617  | scaffold2005                            | 2617                          | ATTTTTTT/ATTTTTTTT                                                                                                     | ACCAGCAACCATAAAA<br>ACGC   | CTTCGAATCCAACCTT<br>GGTG  | 60.0                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2005_P4_31637 | scaffold2005                            | 31637                         | ATTTTTTTTT/ATTTTTTTTTT                                                                                                 | TGGTGAGTGAACCAAA<br>CGAG   | CAGCCGTCTTCATTTTC<br>ATCT | 59.7                             | 302                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2005_P4_32399 | scaffold2005                            | 32399                         | ATTTTTTTTT/ATTTTTTTTTT                                                                                                 | CCAGACCAGACTTCGA<br>AAGG   | GACTGTCTGTCAGGG<br>CCTA   | 59.8                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2018_P4_16998 | scaffold2018                            | 16998                         | CAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AAT/CAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAAT | AAGGCTCACTTGCAAA<br>GACG   | GGTATTGCTGCAGTTT<br>TTGG  | 60.6                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2018_P4_24141 | scaffold2018                            | 24141                         | GTCTCTGTTTTCTCT/GTCTCTGTTT<br>TCTCTGTTTTCTCT                                                                           | TTGAGAGGACGTATTC<br>GGCT   | GCGGAGATTTTGAAG<br>CAAG   | 59.8                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2018_P4_4354  | scaffold2018                            | 4354                          | TGGAG/TG                                                                                                               | CATGGTTTTGTTTGTC<br>GTGC   | TGTTTGCTTTAAGCGAT<br>GTCA | 60.0                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold202_P4_104727 | scaffold202                             | 104727                        | TTA/T                                                                                                                  | TCATTCATCCAATCCAT<br>CCA   | TCGAGTGTGCATCTCA<br>AGGA  | 59.7                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold202_P4_17816  | scaffold202                             | 17816                         | AAA/AAATAA                                                                                                             | TCACAAGGGTAGTTTT<br>GGGTTT | CTGCCAGCTCACCTCC<br>TATC  | 59.8                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold202_P4_19978  | scaffold202                             | 19978                         | GT/G                                                                                                                   | GGAATTTTGCAAAAA<br>CGGA    | CTGTCCGCCTAATTTTC<br>GAG  | 60.1                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold202_P4_20536  | scaffold202                             | 20536                         | CTA/C                                                                                                                  | TGCATCCAACTTTGGT<br>GTGT   | ACACCGTTGTTTATGCA<br>CGA  | 60.0                             | 373                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold202_P4_22635 | scaffold202                             | 22635                         | CG/C                                                          | GGATTACATTCGCTTC<br>TCCG | GCAACAATGCGAAAC<br>AGAA    | 59.7                             | 804                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold202_P4_22768 | scaffold202                             | 22768                         | AT/A                                                          | TTGCAATCATGAGGCA<br>AGTC | GCAACAATGCGAAAC<br>AGAA    | 59.8                             | 235                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold202_P4_36818 | scaffold202                             | 36818                         | TA/TACA                                                       | ACCGCTAAATCGGTGT<br>CAAC | TGGGATCTTGTACCCA<br>AACC   | 60.0                             | 932                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold202_P4_37860 | scaffold202                             | 37860                         | TAAA/TAA                                                      | ATTGGAGGCTGGTTT<br>GTTG  | ATCGTGGGGATGAATT<br>TGAA   | 60.0                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold202_P4_37967 | scaffold202                             | 37967                         | T/TC                                                          | ATTGGAGGCTGGTTT<br>GTTG  | ATCGTGGGGATGAATT<br>TGAA   | 60.0                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold202_P4_38468 | scaffold202                             | 38468                         | ATT/AT                                                        | TTCAAATTCATCCCCAC<br>GAT | CCAAGTGGTACAATTG<br>GTGTCT | 60.1                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold202_P4_38482 | scaffold202                             | 38482                         | AT/ATT                                                        | TTCAAATTCATCCCCAC<br>GAT | CCAAGTGGTACAATTG<br>GTGTCT | 60.1                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold202_P4_39053 | scaffold202                             | 39053                         | CTTTTTTTT/CTTTTTTTT                                           | GCACCGGAAAATACGT<br>AGGA | ATTATCTTGTCGCGGC<br>CTAA   | 60.0                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold202_P4_39185 | scaffold202                             | 39185                         | TATG/TATGATG                                                  | GCACCGGAAAATACGT<br>AGGA | ATTATCTTGTCGCGGC<br>CTAA   | 60.0                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold202_P4_39293 | scaffold202                             | 39293                         | CTTTT/CTTTTT                                                  | GCACCGGAAAATACGT<br>AGGA | ATTATCTTGTCGCGGC<br>CTAA   | 60.0                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2020_P4_11180  | scaffold2020                            | 11180                         | CAAAAA/CAAAA                                                  | GATACAAGAATCGCCC<br>GAAA  | TCCTGGTCCTCGATT<br>CATC   | 60.0                             | 208                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2020_P4_7500   | scaffold2020                            | 7500                          | AATA/AA                                                       | CTTGCTAGAGCTTGGC<br>GATT  | ACATTTCTTTGGCGTT<br>TTG   | 59.8                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2022_P4_115294 | scaffold2022                            | 115294                        | GT/GTT                                                        | ATTCCAAACCAAAACC<br>CTCC  | TGTTGGCGTGAAAACC<br>ATTA  | 60.0                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2023_P4_2321   | scaffold2023                            | 2321                          | CAA/CAAA                                                      | AACACCAACTCCACCA<br>CACA  | TGTTTTGGTTGAGAG<br>AGGG   | 59.9                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2024_P4_1945   | scaffold2024                            | 1945                          | CAAA/CAAAA                                                    | GAATGTTAGGGTTTC<br>GGGT   | GATGAAATCGAGGACT<br>GGGA  | 60.1                             | 338                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2027_P4_125527 | scaffold2027                            | 125527                        | TATAGATGTCAACA/T                                              | TCTTTGAATTTGCACGT<br>TTGA | GAGCCATGGAGTTTGG<br>TTGT  | 59.3                             | 793                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2027_P4_955    | scaffold2027                            | 955                           | GAAAAAAAA/GAAAAAAAA                                           | AGAAAGGCTCAAACGA<br>CCAA  | ACAGAGGAAGCTGCCA<br>CCTA  | 59.9                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2030_P4_4596   | scaffold2030                            | 4596                          | ATT/ATTTT                                                     | AGGGTTTAGGATTTTCG<br>CGTT | CATATCAAAACCCAAA<br>TGACC | 60.0                             | 243                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2033_P4_178950 | scaffold2033                            | 178950                        | TAAAAA/TAAAAA                                                 | GCTCCATTGCTTCAG<br>CTAC   | GGGTAAGCTATGCACC<br>CTGA  | 60.0                             | 427                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2033_P4_3959   | scaffold2033                            | 3959                          | GATATATATATATATATATA/GA<br>TATATATATATATATATA                 | GCGGATCTGCTCTTGA<br>ATT   | TCCAAACATAGTGGTC<br>GTCG  | 59.4                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2033_P4_44747  | scaffold2033                            | 44747                         | GTTTTTTTTT/GTTTTTTTTT                                         | ATGAATACCCCTGCGA<br>GTTG  | GAACAAGCAATCGCAG<br>ACAA    | 60.0                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2033_P4_66509  | scaffold2033                            | 66509                         | TTAT/TTATAT                                                   | ACCCAAGAGGATAAGG<br>GCAC  | AGCCCTCGAAAAGATA<br>CCAA    | 60.3                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2033_P4_92221  | scaffold2033                            | 92221                         | CAAAAAAAAA/CAAAAAAAAA                                         | GAAAATCCTGCCCAAG<br>TTGA  | TCACCTGATGAGGAAA<br>ATGAA   | 60.1                             | 731                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2036_P4_57805  | scaffold2036                            | 57805                         | ATT/ATTT                                                      | ATCACATCCTTTTGAAG<br>CGG  | AAAACCCCATTCATCAT<br>CCA    | 60.1                             | 262                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2040_P4_154810 | scaffold2040                            | 154810                        | AATATATATATATATATAT/AAAT<br>ATATATATATATAT                    | ATTTTGTTTCGGAGGC<br>TTTT  | TCTCTACGCCGTTTTT<br>CTT     | 59.9                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2040_P4_159577 | scaffold2040                            | 159577                        | CA/CAGGTA                                                     | TGAAGAGGGGAATCCA<br>TCTG  | TTAACAACTCCTGGTTC<br>GGG    | 60.0                             | 372                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2040_P4_235335 | scaffold2040                            | 235335                        | GTTTTTTTTT/GTTTTTTTTT                                         | GGATTGAGCCGATACT<br>GATTG | CTCGTTCCATGAACCG<br>ACTT    | 59.5                             | 466                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2040_P4_62407  | scaffold2040                            | 62407                         | ATTTTTTTTTT/ATTTTTTTTTT                                       | TGTTGCAAACTGGGC<br>ATTA   | CTTGTCGGGTACCTC<br>GTGT     | 60.1                             | 411                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2040_P4_75386  | scaffold2040                            | 75386                         | CTTTT/CTTT                                                    | GTCAATCGACTTGGCT<br>GGTT  | GGAACCTCAAGCAATCA<br>AGCA   | 60.1                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold205_P4_130828  | scaffold205                             | 130828                        | TAAAAAAAA/TAAAAAAAA                                           | TTGTTCTGTGAATTTTG<br>ACGC | TTTGGGGAATTTACTTA<br>ATCGAA | 58.7                             | 444                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold205_P4_152979  | scaffold205                             | 152979                        | AATATATATATATATATATA/AATATA<br>TATATATATATATATA               | TATCGATTGGCTGAAATCCA    | CACAAGCGCCGTAAATACA     | 59.1                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold205_P4_41104   | scaffold205                             | 41104                         | GT/GTCT                                                       | TAATGCGCTTCTGATTGTGC    | AGGCCGTATTGCTTTTGAGA    | 60.0                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold205_P4_46882   | scaffold205                             | 46882                         | GAGGA/GAGGAAGGA                                               | GAGAGGATTTGTGTCCGCA     | GGAATGCTCAAAGTTGCAT     | 60.1                             | 235                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold205_P4_75804   | scaffold205                             | 75804                         | G/GCTAGTTAAGAAGAA                                             | TGAAGAGGGGAATCCATCTG    | ACTCCAACGGCATAACAG      | 60.0                             | 745                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2051_P4_195973 | scaffold2051                            | 195973                        | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>A   | TCGATTTTCCAGTCCATTCA    | GGTGCACCTATTGGTCATT     | 59.0                             | 762                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2051_P4_202819 | scaffold2051                            | 202819                        | TAAAAAAAA/TAAAAAAAA                                           | TGTCATGGCGAGTATTCCA     | CTTTTCCATTCTCTGTCACAA   | 60.1                             | 335                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2051_P4_220529 | scaffold2051                            | 220529                        | ATATGTAT/ATAT                                                 | TCCACATCCACTGAGGAACA    | GCATTTTCTTGGCACGTTTT    | 60.1                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2051_P4_51153  | scaffold2051                            | 51153                         | TC/TCC                                                        | AGGTTTGATTTTGTGCTGCG    | TGGCGATTGAGAAGCAAGTA    | 60.0                             | 365                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold206_P4_162025  | scaffold206                             | 162025                        | GTTTT/GTTTT                                                   | CTTGGATTCATTGATCGCT     | GTTTGGTTTTCTTTGGGGT     | 60.0                             | 423                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold206_P4_175737  | scaffold206                             | 175737                        | TTAAATAAA/TTAAA                                               | GCCCTCAGATGAGAGTCAGG    | TGACGCCATGGTGACATACT    | 59.9                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold206_P4_176077 | scaffold206                             | 176077                        | T/TATAG                                                       | CTCTCGCTATGAAAA<br>CGGG   | TGGGTTCAATTGGCAT<br>TTTT     | 59.8                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold206_P4_179036 | scaffold206                             | 179036                        | GAAAAAAAA/GAAAAAAAAA                                          | TTTTCCGAGTTGGTCC<br>CTTA  | TGGAAAAGATAGCAGC<br>CGAT     | 59.5                             | 884                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold206_P4_190834 | scaffold206                             | 190834                        | CATATATATATATATATAT/CATATAT<br>ATATATATATATAT                 | ATCCCTAACGCCGTTT<br>TTCT  | ATATTGGCTCGGAGGC<br>TTTT     | 60.0                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold206_P4_199524 | scaffold206                             | 199524                        | T/TA                                                          | CCGAGCCAAATCCAA<br>AATA   | TCTCAACGATAGCCAT<br>CACG     | 59.9                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold206_P4_25527  | scaffold206                             | 25527                         | GTT/GTTT                                                      | TTTTGGGTGTGAGTTG<br>TGGA  | AACGTACTGCCTATCA<br>CGGG     | 60.0                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold207_P4_6894   | scaffold207                             | 6894                          | AC/A                                                          | GCAAACGACAGGAA<br>AAGC    | TTGGTGAAGATGTCAG<br>CCAG     | 60.0                             | 370                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2072_P4_3202  | scaffold2072                            | 3202                          | CCAA/C                                                        | TTCAATTTGAACTTTTCG<br>GGC | TGACGTAGAACTATAAA<br>ACGGTGA | 60.1                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold208_P4_119748 | scaffold208                             | 119748                        | AACA/AA                                                       | CGTGTATATACGCACA<br>CCCAA | TTGTAAACGGAGAAAT<br>CGGG     | 59.4                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold208_P4_15689  | scaffold208                             | 15689                         | CTATATATA/CTATATATATA                                         | TTTTGGCCATTTCAACT<br>CAA  | TCCAAATACTTAAATGC<br>GAACAAA | 59.1                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold208_P4_157224 | scaffold208                             | 157224                        | CAAGTAAG/CAAG                                                 | ATGTGACACCCTAAAC<br>CCCA  | GATCTATGAGGACAGG<br>GCCA     | 60.1                             | 727                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                              |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold208_P4_174233 | scaffold208                             | 174233                        | GAAAA/GAAA                                                                                                                   | CCTTGGAGTATTCTCG<br>GCAG | TGCTGATCCGTGAGAG<br>ATTG  | 59.8                             | 894                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold208_P4_208390 | scaffold208                             | 208390                        | ATGCATTGCATTGCATT/ATGCATTG<br>CATTGCATTGCATT                                                                                 | TGTTTACCTCGACTGTT<br>GCG | CTTCCAAACCCGAACCTT<br>CAA | 59.9                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold208_P4_37577  | scaffold208                             | 37577                         | CA/CAA                                                                                                                       | CCCCAAGCAACAATCA<br>ATTT | CAACGTGCACCATAAC<br>AAAGA | 59.8                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2089_P4_679   | scaffold2089                            | 679                           | TGTTTGGGGTTT/TGTTTGGGGTTT<br>GGGGTTT                                                                                         | TTGCGGTTCCGTATTA<br>TGTT | AAACCCAAACGCTAAA<br>CCCT  | 60.2                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2089_P4_805   | scaffold2089                            | 805                           | AT/A                                                                                                                         | TTGCGGTTCCGTATTA<br>TGTT | AAACCCAAACGCTAAA<br>CCCT  | 60.2                             | 587                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold209_P4_258029 | scaffold209                             | 258029                        | TA/TAA                                                                                                                       | TCAGGCAACAAGCAG<br>ACAC  | ATCGAATGCCTCAATCT<br>TGG  | 60.0                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold209_P4_378233 | scaffold209                             | 378233                        | AATATATATATATATAGATATATA<br>TATATATAT/AATATATATATATAT<br>ATAGATATATATATATAT                                                  | AAATGGAGGAGAAGGA<br>GGGA | ATTTTGGGTCGGAAGC<br>TTTT  | 60.0                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold209_P4_96741  | scaffold209                             | 96741                         | C/CAT                                                                                                                        | TTGTGCATCCAATCAG<br>GTGT | AGGGAGGACGAAAATG<br>ACCT  | 60.0                             | 262                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2097_P4_4977  | scaffold2097                            | 4977                          | GC/GCC                                                                                                                       | ACATTCCCATCCACAG<br>GGTA | CATGCAGGAATTCAGC<br>AAAA  | 60.1                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2097_P4_50389 | scaffold2097                            | 50389                         | TATAATAATAATAATAATAATAAA<br>TAATAATAATAATAATAATAATA<br>ATAA/TATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAA | TGGCCACTTAATTCAC<br>ATCG | TGGTTCAGTTTTGCCA<br>CATAA | 59.5                             | 318                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                             |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2097_P4_59684  | scaffold2097                            | 59684                         | TTATATATATATATATATATATATAT<br>T/TTATATATATATATATATATATATA<br>T              | TTAAATCCGCAGGAA<br>AACG   | CCACATGATTTTGGCAT<br>GAG    | 60.1                             | 306                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold210_P4_31686   | scaffold210                             | 31686                         | CAA/CAAA                                                                    | TTTTCTCGCAAAACATG<br>CAG  | TTCGCAACTCCACTCTT<br>CCT    | 60.0                             | 712                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold210_P4_32630   | scaffold210                             | 32630                         | TAAAA/TAAAAA                                                                | AGGAAGAGTGGAGTTG<br>CGAA  | TATTTTGGATTTTGGCT<br>CGG    | 60.0                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold210_P4_330740  | scaffold210                             | 330740                        | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATATA<br>TATATATATATATAT | ATGTTTTGGATTTTGG<br>CTCG  | AGGAAGAGTGGAGTTG<br>CGAA    | 59.9                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold210_P4_577121  | scaffold210                             | 577121                        | AGAAATCGATTGG/AGAAATCGATT<br>TGGAAATCGATTGG                                 | TTGCCAAGTGTGGATG<br>TTGT  | GGGTACGAACCGGTAG<br>GATT    | 60.0                             | 947                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2103_P4_113083 | scaffold2103                            | 113083                        | ATTTTTTTT/ATTTTTTTTTT                                                       | CGGTGGGGGAGAACTCT<br>GATA | AACCAACAATTCACATG<br>GCA    | 60.1                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2103_P4_124055 | scaffold2103                            | 124055                        | AT/A                                                                        | AACCCAATCACTGGAG<br>ATGC  | AGGAAGAGTGGAGTTG<br>CGAA    | 59.9                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2103_P4_124113 | scaffold2103                            | 124113                        | AG/AGG                                                                      | AACCCAATCACTGGAG<br>ATGC  | AGGAAGAGTGGAGTTG<br>CGAA    | 59.9                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2103_P4_145039 | scaffold2103                            | 145039                        | GTATATATATATATATATATAT/GTAT<br>ATATATATATATATAT                             | GCCAGAACCCGACCA<br>TACT   | CCAAGTGGTACAACCTG<br>GTGTCT | 60.0                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold212_P4_180804  | scaffold212                             | 180804                        | T/TA                                                                        | CGAAGATTCTGAAGGCA<br>AAAG | CCGTTCTTGGTTTTTAC<br>ACA    | 60.0                             | 722                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                       |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold212_P4_296923 | scaffold212                             | 296923                        | TC/T                                                                  | GTATCAAGTGCACAGC<br>GGAA   | ACGAACGTTGAAAATC<br>CAGC | 59.9                             | 373                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold212_P4_300138 | scaffold212                             | 300138                        | TTATATATATATATATAT/TTATAT<br>ATATATATATATAT                           | CGCACCTTAAGTTTCG<br>AGGA   | TGAGAACTTTTCCGCT<br>GCT  | 60.4                             | 729                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold212_P4_463806 | scaffold212                             | 463806                        | TAA/TA                                                                | AAACGCAATCCTTGAG<br>TTCG   | TGGGTCAAAGAAAAGA<br>TCGG | 60.2                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2126_P4_19827 | scaffold2126                            | 19827                         | AATATATATATATATATATATAT<br>ATATA/AATATATATATATATATAT<br>ATATATATATATA | GGAGAAGGAGGGGAA<br>ATCAG   | TATTTTGATTTTGGCT<br>CGG  | 60.0                             | 394                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2126_P4_3526  | scaffold2126                            | 3526                          | GATATATATATA/GATATATATATA<br>TATA                                     | CCATGAAAAGAAGAAG<br>GGCA   | GCCTTTTACTGCACTTT<br>GGC | 60.2                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2127_P4_32525 | scaffold2127                            | 32525                         | TGATTGGTTTGTGTTGAGATTGGTTT<br>GTTTG/TGATTGGTTTGTGTTG                  | TTTGCAAGAATTTGCC<br>TCA    | TTACGCTACACCGTCA<br>CCAG | 59.4                             | 645                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2131_P4_815   | scaffold2131                            | 815                           | TCTATTGAAATAC/TCTATTGAAATA<br>CTATTGAAATAC                            | TGGTCGCAACAACACTAG<br>CAAC | CTGCAATCGCAAAGT<br>GAAA  | 59.9                             | 975                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2134_P4_5442  | scaffold2134                            | 5442                          | TTA/T                                                                 | GAAAAAGGAACGAAGG<br>GAGG   | AACGGAACGAGCGAGT<br>CTTA | 60.0                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2141_P4_17958 | scaffold2141                            | 17958                         | ATGTGT/ATGT                                                           | TCGATTGGCACGTTGA<br>TTTA   | TCGTTGGTTTTTGGATC<br>TGA | 60.1                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2147_P4_24244 | scaffold2147                            | 24244                         | GT/GTT                                                                | TGGTGGCACAAGATAG<br>GTCA   | CATTTTCGTCCTCCATA<br>GGC | 60.1                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                          | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                        |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2147_P4_5614   | scaffold2147                            | 5614                          | ATTTTTTT/ATTTTTT                                                                                       | TCGATTGGCCCTTAAG<br>TCAG | ACCTGAGTATCTCCA<br>TGCG     | 60.2                             | 562                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2152_P4_108576 | scaffold2152                            | 108576                        | CT/CTATATTTTCATATCTT                                                                                   | TTTCAGCTTCATCGCAT<br>TCA | GAGATTGCCAAGAACA<br>AGGC    | 60.5                             | 448                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2152_P4_132652 | scaffold2152                            | 132652                        | CTATTATTATTATTATTATTATTA<br>TTATTATTATTATTAT/CTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTAT | TCAATGTTGAGTGAGC<br>CGAG | TTTCGAAAAACAACACTG<br>AAAAA | 60.0                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2152_P4_340315 | scaffold2152                            | 340315                        | TAATCA/TAATCAAATCA                                                                                     | CTTGCCCCCTAATCATT<br>TCA | AATGAATTCGGCGCTA<br>GAGA    | 59.9                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2152_P4_34103  | scaffold2152                            | 34103                         | CTTTTT/CTTTT                                                                                           | GGGGTGCTCAACTTGT<br>TTGT | TGATCAAATCCCCCAC<br>ACT     | 60.0                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2152_P4_380109 | scaffold2152                            | 380109                        | TTATATA/TTATATATATATA                                                                                  | ACCCAATTACTGGAGA<br>TGCG | CCTTTCCCTCAAACAA<br>ACA     | 60.0                             | 285                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2152_P4_76335  | scaffold2152                            | 76335                         | ATTATTGTTATT/ATTATT                                                                                    | TTTATGGGAACACAAG<br>CAAG | GAAGGAAAGGGTCAAG<br>GCTC    | 59.7                             | 258                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2152_P4_76522  | scaffold2152                            | 76522                         | AATTATTATTATTATTATTATTAT<br>TAT/AATTATTATTATTATTATTA<br>TTATTATTATTAT                                  | GAGCCTTGACCCCTTC<br>CTTC | TGGGGGTATAAACCAT<br>CAAAA   | 60.2                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2152_P4_76564  | scaffold2152                            | 76564                         | AATTATTATTATTATTA/AATTATTAT<br>TATTATTATTA                                                             | GAGCCTTGACCCCTTC<br>CTTC | TGTCACCGCTTGCTTA<br>AGAG    | 60.2                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2153_P4_19763  | scaffold2153                            | 19763                         | CTATTTATTTATTTATTT/CTATTTAT<br>TTATTTATTTATTT                                                          | TGGAAAACACAAGAAA<br>GGGG | TGGGGATACGTAGGAG<br>CAAG    | 59.9                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                       | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                     |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2153_P4_34924  | scaffold2153                            | 34924                         | TCC/TC                                                                              | ATCTTCACGCACGTCA<br>ACTG   | CGTGCCTCAAAATTCAA<br>GGA | 59.9                             | 957                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2153_P4_6068   | scaffold2153                            | 6068                          | TAAAAAAAAA/TAAAAAAAAA                                                               | CCGCTGTCAATTCTCC<br>ATT    | TAACATGCGCTATTTGC<br>AGG | 60.1                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2158_P4_155467 | scaffold2158                            | 155467                        | GAAAAAAAA/GAAAAAAAA                                                                 | CGGCAATTCGAAGAA<br>GAAG    | TCCTCCCTCCTTAGG<br>AAAA  | 60.0                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2158_P4_64854  | scaffold2158                            | 64854                         | ATTTT/ATTTT                                                                         | CGTGGTAATCGCGTAG<br>GAAT   | CTCTCATCTGAGGGCA<br>AAGC | 60.0                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2158_P4_70847  | scaffold2158                            | 70847                         | TAAT/TAATACAATAAAAAAAT                                                              | TCTTTGTAAACACCCC<br>GACC   | ATAATTCGACCTCTCCT<br>GCG | 59.8                             | 394                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2158_P4_71695  | scaffold2158                            | 71695                         | A/AATACCATTGT                                                                       | TCGCGTAAGCAGACTC<br>GTAA   | GCTACCTCACGACCTT<br>CTCG | 59.8                             | 212                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2158_P4_81348  | scaffold2158                            | 81348                         | AATATATATATATATATATATATAT<br>ATTTATATATATAT/AATATATATATA<br>TATATATATATTTATATATATAT | GGATTTTGGCTAGGAG<br>GCTT   | AAATGGAGGAGAAGGA<br>GGGA | 59.7                             | 438                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2161_P4_108150 | scaffold2161                            | 108150                        | AT/ATATATATGT                                                                       | TTTTGGGATTCATGAC<br>AACAAG | GCATGGGACCACCATA<br>ACTC | 59.8                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2161_P4_111313 | scaffold2161                            | 111313                        | ATT/ATTT                                                                            | AGAAATTGTTGATGGC<br>GTCC   | GGTTGCATCAGGGTCA<br>ATCT | 59.9                             | 240                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2161_P4_157590 | scaffold2161                            | 157590                        | GCTAATCGATTGC/GCTAATCGATT<br>GCCTAATCGATTGC                                         | CAATCGATTCCCTCAG<br>CACT   | ACTTGGCACAAGATCC<br>ATCC | 60.2                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                   |                          |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2163_P4_71476  | scaffold2163                            | 71476                         | AC/A                                                              | AGGGAGGACGAAATG<br>ACCT  | TTGCGTTTGTGTCATTG<br>GAT   | 59.9                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2164_P4_44615  | scaffold2164                            | 44615                         | CAAAAAAAAAAAAA/CAAAAAAAAAAA<br>AA                                 | TGGACATAGCCTTCAT<br>TGGG | ACACTCGACTCGCTCG<br>ATCT   | 60.9                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2166_P4_115052 | scaffold2166                            | 115052                        | GAAAAAAAAA/GAAAAAAAAA                                             | AAGGAAGCGTTGCAAG<br>GTAA | TCTATCCAAAAAGAATG<br>CAACA | 59.9                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2166_P4_183523 | scaffold2166                            | 183523                        | AAGTCTCTTTAATTGA/AA                                               | CAGAGGAAATCCAGGG<br>ACAA | GTTGTGGGATGAACTG<br>ACCC   | 60.0                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2166_P4_202348 | scaffold2166                            | 202348                        | TAAAAAAAAA/TAAAAAAAAA                                             | GTGTCGCGACTGATT<br>GCTA  | TCCTTTGTGTAACCTCCT<br>TGCC | 60.0                             | 769                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2166_P4_41038  | scaffold2166                            | 41038                         | AG/AGG                                                            | GCTCGAAACTGGTGGC<br>TACT | TCCACAACACCTACG<br>TCCA    | 59.5                             | 245                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2166_P4_76274  | scaffold2166                            | 76274                         | AATATATATATATATATATATATAT<br>AT/AATATATATATATATATATATA<br>TATATAT | TGCTCATTTGTTTTAT<br>GCCA | TCATAATGCAGCAGAA<br>ACGG   | 59.2                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2166_P4_85838  | scaffold2166                            | 85838                         | AATATATATATATATATATAT/AA<br>TATATATATATATATATATATATAT             | TTTCAAGGATTCACTG<br>CCC  | GCACCATAATGCCCT<br>GTAT    | 60.1                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2173_P4_19619  | scaffold2173                            | 19619                         | TAAAAA/TAAAAA                                                     | GGATGACACAAACGCA<br>CCTA | ATTTTGTCTCCTTG<br>GCT      | 59.6                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2173_P4_19824  | scaffold2173                            | 19824                         | A/AG                                                              | CCAAGGGAGGACAAA<br>ATGA  | TTTCGTCCTTCACAGG<br>CTT    | 59.9                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                               |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2173_P4_56248 | scaffold2173                            | 56248                         | ATT/AT                                                        | CCTTGGGAAGACGAAA<br>ATGA | CCATCCAATACGTGTG<br>CTTG      | 60.0                             | 363                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2173_P4_56515 | scaffold2173                            | 56515                         | GACACCAACACACCAA/GACACCAA                                     | CCTTGGGAAGACGAAA<br>ATGA | TCCAATCTGGTCCATC<br>CAAT      | 60.0                             | 673                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2179_P4_20727 | scaffold2179                            | 20727                         | CTTTT/CTTTT                                                   | GTGAGGCCATCCTTGA<br>CATT | TGCTACCAGCCCAGTT<br>CTCT      | 59.9                             | 673                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2179_P4_20793 | scaffold2179                            | 20793                         | TCCCC/TCCCC                                                   | ATCAGCGAGGATGCAG<br>AACT | CATCGCTCAGTTTGA<br>CTCA       | 60.0                             | 789                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2179_P4_34814 | scaffold2179                            | 34814                         | AATATATATATATATATATATATA/<br>AATATATATATATATATATATATAT<br>A   | GCGGTTAAGGATGGCA<br>ATAA | AAAGTGGATGGCACA<br>CACA       | 59.9                             | 565                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2179_P4_35934 | scaffold2179                            | 35934                         | TG/TGCG                                                       | GAATTTGAACCTCCAA<br>GCCA | ATAGCGGAGAAGCCCA<br>TACA      | 60.1                             | 404                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2179_P4_35973 | scaffold2179                            | 35973                         | TC/TCC                                                        | GAATTTGAACCTCCAA<br>GCCA | ATAGCGGAGAAGCCCA<br>TACA      | 60.1                             | 404                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2179_P4_36066 | scaffold2179                            | 36066                         | ATAG/A                                                        | GAATTTGAACCTCCAA<br>GCCA | TGCATTCCACATACAAG<br>GGA      | 60.1                             | 582                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2183_P4_16999 | scaffold2183                            | 16999                         | AATATATATA/AATATATATATA                                       | TTGGCAAATTGATTCA<br>TCT  | AACACACGCACCAACA<br>AAGA      | 59.1                             | 437                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2183_P4_19955 | scaffold2183                            | 19955                         | TATTAATTAATT/TATTAATT                                         | TAGGGCGATTTTCGTA<br>CCAC | TTTTCGCATATTTATTT<br>GACAACTC | 60.0                             | 468                                           | INTERGENIC                                           | --                                  | --                    | --  |



| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)      | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                    |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2183_P4_65749  | scaffold2183                            | 65749                         | A/AG                                                               | CCCATCGATGATAATG<br>GACC  | CTAGTCATCGTCTGGT<br>GCGA | 60.0                             | 380                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2183_P4_67523  | scaffold2183                            | 67523                         | GT/G                                                               | AGTCGCTCGAAAAGTC<br>CAAA  | TCCTGGTCCTCGATTT<br>CATC | 60.0                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2183_P4_67873  | scaffold2183                            | 67873                         | ATTTTT/ATTTT                                                       | GATGAAATCGAGGACC<br>AGGA  | TTTCATCTGGACTTTTC<br>GGG | 60.0                             | 333                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2183_P4_70044  | scaffold2183                            | 70044                         | AGGGG/AGGGGG                                                       | AGGGTCTGCGCTAGAT<br>TTCA  | AGGGTTTCTCGGTCCT<br>TGAT | 60.0                             | 127                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2183_P4_71587  | scaffold2183                            | 71587                         | GT/G                                                               | AGTTTCGGGTTCACAC<br>TCAG  | GGTCATCGATTTCTCT<br>GGA  | 60.0                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2192_P4_106941 | scaffold2192                            | 106941                        | CTATTATTATTATTATTATTATTA<br>TT/CTATTATTATTATTATTATTATA<br>TTATTATT | TGGTCTCCCTCTCCTT<br>CTCA  | TTCCATTGCGCAAAATC<br>ATA | 59.9                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2192_P4_128967 | scaffold2192                            | 128967                        | CTTTTTTTTTTTTT/CTTTTTTTTTTT<br>TT                                  | TTGATTTCTCAATCGCA<br>CCA  | TCGATTATGCGTAGGG<br>AAGG | 60.2                             | 264                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2192_P4_209113 | scaffold2192                            | 209113                        | TTATATATATATATATATATATA/TTA<br>TATATATATATATATATATATATA            | GAAAGAAAGCGTTTCGT<br>GAGG | CGGGTTGCTGAAAAAT<br>TCAT | 60.0                             | 240                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2192_P4_2178   | scaffold2192                            | 2178                          | GA/GAGAA                                                           | CATGGAGTTGAAATGG<br>CAAA  | CGTTGTTAAAAATCGG<br>GGTG | 59.5                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2192_P4_8042   | scaffold2192                            | 8042                          | CATATATATATATATATATATAT/C<br>ATATATATATATATATATATATATA<br>T        | AGGAAGAGTGGAGTTG<br>CGAA  | ATGTTTTGGATTTTGGC<br>TCG | 60.0                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2193_P4_162789 | scaffold2193                            | 162789                        | ATTT/ATT                                                      | GCATTCTTGTCGGGCA<br>TAAT | TGTTTTGGAGGTGGTC<br>AACA | 59.9                             | 620                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2193_P4_31580  | scaffold2193                            | 31580                         | AA/AAACACA                                                    | GCCAATAGAGGATGGA<br>AGCA | TATGCCAAAGCCATGT<br>TTCA | 60.2                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold22_P4_24507    | scaffold22                              | 24507                         | AAT/A                                                         | ATGAGGCTCAAAATGC<br>CATC | GCCAACTTTTCCAATG<br>CCTA | 60.0                             | 727                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold22_P4_34524    | scaffold22                              | 34524                         | GTTTT/GTTTTTTT                                                | GCAGCATCGCAGATCA<br>TAGA | CGAATTGGGTTTTCGT<br>TCTC | 60.1                             | 181                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2205_P4_49159  | scaffold2205                            | 49159                         | ATT/ATTT                                                      | TTTTTAACCAATCTTCG<br>GCG | AGGGAGGACGAAAATG<br>ACCT | 60.1                             | 272                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2208_P4_20005  | scaffold2208                            | 20005                         | CA/CATA                                                       | CAACACACCTGTTGG<br>ATGC  | CCCTAGGCTTATTCTTG<br>CCC | 60.0                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2208_P4_5970   | scaffold2208                            | 5970                          | AC/A                                                          | CGGAGGACGAACACAA<br>AAAT | TCCAATCTTGTCATCC<br>AAC  | 60.0                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold221_P4_61534   | scaffold221                             | 61534                         | CT/CTAAGTGTTATGT                                              | CCCGTGATAGGCAGTA<br>CGTT | CGATTTCCCTGCATGTT<br>TTT | 60.0                             | 352                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold221_P4_94058   | scaffold221                             | 94058                         | C/CA                                                          | GAAGGAGCAGTTGGAG<br>AACG | AACAATGGCTCGAAC<br>AAAC  | 60.0                             | 724                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2210_P4_15184  | scaffold2210                            | 15184                         | CG/CGGATTTG                                                   | TCCAGATGAAATCGAG<br>GACC | AAATCCGACACGTAAC<br>TCGG | 60.0                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2210_P4_61082 | scaffold2210                            | 61082                         | AGTGTATTCTGAATACA/AGTGTATTC<br>GAATACACGTGTATTCTGAATACA       | TTTAGGGTTTAAGATTC<br>GGGG | TCTTAAGATGCGTGCC<br>CAAT  | 59.3                             | 735                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2214_P4_16473 | scaffold2214                            | 16473                         | G/GA                                                          | TTGGATGCACAAGATT<br>GGTT  | TTTCGTTCTCCCTAGG<br>CTCA  | 59.0                             | 561                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2222_P4_1209  | scaffold2222                            | 1209                          | G/GGATGCACAA                                                  | TGGATGCACAAGTTG<br>GTTA   | AGGTCATTTTCGTCCTC<br>CCT  | 60.0                             | 559                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2227_P4_40022 | scaffold2227                            | 40022                         | AATATATATATATATATATAT/AAT<br>ATATATATATATATATATATAT           | CCATTTGGTCGTGAGA<br>ATGA  | CACCACCTGGAGAATC<br>CACT  | 59.5                             | 311                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2227_P4_7924  | scaffold2227                            | 7924                          | ATTTTTTTTT/ATTTTTTTTT                                         | ATCAATGGTCGCCTTC<br>TTCA  | GGTCCTCGATTTCATCT<br>GGA  | 60.6                             | 832                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2227_P4_7998  | scaffold2227                            | 7998                          | TAAAAAAAAA/TAAAAAAAAA                                         | TTTGACCAAACTCATT<br>TGCAC | GGTCCTCGATTTCATCT<br>GGA  | 60.0                             | 418                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold223_P4_133920 | scaffold223                             | 133920                        | TAAAAAAAAAAAAAAAAA/TAAAAAAAAA<br>AAAAAAAAA                    | TAACAATCAAGCGTCG<br>CAAA  | AGCAGGCGTTGAAAAG<br>CTAA  | 60.4                             | 500                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold223_P4_150454 | scaffold223                             | 150454                        | GTTTTTTTTT/GTTTTTTTTT                                         | TTGCTTTGGTTTGATGT<br>GGA  | AAAAATCTGGGGCGTT<br>ACATT | 60.1                             | 474                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold223_P4_67883  | scaffold223                             | 67883                         | CATATATATATATATA/CATATATA<br>TATATATATATA                     | TAGCGTGAATCACCA<br>TCCA   | TGATTTGTGTTCTTTG<br>CGA   | 60.1                             | 246                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold223_P4_95879  | scaffold223                             | 95879                         | AGCGACTACT/A                                                  | TTGGTCTCCTTGTT<br>GTGC    | TGGAGACCCCTTGATG<br>AAAC  | 59.7                             | 502                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                         | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                       |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold223_P4_9943   | scaffold223                             | 9943                          | AATATATATATATAT/AATATATAT<br>ATATAT                                                   | ACTTCCGACCCAAGGG<br>ATAC | TCCAGCCAGATTTCAA<br>CTCC | 60.2                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold224_P4_180994 | scaffold224                             | 180994                        | C/CTCTT                                                                               | GCTACCGTGCGTTGGA<br>TTAT | GTCACGGGCGTTGAAT<br>AAGT | 60.0                             | 545                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold224_P4_202990 | scaffold224                             | 202990                        | TTTATTATTATTATTATTATTATT<br>ATTATTATTAT/TTTATTATTATTATT<br>ATTATTATTATTATTATTATTATTAT | CCCCCTCACGTACTAT<br>TGGA | TTTCCTTCCAACATCAT<br>GCT | 59.8                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2249_P4_1002  | scaffold2249                            | 1002                          | CT/CTTTT                                                                              | TATTCCACCCACGAT<br>CATT  | CAACCAAGCCATTTTCC<br>ATT | 60.0                             | 871                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2269_P4_12097 | scaffold2269                            | 12097                         | GTTT/GTT                                                                              | CCCTTCTGACCAAGGG<br>TACA | ATGGCCACGAATCTGA<br>AGAG | 60.0                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2269_P4_68414 | scaffold2269                            | 68414                         | A/ATTATATAT                                                                           | CGTGTGAGAAAACCTC<br>GACA | GTTCGAAATGCCGATT<br>TCAC | 59.9                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold227_P4_195682 | scaffold227                             | 195682                        | CAA/CAAA                                                                              | AGACACAAACCCCGCA<br>ATAG | GGATGCCACCATTCAA<br>GTTT | 60.0                             | 338                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold227_P4_195989 | scaffold227                             | 195989                        | ATTTTTTTTTTTTT/ATTTTTTTTTT                                                            | AAACTTGAATGGTGGC<br>ATCC | AGTAATGAATGGGCGA<br>GTGG | 59.8                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold227_P4_196111 | scaffold227                             | 196111                        | TAAAAAAA/TAAAAAAA                                                                     | AAACTTGAATGGTGGC<br>ATCC | AGTAATGAATGGGCGA<br>GTGG | 59.8                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold227_P4_196280 | scaffold227                             | 196280                        | TAAAA/TAAAA                                                                           | AAACTTGAATGGTGGC<br>ATCC | AGTAATGAATGGGCGA<br>GTGG | 59.8                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold227_P4_197474 | scaffold227                             | 197474                        | TAAAAAAAA/TAAAAAAAAA                                          | CCTAATGGCGGAAATT<br>GTGT | TAATCAGACCGTGTGG<br>GTGA   | 59.8                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold227_P4_238383 | scaffold227                             | 238383                        | TG/T                                                          | GACTTTTCTCGCGATT<br>TCG  | CCCCTCAGATGAGAGT<br>CAGG   | 60.0                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold227_P4_34781  | scaffold227                             | 34781                         | TAAAAAAAAA/TAAAAAAAAA                                         | TGAATAGCGAGTGTGT<br>TGGG | TGCACATAGTAAACTT<br>GGCG   | 59.7                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold227_P4_389083 | scaffold227                             | 389083                        | TAGA/TA                                                       | TGTGATCAATTGGAG<br>CAGC  | GGCGTGTATGTTTTG<br>GACC    | 59.8                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold227_P4_59565  | scaffold227                             | 59565                         | TAAA/TAAAA                                                    | ACATCATCGGTGTCAA<br>ACGA | GGGAGAATTGTAAAC<br>CCCA    | 60.0                             | 708                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2275_P4_15734 | scaffold2275                            | 15734                         | AATATATATATATATATATATAT/A<br>ATATATATATATATATATATAT           | AGTGTATAACCCGTGC<br>GTCG | TTGGAGTCATGCTTTTC<br>ATCA  | 61.0                             | 229                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold228_P4_136549 | scaffold228                             | 136549                        | A/AC                                                          | GATGAAATCGAGGACA<br>GGGA | TGCGTCTTTCTCAAGT<br>GCAT   | 60.0                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold228_P4_183161 | scaffold228                             | 183161                        | ATTT/ATT                                                      | CACGCCTAAAAGAGTC<br>GTGG | AAGTTTGACTGCAAAAC<br>GAAGA | 60.8                             | 783                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2289_P4_12871 | scaffold2289                            | 12871                         | ATTT/ATTTT                                                    | TGTGTTTGTGCCATTG<br>GATT | AGGGAGGATGAAAACG<br>ACCT   | 59.8                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold229_P4_13268  | scaffold229                             | 13268                         | TAA/TA                                                        | GCATAGGGTGGACCAA<br>AATG | AGGCAGTCTTAGGCAT<br>CCAA   | 60.2                             | 774                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold229_P4_13642  | scaffold229                             | 13642                         | A/AG                                                          | TTGGATGCCTAAGACT<br>GCCT | AGGTCATTTTCGTCCTC<br>CCT        | 59.8                             | 168                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2301_P4_1549  | scaffold2301                            | 1549                          | GA/GAGAACCCAAA                                                | TGCAACGTCGTTCTCT<br>CTTG | CAGACTTTCAGCGTC<br>ACAA         | 60.2                             | 441                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2301_P4_22791 | scaffold2301                            | 22791                         | CTT/CT                                                        | CAAACACACCTGTTGG<br>ATGC | CCTCGCTTGGCTTATT<br>CTTG        | 60.0                             | 466                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2301_P4_54382 | scaffold2301                            | 54382                         | ATG/ATGTG                                                     | CCAAAGGAGGACGAAA<br>ATGA | GCGTGTTTGTGACATT<br>GGAG        | 60.0                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2301_P4_54476 | scaffold2301                            | 54476                         | C/CA                                                          | TGGATGCACATGATTG<br>GTTT | AGGTCATTTTCGTCCTC<br>CCT        | 59.8                             | 316                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2301_P4_6372  | scaffold2301                            | 6372                          | AAAATG/AAAATGACCTAAATG                                        | AGGGAGGACGAAAATG<br>ACCT | AACCAATCATGTGCATC<br>CAA        | 59.9                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2301_P4_64464 | scaffold2301                            | 64464                         | AAAAAAA/AAAAAAAAAAAA                                          | CCGTGCATGACGTTTA<br>TCAT | AAGGCATCGTCACATC<br>TTCC        | 59.4                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2301_P4_64669 | scaffold2301                            | 64669                         | TATTAT/TATTATTAT                                              | CCGTGCATGACGTTTA<br>TCAT | AAGGCATCGTCACATC<br>TTCC        | 59.4                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2301_P4_65310 | scaffold2301                            | 65310                         | A/AG                                                          | GCTTAATTTCAAGAA<br>GGCG  | TGAAATTCAAATAAAGT<br>CAACATATTC | 59.1                             | 224                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold231_P4_18150  | scaffold231                             | 18150                         | AC/A                                                          | GTTTCGTACCCCTCGA<br>CAAA | TCCAGATGAAATCGAG<br>GACC        | 60.0                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                                |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2325_P4_58923  | scaffold2325                            | 58923                         | CA/C                                                          | TTTCCTTCTCCCTAG<br>GCTT        | TCCTGAATGGATGCAC<br>AAGA | 59.3                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2328_P4_13583  | scaffold2328                            | 13583                         | GTTTT/GTTTTT                                                  | TGTGTTTGTGCCATTG<br>GAGT       | AGGGAGGACGAAAATG<br>ACCT | 60.0                             | 245                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2343_P4_16033  | scaffold2343                            | 16033                         | ATTAGGGTTTAGGGTTTA/ATTAGG<br>GTTTAGGGTTTAGGGTTTA              | AGGCGAGTTTTTGTCA<br>TTGG       | AGGGAGGACGAAAATG<br>ACCT | 60.1                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2345_P4_11872  | scaffold2345                            | 11872                         | TG/T                                                          | TAGTGGTACGAAAAT<br>CGCC        | TTTCATCTGGACTTTTC<br>GGG | 60.0                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2345_P4_549    | scaffold2345                            | 549                           | C/CA                                                          | CCCGAAAAGTCCAGAT<br>GAAA       | TTCGGACTAGACGAGG<br>GCTA | 60.0                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2346_P4_28393  | scaffold2346                            | 28393                         | GA/GAA                                                        | TGGGCGATTTTGTAC<br>TTCC        | CCCGAAAAGTCCAGAT<br>GAAA | 59.9                             | 395                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2348_P4_105897 | scaffold2348                            | 105897                        | T/TACAAG                                                      | GTGGTGCTTGCCAATT<br>TCTT       | CGTGCCACTTTTCTCTA<br>GGC | 60.1                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2348_P4_52479  | scaffold2348                            | 52479                         | GAAAAAAAA/GAAAAAAAA                                           | AAGCCAAGTAATACTA<br>GATCACAAAA | TAATTCTCGACCTTGT<br>GGG  | 58.2                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2348_P4_64435  | scaffold2348                            | 64435                         | CTTTTTT/CTTTTTT                                               | TAAAGAAATTCGTCCC<br>CGA        | TGGCACCGTATTAGGC<br>TCTT | 59.5                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold235_P4_139406  | scaffold235                             | 139406                        | TAAAAAAAAA/TAAAAAAAAA                                         | TGCATCGAGGCGTACA<br>ATAG       | AATTCACCATCCCCAAT<br>CAA | 59.9                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold235_P4_146229  | scaffold235                             | 146229                        | CTTTT/CTTT                                                    | CCTCAGATGAGAGCCA<br>GGAC  | TAACCAAAGGTTCCAC<br>AGCC       | 59.9                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold235_P4_57295   | scaffold235                             | 57295                         | TAAAAA/TAAAAA                                                 | GCCAAAACGACCACAA<br>AGTT  | GGGAGTAGAGCTGATC<br>AGAGGA     | 60.0                             | 779                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2356_P4_133224 | scaffold2356                            | 133224                        | T/TA                                                          | GTTGATTCGTTTGCTG<br>CTGA  | CGTCGATAATTATGAGT<br>GATTAGGTG | 60.0                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2358_P4_1353   | scaffold2358                            | 1353                          | ATTTTT/ATTTT                                                  | GATGAAATCGAGGACT<br>GGGA  | CTTTTCGGGCGATTTT<br>CATA       | 60.0                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold236_P4_25371   | scaffold236                             | 25371                         | CATATATATATAT/CATATATATATAT<br>AT                             | GAGGTTGTCCAGCTCA<br>CACA  | TTGGCACATTGATTTTG<br>ACC       | 59.9                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold236_P4_41897   | scaffold236                             | 41897                         | TTATATATATATAT/TTATATATATAT                                   | CCAGATTTTCAGCCTTT<br>CCAA | GATATGCGTCGACTGA<br>GCAA       | 60.2                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold236_P4_60071   | scaffold236                             | 60071                         | TCC/TC                                                        | GGTTCCGCGTTAGATT<br>TCAA  | GCGGAACCTGAAACAC<br>ATTT       | 60.1                             | 820                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2361_P4_45704  | scaffold2361                            | 45704                         | A/AG                                                          | AACGAAAGCGATCGAG<br>AAAA  | TTAACCAAGATGCATG<br>CGAG       | 60.0                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2371_P4_10396  | scaffold2371                            | 10396                         | GAATAATAATAATAATAAA/GAAT<br>AATAATAATAATAATAAA                | TCCTGAAACAAACGCA<br>TTCA  | GCAAGACAATGGTACG<br>TGGA       | 60.2                             | 887                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2371_P4_139701 | scaffold2371                            | 139701                        | AATATATATATATATATA/AATATA<br>TATATATATATATA                   | AGAATGAGACTCGCAC<br>GTTG  | CAACAAGAAACCTCAA<br>CCTCA      | 59.0                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2371_P4_149994 | scaffold2371                            | 149994                        | GT/GTT                                                        | CAGCTTTTGGCTGAT<br>GTGA    | TCCTCCTTCATGGACA<br>ATTA    | 60.0                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2371_P4_150056 | scaffold2371                            | 150056                        | TGGG/TGG                                                      | GCATTCGGGGGTATGT<br>TTTA   | CATCTTCCTTCCACAAT<br>TTCTTT | 59.7                             | 970                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2371_P4_274661 | scaffold2371                            | 274661                        | ATT/AT                                                        | TAGGAGGTCACATCCC<br>CAAG   | CGGTTACAAGCATCTC<br>CCAT    | 59.9                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2371_P4_287452 | scaffold2371                            | 287452                        | CTTTTTTTTT/CTTTTTTT                                           | CGACTCGTGTCTAA<br>ACTCAA   | TTTCATGCCATAAGTCA<br>TTGTG  | 59.4                             | 884                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2371_P4_73153  | scaffold2371                            | 73153                         | TAAAAAAAAA/TAAAAAAAA                                          | TGTGTCCGAGAATCTT<br>CCCT   | ATCGACGATAAGTCAT<br>CGGG    | 59.7                             | 950                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2371_P4_73366  | scaffold2371                            | 73366                         | ATTTTTATTTT/ATTTTTATTTTATTT<br>TTTATTTT                       | CAAGAAAAAGTTTGA<br>CTTCCGA | ATCCACGCCACATAAA<br>CCAT    | 59.8                             | 919                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2371_P4_73819  | scaffold2371                            | 73819                         | GTT/GT                                                        | ATGGTTTATGTGGCGT<br>GGAT   | TGAATGAAGCGAAAAT<br>GTGC    | 60.1                             | 321                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2371_P4_74028  | scaffold2371                            | 74028                         | AG/A                                                          | ATGGTTTATGTGGCGT<br>GGAT   | TGAATGAAGCGAAAAT<br>GTGC    | 60.1                             | 321                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2371_P4_74656  | scaffold2371                            | 74656                         | ATTTTTT/ATTTTT                                                | GGGTGCTTTAGATGAT<br>GTGCT  | GCCCCGGAGTCTCATA<br>AAA     | 59.2                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2371_P4_87188  | scaffold2371                            | 87188                         | TACA/TA                                                       | ATCCGAGACATTTGAC<br>ACCA   | CCAAATCATGTTGAAGA<br>GTGGA  | 58.9                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2371_P4_87272  | scaffold2371                            | 87272                         | T/TG                                                          | TGAGAAGAATGCAAAG<br>AGGAAA | ACCTAAGGGCATAGCA<br>CTGG   | 59.1                             | 794                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2373_P4_122303 | scaffold2373                            | 122303                        | CAAAAA/CAAAA                                                  | TCCGCTTCCATTGTCTT<br>ACC   | CCCCTCAGATGAGAGT<br>CAGG   | 60.1                             | 611                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2373_P4_151036 | scaffold2373                            | 151036                        | TC/T                                                          | CCCCAACTTTGTCTTT<br>GGA    | ACCGGTGAATACAGAC<br>GAGG   | 59.9                             | 720                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2373_P4_39509  | scaffold2373                            | 39509                         | GAA/GA                                                        | CGAACCGCAAATCTAC<br>CAAC   | ATGTGTTCTCCTCCACT<br>GCC   | 60.5                             | 170                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2373_P4_39709  | scaffold2373                            | 39709                         | TG/T                                                          | GGCAGTGGAGGAGAA<br>CACAT   | TCAAACAGATGCTAAAA<br>TGCAA | 60.1                             | 269                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2373_P4_4581   | scaffold2373                            | 4581                          | TGGTGAGGGTGAGGGTGAGGG/TG<br>GTGAGGGTGAGGGTGAGGGTGAG<br>GG     | AGGATGTGGGTGAGGT<br>TGAG   | TCACCAGCAGCAGAAA<br>CATC   | 60.0                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2373_P4_57552  | scaffold2373                            | 57552                         | CAAAAAAAAA/CAAAAAAAAA                                         | GTTTTGGCGTTGGTTT<br>CACT   | TTTTTATGTGCGTTTGA<br>CTGAT | 60.0                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold238_P4_8477    | scaffold238                             | 8477                          | GCC/GC                                                        | ATGACACGGAACACGA<br>AACA   | TATGAAAATCGCCGA<br>AAAG    | 60.0                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2385_P4_5093   | scaffold2385                            | 5093                          | TCC/TC                                                        | GAGTGAATTGTAACAG<br>CCCAAA | GGACTTGCGGTGAAGA<br>AGAA   | 59.1                             | 720                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2385_P4_5335   | scaffold2385                            | 5335                          | TT/TTTCAAT                                                    | GAGTGAATTGTAACAG<br>CCCAAA | TCATTCGACGCTTTCA<br>CAC    | 59.1                             | 968                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2386_P4_169680 | scaffold2386                            | 169680                        | A/AT                                                          | TAACCCACTCGGCCTT<br>ACAG | GACTGGTTTGACCCTG<br>CATT  | 60.1                             | 481                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2389_P4_13043  | scaffold2389                            | 13043                         | C/CA                                                          | GGTCCTCCCTTGGCTT<br>ATTG | GGGAGGACGAAAAGAC<br>CTAAA | 59.9                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold239_P4_109046  | scaffold239                             | 109046                        | T/TGTCTGA                                                     | TGCCTTAACGTACAAA<br>GGGG | CAATCGATTCCCTCAG<br>CACT  | 60.1                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold239_P4_109266  | scaffold239                             | 109266                        | C/C                                                           | GGTTTCAACCCCAATG<br>CTTA | TCGACTTGTCATCGC<br>TTTG   | 59.8                             | 808                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold239_P4_61563   | scaffold239                             | 61563                         | A/AT                                                          | ATCCATTGTTGTGCAT<br>CCAA | GCGATGGAGGACGAAA<br>GTTA  | 59.8                             | 466                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold239_P4_64716   | scaffold239                             | 64716                         | GTTTTTTTT/GTTTTTTTTT                                          | CGTCCTCCATCGCCTT<br>AGTA | AGGGAGGACGAAAATG<br>ACCT  | 60.2                             | 898                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2392_P4_10736  | scaffold2392                            | 10736                         | TA/TATATAAAGA                                                 | TAGGCTCCACCACTTG<br>GGTA | TTGGAAGGAGCCCTTA<br>CCTT  | 60.5                             | 745                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2392_P4_10820  | scaffold2392                            | 10820                         | TTTCTTCTTCTTCTTCT/TTTCTTCTT<br>CTTCTTCTTCT                    | GGTAGGCCTTGGGCTA<br>GTGT | TTGGAAGGAGCCCTTA<br>CCTT  | 60.5                             | 729                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2392_P4_18113  | scaffold2392                            | 18113                         | A/ATAATAAAATAATAT                                             | TTGCTCCACGAACATC<br>TCTG | CTGAGTTGCATTGATCT<br>CGC  | 60.0                             | 870                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2392_P4_259018 | scaffold2392                            | 259018                        | TTCTCTCTCTCTCTCTCT/TTCTCTC<br>TCTCTCTCT                       | ATCCTCCACCACCATA<br>ACCA | GCAGATCGCACCCAAA<br>TAAT  | 60.1                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2392_P4_323618 | scaffold2392                            | 323618                        | GACTA/GACTAACTA                                               | AATCCTTGCTTCCGAG<br>TTCA  | TGCACGTGGTTATGAT<br>TGCT | 59.8                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2392_P4_326211 | scaffold2392                            | 326211                        | AATATTTT/A                                                    | TCATTCCCCACCTACA<br>CAAG  | GTGCATGTGGCTGAAA<br>AACA | 58.4                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2392_P4_355152 | scaffold2392                            | 355152                        | ATTT/ATTTT                                                    | TGCACCCAATCTGCAA<br>ATAA  | TGGGCTAGTTAGCTTT<br>TGCC | 60.1                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2392_P4_355244 | scaffold2392                            | 355244                        | AAATTATATT/AAATTATATTTAATT<br>ATATT                           | TGCACCCAATCTGCAA<br>ATAA  | TGGGCTAGTTAGCTTT<br>TGCC | 60.1                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2392_P4_83496  | scaffold2392                            | 83496                         | GATTT/GATTTATCCGTACATATTT                                     | GGCCGAATCCAACAAG<br>ACT   | AGGGGAGGGTTTGT<br>TTGT   | 60.1                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold240_P4_126879  | scaffold240                             | 126879                        | GACA/GA                                                       | TTTTGCTTGTGGATGA<br>TGGA  | CCCACAAGTCATTGCA<br>ACCT | 60.0                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold240_P4_150038  | scaffold240                             | 150038                        | GTATATATATATATATATATAT/GT<br>ATATATATATATATATATATAT           | GGAGGCTTTGAAATTA<br>GGGC  | CTCCAGCGCACAACT<br>CTAA  | 60.0                             | 783                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold240_P4_151385  | scaffold240                             | 151385                        | TAAAAAA/TAAAAAA                                               | AGATGCATGTGATGAA<br>ACCAA | TACTCCCATTTCTCCC<br>CTT  | 59.0                             | 727                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold240_P4_156860  | scaffold240                             | 156860                        | AAACAACA/AAACA                                                | GACAATCGCAGGAAGT<br>GGTT  | GCATTGCACCAAAACA<br>CAAC | 60.1                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold240_P4_38776   | scaffold240                             | 38776                         | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATAT               | TATTTTGATTTTGGCT<br>CGG   | TAGGAGAAACGGAGGG<br>GTTT | 59.9                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                       |                           |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold240_P4_73279  | scaffold240                             | 73279                         | AT/A                                                                  | CAAGGTGTCGATGTTG<br>GTTG  | CTGGTGGCTACTTTCT<br>TGGG      | 60.0                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2408_P4_3902  | scaffold2408                            | 3902                          | TAAAA/TAAA                                                            | GACGCATTGTCCTGCA<br>AAATA | CAAAGAATTCACCTTGAT<br>ACATGGC | 59.8                             | 725                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2408_P4_509   | scaffold2408                            | 509                           | AATATATATATATATATATA/AATA<br>TATATATATATATATA                         | TCGAAGTGAAACTCGT<br>CCCT  | ACATCACCACACGGT<br>CTGA       | 59.8                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2410_P4_15231 | scaffold2410                            | 15231                         | TTATATATATATATAT/TTATATAT<br>ATATATAT                                 | CTTGGGAAGTGGAGAG<br>CAAG  | AAATCGGAGAAGGAGG<br>GAAA      | 60.0                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2415_P4_27032 | scaffold2415                            | 27032                         | AATATATATATATATAT/AATATAT<br>ATATATATATATAT                           | CAAAATTCGGGAAGC<br>TCAC   | TTTTTGGCCTACAAAT<br>CGG       | 59.7                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2415_P4_6685  | scaffold2415                            | 6685                          | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATA<br>TATATATATAT | ATCGACTCCCGAACTC<br>AAAA  | TGGTTTTACGCGTTTG<br>ACA       | 59.7                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_230913 | scaffold242                             | 230913                        | CTTTTTTTTT/CTTTTTTTTTT                                                | AGCTTCCATGTTTCCC<br>TCCT  | TCTAAGGATCCCCAGT<br>GCAA      | 60.1                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_258886 | scaffold242                             | 258886                        | CCTTTTCTTTCTTTTCT/CCTTTTCT                                            | GTTGGTCCCTAGCAC<br>CGTA   | AGGTGAAAGTGGATTG<br>GTCG      | 60.0                             | 681                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_268692 | scaffold242                             | 268692                        | CTTTTTTTTT/CTTTTTTTTTT                                                | CTTGGGCTCATGTTGT<br>GCTA  | ACGCAGAAACCAAC<br>AAAC        | 59.9                             | 720                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_284468 | scaffold242                             | 284468                        | ATATATATTTATATTTAT/ATATAT<br>ATTTATATATTTATATATTTATATATT<br>TAT       | TTTGGGTTCCCAAGTG<br>AAAG  | CACCAATGCGTCTAAT<br>CCCT      | 59.9                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold242_P4_301834 | scaffold242                             | 301834                        | ATTTTTTTTT/ATTTTTTTT                                          | GATTCCTGACACAA<br>AATCG  | TCATGTTGCTCCTCTC<br>GTG  | 59.5                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_307052 | scaffold242                             | 307052                        | CTTTTTTTTT/CTTTTTTTTTTTT                                      | TTGCGTACGAGCATAT<br>CCAT | ATGGGTGCTTTCTATG<br>GTCG | 59.2                             | 177                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_316132 | scaffold242                             | 316132                        | TAAAAAAAAA/TAAAAAAAAA                                         | CAGATGGCTGCTGTTC<br>TCAA | GAAGGACATCGTGAA<br>GGAA  | 60.1                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_316249 | scaffold242                             | 316249                        | TAAAAAAAAA/TAAAAAAAAA                                         | CAGATGGCTGCTGTTC<br>TCAA | GAAGGACATCGTGAA<br>GGAA  | 60.1                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_316920 | scaffold242                             | 316920                        | ATTTTTTTTT/ATTTTTTTTTT                                        | TTCTTCCACGATGTC<br>CTTC  | TTATTCAGCATTCCCGA<br>TCC | 60.1                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_338467 | scaffold242                             | 338467                        | ATTTTTTTTT/ATTTTTTTTTT                                        | CCCAATCCTCCTTTTGT<br>CCT | TCCAACCAAAGCAAG<br>ATCC  | 60.3                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_357065 | scaffold242                             | 357065                        | AATAT/AATATAT                                                 | TCATTTTCCACCAATCC<br>ACA | GAGCAAAAAGATTTCG<br>GTGC | 59.8                             | 295                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_359392 | scaffold242                             | 359392                        | TAAAAAAAAA/TAAAAAAAAA                                         | CTGGTCAAGTAAGGGG<br>CAAA | CTTCGGCTCTTCAAAT<br>TGC  | 60.1                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_360673 | scaffold242                             | 360673                        | CTTTTTTTTTTTTT/CTTTTTTTTTT<br>T                               | CCAGAAAATCATCGGA<br>AAGC | CCCAAGGAAATGAAGC<br>AAAC | 59.6                             | 761                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_368643 | scaffold242                             | 368643                        | CAAAAAAAAA/CAAAAAAAAA                                         | AATGCATTAATTGAGG<br>GGGA | AGGCAAAAGCTTCGTT<br>GAAA | 59.2                             | 384                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold242_P4_393693 | scaffold242                             | 393693                        | CAAAA/CAAAA                                                   | TTAGAGGGGCTAGGAG<br>GGAA | TCGCCTTTGCAAACAC<br>ATAC  | 60.2                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_393992 | scaffold242                             | 393992                        | TTATATATATATATATATATA/TTA<br>TATATATATATATA                   | TATGTGTTTGCAAAGG<br>CGAC | CCGTCTCTCGCAAATC<br>TCTC  | 59.7                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_405656 | scaffold242                             | 405656                        | AAAAAATAAAGAATAAAAAATAAA/<br>AAAAAATAAAA                      | CATCACGATCTTTGTC<br>CACG | ACAAAAACCACATTGCG<br>ACA  | 60.1                             | 691                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_416343 | scaffold242                             | 416343                        | GAAAA/GAAAA                                                   | CCAGGAGATGAGAGGT<br>CCAA | TGGCTTTCAACCATTTT<br>TCC  | 60.2                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_422391 | scaffold242                             | 422391                        | ATTTTTT/ATTTTTTTT                                             | CAGGGGCCAAATGTTT<br>CTTA | AGCTCTGTTCAATGTC<br>GTTCA | 59.9                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_422853 | scaffold242                             | 422853                        | ATTTTTTTTT/ATTTTTTTTTTT                                       | TGAACGACATTGAACA<br>GAGC | GCACACTTCACCAAAC<br>GTCA  | 57.4                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_423606 | scaffold242                             | 423606                        | CAAAA/CAAAA                                                   | TTTTCTCGCAGTTAGG<br>GGTG | TGAACTAAAATCGCTG<br>CATGA | 60.2                             | 223                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_451161 | scaffold242                             | 451161                        | ATTTTT/ATTTTT                                                 | GGCGCATGTCATAAGA<br>ACCT | TCGATCAATTCGTTCC<br>TCC   | 60.1                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_454823 | scaffold242                             | 454823                        | GT/GTTTATTATATATAT                                            | TTGTACAGGTGTCTGC<br>CGAG | GTGGAGGCAAATCGAA<br>CCTA  | 59.9                             | 457                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_455243 | scaffold242                             | 455243                        | CTTTT/CTTT                                                    | TAGGTTTCGATTTCCT<br>CCAC | TGTGAGGGGAATTTCC<br>AAAA  | 60.1                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold242_P4_462385 | scaffold242                             | 462385                        | ATTTTTTTT/ATTTTTTTTTT                                         | GATCCAACTCGGGTCA<br>AAGA  | CATTCAAAGGGTTTGT<br>CCG       | 60.1                             | 209                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_464262 | scaffold242                             | 464262                        | CA/CAA                                                        | CGGAAGTTTGAAGTGT<br>GCAA  | GCATGCTTCATTGCA<br>GAAA       | 59.9                             | 214                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_470407 | scaffold242                             | 470407                        | AATATATATAT/AATATATATATAT                                     | GGAAAAGAATGGCCAA<br>GTGA  | GTTCGAAATTAGGATC<br>AACAGTG   | 60.1                             | 348                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_470704 | scaffold242                             | 470704                        | C/CT                                                          | GGAAAAGAATGGCCAA<br>GTGA  | CTTGTCGGATATTTT<br>GGCT       | 60.1                             | 846                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_490912 | scaffold242                             | 490912                        | TAAAAAAA/TAAAAAAA                                             | AGCGGTGCTCCAATAG<br>TCAC  | AGATTTCATCATACCC<br>CCA       | 60.3                             | 702                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_502881 | scaffold242                             | 502881                        | GAAAAAAA/GAAAAAAA                                             | AATTTCCGGTTCATTG<br>CAG   | TCTGTTTGGCAAAGG<br>CTCT       | 59.9                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_536515 | scaffold242                             | 536515                        | ATTTTTTTTT/ATTTTTTTTTT                                        | TTACGTGTTGAGAGTT<br>GCCG  | TCTCGCGATTGCCTTA<br>CTT       | 59.9                             | 302                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_552302 | scaffold242                             | 552302                        | CAAAGAAATAAGAAA/CAAAGAAA                                      | CGGATATGAATCAAAC<br>AAGCC | TGGAATAAGAAATGATG<br>GCAGC    | 59.4                             | 234                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_577314 | scaffold242                             | 577314                        | GTTTTTTTTT/GTTTTTTTTT                                         | GCAAGTTAAATGCGAT<br>TGTGT | GAGTTTTTGAGATGTG<br>AATCAAACA | 57.8                             | 744                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_578423 | scaffold242                             | 578423                        | AGTG/AG                                                       | CCAAGCTTGGCCATGA<br>GTTT  | AAAATGCACTAGTTTCA<br>ACCG     | 60.2                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')         | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|---------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                   |                                 |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold242_P4_587277 | scaffold242                             | 587277                        | GCTATAACTAT/GCTATAACTATAAC<br>TAT                                 | CCAATACTTTGCGGCA<br>TCTT        | CAGCTACCTTTTCACG<br>CAGA  | 60.1                             | 739                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_593752 | scaffold242                             | 593752                        | ACCC/ACC                                                          | GGTTGTTTGAGCAAAC<br>TGCAT       | TTTGATTGTGTTGATGA<br>GCCA | 60.2                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_667084 | scaffold242                             | 667084                        | CTTTTTTTT/CTTTTTTTT                                               | CTTGGTGGCTTTGCCT<br>TAAA        | TTTATCTGGGGACTT<br>CGTG   | 60.2                             | 368                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_687481 | scaffold242                             | 687481                        | A/AT                                                              | ATGTTTGCCAAAAGG<br>CAAG         | AGCTTCATCGGCTTCA<br>ACAT  | 60.1                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_698186 | scaffold242                             | 698186                        | GAAA/GAAAA                                                        | GGCATTTTAAGGTGTA<br>TCAATAA     | GACATTGGAGGCGATT<br>GTTT  | 57.3                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_70770  | scaffold242                             | 70770                         | GTATATATATATATATATATATAT<br>ATATAT/GTATATATATATATATATAT<br>ATATAT | TGGCTGCCACATGATA<br>TGAA        | GATTTTGCGAGGATGG<br>AAAA  | 61.1                             | 848                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_710124 | scaffold242                             | 710124                        | CATAAATATATTTATAAATATATTTA<br>TA/CATAAATATATTTATA                 | ACTTGTTTCACCACATG<br>CCA        | CTTCACGTGAGCCAAA<br>CTCA  | 60.0                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_710240 | scaffold242                             | 710240                        | TTTATTATTA/TTTATTA                                                | ACTTGTTTCACCACATG<br>CCA        | CTTCACGTGAGCCAAA<br>CTCA  | 60.0                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_722081 | scaffold242                             | 722081                        | GAAAAA/GAAAA                                                      | CACAAGATCTTTAAGTT<br>CATATTTTCA | TTTCTCCATCCAAATTC<br>CCA  | 57.3                             | 951                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_730900 | scaffold242                             | 730900                        | GAAAA/GAAA                                                        | ACTACGAGACGGTGTA<br>GCCG        | CTCCACCACCTTGAG<br>TTGT   | 60.3                             | 916                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                              | Forward primers (5'-3')         | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------|---------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                            |                                 |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold242_P4_735528 | scaffold242                             | 735528                        | ACC/AC                                                                                     | CGAACTTGAGAATTCA<br>CCGC        | GTGGAAAAGGGGATTG<br>GATT       | 60.8                             | 371                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_735562 | scaffold242                             | 735562                        | A/AC                                                                                       | CGAACTTGAGAATTCA<br>CCGC        | GTGGAAAAGGGGATTG<br>GATT       | 60.8                             | 371                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_768388 | scaffold242                             | 768388                        | ATTTT/ATTTT                                                                                | CGATGCCCTAGGTGAT<br>TGTT        | GCATCCACGGTGATAG<br>TGAA       | 60.0                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_793808 | scaffold242                             | 793808                        | TCCC/TCC                                                                                   | CCTTCTTTCTTAGGGTT<br>CCACC      | TAGACACTGAACGCCA<br>ATCG       | 60.3                             | 320                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_804134 | scaffold242                             | 804134                        | CTTT/CTTTT                                                                                 | TGAAATGGAAATGCTA<br>CCATCA      | TGGTCAGAAACAACGC<br>AAGA       | 60.3                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_804233 | scaffold242                             | 804233                        | CTTTTTTTTT/CTTTTTTTTTT                                                                     | TGAAATGGAAATGCTA<br>CCATCA      | TGGTCAGAAACAACGC<br>AAGA       | 60.3                             | 710                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold242_P4_87361  | scaffold242                             | 87361                         | TA/T                                                                                       | GTTGCAAAGGCTCTGGT<br>GGTT       | CAACTTGGAGATTTTAA<br>AGTTCATTT | 60.0                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2421_P4_50421 | scaffold2421                            | 50421                         | C/CA                                                                                       | GAATAGGCCTAGGGAG<br>GACG        | AACCCATCTTGTCATC<br>CAA        | 60.1                             | 379                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2434_P4_76263 | scaffold2434                            | 76263                         | TGG/TG                                                                                     | TTCTTCGTTTTGTAGTT<br>GTACTCAATG | GGCAAACAAGAACCGA<br>AAAC       | 60.0                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2434_P4_76397 | scaffold2434                            | 76397                         | AAATAATAATAATAATAATAATA<br>ATAATAATAATAA/AAATAATAATAAT<br>AATAATAATAATAATAATAATAATA<br>TAA | TGTTGACACCTAATTTT<br>GTCCG      | AGAGGCCAAACAAGAAC<br>CGAA      | 59.9                             | 182                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2446_P4_7253  | scaffold2446                            | 7253                          | A/AC                                                          | TTCTCTGCGAAAATAA<br>ACCTC | TGCCCTTGTTTTCAGTT<br>CAA  | 59.7                             | 394                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2459_P4_20215 | scaffold2459                            | 20215                         | TCTGGAA/T                                                     | AATCGATTGATTCAGC<br>CCAG  | TGTTGTCCCACTTCCAT<br>TCA  | 60.0                             | 355                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2459_P4_42306 | scaffold2459                            | 42306                         | TCA/TA                                                        | TCAAACTTTTCCGCTG<br>CTT   | TCGAGAATTGAAACCC<br>AAGG  | 60.0                             | 287                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2459_P4_77337 | scaffold2459                            | 77337                         | GTT/GTTT                                                      | GTCCCGGGTTTAGGGT<br>TTAG  | TTGATGCATTGAGACA<br>GTTGC | 59.7                             | 301                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2466_P4_8204  | scaffold2466                            | 8204                          | CT/CTT                                                        | CGATTGTGTTTGTCAC<br>AGGG  | TCATTTTCGTCTCCAA<br>AGG   | 60.0                             | 769                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2489_P4_2070  | scaffold2489                            | 2070                          | CATA/CA                                                       | TTGGATGCACATGATT<br>GGTT  | CGTCCCCTCTTGGCTT<br>ATTT  | 59.8                             | 214                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold249_P4_144782 | scaffold249                             | 144782                        | AAGG/AAGGTAAAAGAGG                                            | TGGATGCTCAAGATTG<br>GTGA  | CATTTTCGTCTCCATA<br>GGC   | 60.2                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold249_P4_145492 | scaffold249                             | 145492                        | TGG/TG                                                        | AGCCTAGGGAGGACGA<br>AAAT  | TTTTCATTTGCGTCATT<br>GGA  | 59.2                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold249_P4_69062  | scaffold249                             | 69062                         | C/CG                                                          | TTGGTGCTTGCAGTG<br>TTTC   | AACCCTCAGATGCGTC<br>AATC  | 59.9                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2491_P4_6330  | scaffold2491                            | 6330                          | TTGTGT/TTGT                                                   | TCGAGGACCGAGAGAC<br>ACTT  | GCATTTTGGACCAGA<br>CGAT   | 60.0                             | 863                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2498_P4_24688 | scaffold2498                            | 24688                         | GTTTTTTTTT/GTTTTTTTTT                                         | TGGCAATTCAAGAAA<br>AGGG  | GGCAACAACAGTAACG<br>AGCA   | 60.0                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2498_P4_40654 | scaffold2498                            | 40654                         | CAAAAAAAAA/CAAAAAAAAA                                         | GCCGCCTTCGTACTCT<br>TAAA | GAAACAAACAAGCATT<br>TGGCA  | 59.5                             | 678                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold250_P4_12032  | scaffold250                             | 12032                         | ATT/ATTATTATTGTT                                              | GAAAGAAGCATGAATG<br>GGGA | TTGATTAACCCGATC<br>TAGCC   | 60.0                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold250_P4_82632  | scaffold250                             | 82632                         | AT/ATAATTTTCTT                                                | CCGGATCACTTTTTC<br>TTGA  | GTGATGATAGCCCTCC<br>TCCA   | 60.0                             | 235                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold250_P4_87679  | scaffold250                             | 87679                         | TGTG/T                                                        | TTCTGTGGTAAACATG<br>GGCA | TATGACCACCTCTTTG<br>GGC    | 60.0                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2501_P4_7458  | scaffold2501                            | 7458                          | TG/T                                                          | AACCGATCTTGTCGAT<br>CCAA | AGGGAGGACGAAATG<br>ACCT    | 60.5                             | 373                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2505_P4_1462  | scaffold2505                            | 1462                          | TCCC/TCCCC                                                    | ATTCCAAACCAAAACC<br>CTCC | TTGCTCACTACCACGC<br>TACG   | 60.0                             | 884                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2505_P4_1793  | scaffold2505                            | 1793                          | TG/TGGAAGG                                                    | CGTTCCACACAACCA<br>CAAA  | TTGCTCACTACCACGC<br>TACG   | 60.4                             | 112                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2511_P4_5221  | scaffold2511                            | 5221                          | A/AT                                                          | ATAAAGCACCTGGCTC<br>TCCA | GGCTGAAGAAGAAAT<br>CATCAGA | 59.8                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2511_P4_7402  | scaffold2511                            | 7402                          | CT/C                                                          | TGTTGAAGAAGGTTTT<br>GGGG | CCAATAACGATCAAGC<br>AATCG  | 59.9                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2516_P4_114083 | scaffold2516                            | 114083                        | TAAAAA/TAAAA                                                  | CACATTACTTCCACA<br>CCCC    | GTCGTGTTAGGCCAAT<br>TGCT  | 60.1                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2516_P4_87448  | scaffold2516                            | 87448                         | AAC/AACCAC                                                    | GGCGATTCAGAAGCCA<br>ATAC   | TGTTGGAGTTATTAGC<br>CGCA  | 59.7                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2521_P4_31107  | scaffold2521                            | 31107                         | CAAA/CAAAA                                                    | ATGCAATGCGTATATG<br>CCAA   | TAAATCGTGTGACCC<br>GTGA   | 59.9                             | 232                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2528_P4_19502  | scaffold2528                            | 19502                         | GTTTT/GTTTT                                                   | GTCCTCCGTTGGCTTA<br>TTCA   | GGACGAAAATGACCAA<br>AAGG  | 60.1                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2535_P4_23039  | scaffold2535                            | 23039                         | AATATATATATATATATA/AATATA<br>TATATATATATATATA                 | CCCAAGGCAGACTCTT<br>TCTG   | ACCAACCATTGCAAA<br>CAAT   | 60.0                             | 249                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2535_P4_4512   | scaffold2535                            | 4512                          | TTATATATATATATATAT/TTATAT<br>ATATATATATATATATAT               | TCACACAAATTTAGCCT<br>GGACT | GATGAGGTGGCATCGA<br>GAGT  | 58.8                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2542_P4_2207   | scaffold2542                            | 2207                          | TAGGAG/TAG                                                    | TCATTTGGACTTTTCG<br>GGAG   | TCAATTTGGGTTTCAGG<br>GTGT | 60.0                             | 816                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2542_P4_2507   | scaffold2542                            | 2507                          | ATATTATTAT/ATATTATTATTAT                                      | GTACCACCCGACAAAA<br>ATGG   | AACCGCTGCGAATCTC<br>TTTA  | 60.1                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2548_P4_1044   | scaffold2548                            | 1044                          | TTTTCTTTCT/TTTTCT                                             | AACAAAGGAACAAAT<br>GGCG    | AGGGAGGACGAAATG<br>ACCT   | 60.0                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2555_P4_18388  | scaffold2555                            | 18388                         | CACATATATA/CA                                                 | CACATGCATCAGGAAA<br>CGAC   | TTGTAGCCGTTGACTA<br>CCAAA | 60.1                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                       |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2557_P4_49964 | scaffold2557                            | 49964                         | AA/AATTA                                                              | CTTGGGCAAAACACCTC<br>CTAA | TGCATTGGTATATGGA<br>GGCT   | 60.1                             | 907                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2557_P4_51883 | scaffold2557                            | 51883                         | TTTTG/T                                                               | AACCACAAAATTGGAC<br>CAACA | TCATTGCATTTCATGG<br>AGT    | 60.1                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2557_P4_57413 | scaffold2557                            | 57413                         | TTCAATCAAT/TTCAAT                                                     | GAAACTGAAACGCGAC<br>AACA  | TCGAAAACATTCCGCT<br>GCT    | 59.9                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2557_P4_61886 | scaffold2557                            | 61886                         | ATTTTTT/ATTTTTT                                                       | GCTAGAAATTCGCCA<br>CACC   | TCGGCAAAATATTAGG<br>GACA   | 59.7                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2557_P4_6548  | scaffold2557                            | 6548                          | ACA/ACAATTTCCCTACA                                                    | GTGCCAACTTCATCCT<br>TGGT  | TCCTACGGTAGATCC<br>CAAA    | 60.0                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2557_P4_79849 | scaffold2557                            | 79849                         | TTATATATATATATATATATA/TTA<br>TATATATATATATATATA                       | TTCAATTAGGATTTTGT<br>GCGG | TCAACAAGACGACGAG<br>ATGC   | 60.0                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold256_P4_141629 | scaffold256                             | 141629                        | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATA<br>TATATATATAT | ATTTTGGCTCGGAGGC<br>TATT  | CGTTTTCGGATCAAAG<br>AGGA   | 60.1                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold256_P4_43420  | scaffold256                             | 43420                         | ATTT/ATTTT                                                            | TCACCTATCACGGGTC<br>AACA  | TGGTTTTGTCGTGAAAT<br>TGG   | 60.0                             | 621                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold256_P4_43496  | scaffold256                             | 43496                         | C/CAT                                                                 | TCACCTATCACGGGTC<br>AACA  | GGGAGGGAATTTGTCA<br>AGGT   | 60.0                             | 906                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2560_P4_60001 | scaffold2560                            | 60001                         | T/TCAATTGACG                                                          | TGCCAAACAACCTGG<br>AGAA   | CACGAATTAGCAAGAC<br>CAAACA | 59.3                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                            | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                          |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2560_P4_60629  | scaffold2560                            | 60629                         | T/TA                                                                                                     | GGAGAACATTATCCGT<br>TTTCCA | TCAAATTTTCATCTCAC<br>CCA  | 60.2                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2560_P4_61168  | scaffold2560                            | 61168                         | ACACGCACGCAC/ACACGCACGCAC<br>GCACGCAC                                                                    | GGGTGAGGATGAAATT<br>TGAAGA | ATTCGGTAGCACATT<br>GTCC   | 60.3                             | 864                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2560_P4_61734  | scaffold2560                            | 61734                         | TC/T                                                                                                     | GGACGAATGTGCTACC<br>GAAT   | GCACCCGCAAAGAATA<br>ACAT  | 60.0                             | 121                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2560_P4_62813  | scaffold2560                            | 62813                         | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATA/AAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATA | TAATGTTGGGCTTGCC<br>TTTC   | GCATCAACAACTATTC<br>TTGCC | 60.1                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2569_P4_65788  | scaffold2569                            | 65788                         | GATATATATATATATATATATAT/G<br>ATATATATATATATATATATATAT                                                    | GCCGCGTCTATTTGT<br>GTAT    | CCCTGTCCAGATTGAG<br>TGGT  | 60.0                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2575_P4_124736 | scaffold2575                            | 124736                        | TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATT/TTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATT    | TGAATCGCGAAAGTAG<br>TCCC   | CCTGGTTTTTGGGAGT<br>GAAA  | 60.2                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2575_P4_184922 | scaffold2575                            | 184922                        | ATTTTTTTTT/ATTTTTTTTTT                                                                                   | AGATCCATCCCTGCTT<br>GTTG   | CAAGCAAATTCGCAAC<br>ACAT  | 60.1                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2575_P4_196132 | scaffold2575                            | 196132                        | C/CA                                                                                                     | ACTTTTCACCACATCCC<br>TCG   | ATCCATTCCCACATTG<br>AAA   | 60.0                             | 347                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2575_P4_203148 | scaffold2575                            | 203148                        | ATATATG/A                                                                                                | ACCACACAAGCTTCAT<br>TCCC   | GTTGTTGGTCCACCAG<br>AGGT  | 60.0                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2575_P4_245742 | scaffold2575                            | 245742                        | ATTTTTTTTT/ATTTTTTTTTT                                                                                   | CGCAATAAATTTTGGAC<br>GCC   | TACCCATCAGGGCAGA<br>ACTC  | 60.4                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                 | Forward primers (5'-3')     | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------|-----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                               |                             |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2575_P4_247902 | scaffold2575                            | 247902                        | G/GA                                                                                                          | AGCCATAACTTGCTTG<br>AGGC    | CCATCCTCACGTGGTT<br>TTCT       | 59.5                             | 374                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2575_P4_278772 | scaffold2575                            | 278772                        | TGAAGAAG/TGAAG                                                                                                | TGGTGGCAAATGATGA<br>AGAA    | CAGGGACTACATCCAA<br>CAAAAA     | 60.0                             | 769                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2575_P4_279175 | scaffold2575                            | 279175                        | CTAT/CTATTAT                                                                                                  | TTTGATTGACTTAGCAC<br>CACG   | TAAAAGATGATGTGTG<br>GTGTGT     | 58.8                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2575_P4_279306 | scaffold2575                            | 279306                        | TAA/TA                                                                                                        | TTTTTGTGGATGTAGT<br>CCCTG   | CATGAACATTTAAGAGT<br>TTGCAITTT | 59.0                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2575_P4_280082 | scaffold2575                            | 280082                        | C/CATTGATA                                                                                                    | TCCCAAGGTATCATTG<br>TCTCTTT | TCGGAGTTTTGTGTGA<br>GTGTG      | 59.0                             | 316                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2575_P4_282172 | scaffold2575                            | 282172                        | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT/TTT<br>ATTATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATT | GAACCCGCCTAAACAT<br>TTCA    | GAAGAGAGACTATGTG<br>GGAACCA    | 59.9                             | 953                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2591_P4_5293   | scaffold2591                            | 5293                          | ACCTAAACCCTAAACCCTAAACCCT<br>AA/ACCTAAACCCTAAACCCTAAACC<br>CTAAACCCTAAACCCTAA                                 | TAACCATAAACCCGAA<br>ACGC    | TTTTTGTGTTGTCCAT<br>TTTTGTT    | 59.8                             | 236                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2598_P4_2362   | scaffold2598                            | 2362                          | TG/T                                                                                                          | CCCATGTAATTGTCAC<br>GCAA    | TTGTGGCAGACTTTGC<br>TTTG       | 60.4                             | 291                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold26_P4_227722   | scaffold26                              | 227722                        | AA/AAACTA                                                                                                     | CGTTGAGCCCATTTTT<br>CATT    | ATGTGTCAGCTGCAAA<br>CTGC       | 59.9                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold26_P4_506230   | scaffold26                              | 506230                        | GTT/GTTT                                                                                                      | ATTGGCGTGAAAACCG<br>TTAG    | TGACGGGTCTGCACAA<br>TTTA       | 60.0                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                    | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                  |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold26_P4_84614   | scaffold26                              | 84614                         | CATATATATATATA/CATATATATATA<br>TATA                                                              | TACAGAAACGGAGGGG<br>TTTG | GGAGGCTTTTAGGCCA<br>AAGT    | 60.0                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold260_P4_1842   | scaffold260                             | 1842                          | TAAA/TAA                                                                                         | AATGCACTCCAGGACC<br>AAAC | CCTTCTTCAGCCGTAT<br>CAGC    | 60.0                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold260_P4_330722 | scaffold260                             | 330722                        | G/GC                                                                                             | AGGCAATGCAATCCGA<br>TAAG | GAAGAGTTACGCGGAC<br>AAGC    | 60.1                             | 186                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold260_P4_356607 | scaffold260                             | 356607                        | T/TC                                                                                             | TTGATTTAGCCAGG<br>ATTC   | TTCTCATCTCCATTCCC<br>GTC    | 60.0                             | 149                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold260_P4_40057  | scaffold260                             | 40057                         | TNNNNNNNNNN/TNNNNN                                                                               | TAGGTTGTTTGCGAGC<br>TCCT | CCAACAATATCCCAATC<br>GCT    | 60.0                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold260_P4_58616  | scaffold260                             | 58616                         | AATATATATATATATATATATA/AA<br>TATATATATATATATATATATA                                              | TTCATAGCGCGATTCT<br>CCTT | CTGCACTTGCGGTCTT<br>ATCA    | 59.9                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold260_P4_73419  | scaffold260                             | 73419                         | TTATATATATATATATATATATATA<br>TATATATATATATATAT/TATATATAT<br>ATATATATATATATATATATATA<br>TATATATAT | CTTGGGAGTTGGAGAG<br>CAAG | AGGAAGAGTGGAGTTG<br>CGAA    | 60.0                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2603_P4_6448  | scaffold2603                            | 6448                          | ATCATAAGTGAT/A                                                                                   | AGCAGCTTCAAGCAAA<br>GCTC | TGAACCAAGTCCAATTCA<br>ACAGT | 60.0                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2603_P4_6501  | scaffold2603                            | 6501                          | CCA/CCACA                                                                                        | AGCAGCTTCAAGCAAA<br>GCTC | TGAACCAAGTCCAATTCA<br>ACAGT | 60.0                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2603_P4_67369 | scaffold2603                            | 67369                         | GTT/G                                                                                            | AATCCGCAACGGAGTT<br>TATG | TGAACGAGCTGAGAGA<br>AGCA    | 60.0                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                         | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                                       |                          |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2610_P4_5915   | scaffold2610                            | 5915                          | GAAAA/GAAAAA                                                                                                          | CCTTGGGAGGACGTAA<br>TTGA | TTTCGTCCTTCCTGG<br>CTTA      | 59.9                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2617_P4_324497 | scaffold2617                            | 324497                        | TGTG/T                                                                                                                | AAACAAGTTGGTGGTG<br>GAGC | AAAGTTAATTCAAATGC<br>ACTGTCA | 60.0                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2617_P4_402483 | scaffold2617                            | 402483                        | GAA/GAAA                                                                                                              | GTTGCAAGGGTGGAGT<br>GATT | AACAATTGTGAAACGTC<br>TCCG    | 60.0                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2617_P4_402519 | scaffold2617                            | 402519                        | TG/T                                                                                                                  | GTTGCAAGGGTGGAGT<br>GATT | AACAATTGTGAAACGTC<br>TCCG    | 60.0                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2617_P4_402584 | scaffold2617                            | 402584                        | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATA/AAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATA                    | GTTGCAAGGGTGGAGT<br>GATT | AACAATTGTGAAACGTC<br>TCCG    | 60.0                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2617_P4_402777 | scaffold2617                            | 402777                        | ATTTTTTT/ATTTTTTTTTT                                                                                                  | GTTGCAAGGGTGGAGT<br>GATT | AACAATTGTGAAACGTC<br>TCCG    | 60.0                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2617_P4_440937 | scaffold2617                            | 440937                        | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>A/AAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATA | GGCAATCCCACAAATG<br>TTCT | TCGCCAAATTGAAGCT<br>ATTG     | 59.8                             | 729                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2617_P4_444240 | scaffold2617                            | 444240                        | GACACACAC/GACAC                                                                                                       | CGTTGTGGACGTGTAT<br>TTGG | GCACTCCGCTTTCAC<br>TTAC      | 59.9                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2617_P4_476335 | scaffold2617                            | 476335                        | GTTTTTT/GTTTTTTT                                                                                                      | CATTAATGCACGGGCT<br>TTTT | AACTACGGCATAACAA<br>CCGC     | 60.0                             | 760                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold263_P4_177694  | scaffold263                             | 177694                        | A/AC                                                                                                                  | TCTGATGCAGTGTTTG<br>GCTC | TTTTCTGGTCTGCCTTG<br>GTC     | 60.0                             | 329                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                          | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                        |                            |                          |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2692_P4_14114 | scaffold2692                            | 14114                         | TATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATA/TATAATAATAATAATAATAA<br>TAATAATAATAATAATAATA | TAACCTGGGGCTTTAG<br>AGGG   | TTTGACAGTCAATTC<br>AAACC | 60.4                             | 654                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2692_P4_14319 | scaffold2692                            | 14319                         | GAAAAAAAA/GAAAAAAAAA                                                                                   | CATTGTATTGGAATGAA<br>CACCA | TTTCCTTCACCAACCA<br>ACA  | 58.3                             | 884                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2692_P4_1438  | scaffold2692                            | 1438                          | AAAAATATTATCAAATATTAT/AAAA<br>ATATTAT                                                                  | CCCTCAAGTCAAACAT<br>AGGCA  | AAGGAAATCCGAGTCT<br>GCAA | 60.1                             | 511                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2692_P4_14565 | scaffold2692                            | 14565                         | ATTTTTTT/ATTTTTTTT                                                                                     | ACCTGTCAAAGTTTTT<br>AAGCA  | TCCTTCACCAACCAAC<br>AAA  | 58.9                             | 420                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2692_P4_14759 | scaffold2692                            | 14759                         | ATTTTTTT/ATTTTTTT                                                                                      | ACCTGTCAAAGTTTTT<br>AAGCA  | TTTCCTTCACCAACCA<br>ACA  | 58.9                             | 422                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2692_P4_1521  | scaffold2692                            | 1521                          | CTATATATATATAT/CTATATATAT<br>ATATATAT                                                                  | CCCTCAAGTCAAACAT<br>AGGCA  | AAGGAAATCCGAGTCT<br>GCAA | 60.1                             | 511                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold2705_P4_1514  | scaffold2705                            | 1514                          | TAAAAAAAA/TAAAAAAAAA                                                                                   | TGCACGTGAACAAATA<br>TCTCAA | TTCCCCATGTTGAGTTA<br>GGC | 59.2                             | 623                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold271_P4_169460 | scaffold271                             | 169460                        | TTTATTATTATTATTATTATTATT<br>ATTATT/TTTATTATTATTATTAT<br>TATTATTATT                                     | GGATTGATTATGGCG<br>TTGC    | GTTTTGGGGTGGCACA<br>TATC | 60.3                             | 960                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold271_P4_196964 | scaffold271                             | 196964                        | ATTTTTTTTT/ATTTTTTTTT                                                                                  | TATCATTTAGGGTGAG<br>GGCG   | AGAAGTGGAAGGGT<br>GCCT   | 59.9                             | 605                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold271_P4_267926 | scaffold271                             | 267926                        | GATATATATATATATATATAT/GAT<br>ATATATATATATATAT                                                          | GGGGTGCTCAACTTGT<br>TTGT   | GGCCAAGGTAAGGGTG<br>AGAT | 60.0                             | 223                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')         | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                                 |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold271_P4_57742  | scaffold271                             | 57742                         | TGAGATGATTAG/TG                                               | TGGGGTGTTCATAGC<br>ATCA         | TTCATCCCATGCATCA<br>GAAA    | 59.9                             | 444                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold271_P4_6286   | scaffold271                             | 6286                          | GCC/GC                                                        | GCCAAAAATCGTGTGG<br>AGTT        | CAGTTGGGATTGGTCG<br>AGTT    | 60.0                             | 355                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2720_P4_26440 | scaffold2720                            | 26440                         | A/ACTGTG                                                      | TATTTTGGGGTTATCG<br>AGCG        | TTGTTTATTGGGTTG<br>GGA      | 59.9                             | 792                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2720_P4_26585 | scaffold2720                            | 26585                         | CATATATATATATA/CATATATATATA                                   | TTGCAACATCACAA<br>CCA           | TTTGAATCCCATGATGC<br>GTA    | 59.6                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2722_P4_55693 | scaffold2722                            | 55693                         | GAAAAAAAAA/GAAAAAAAAA                                         | CAACCACTTTGGATGA<br>AGCA        | TTTGGTTCCACAGTCT<br>CCC     | 59.7                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2722_P4_70279 | scaffold2722                            | 70279                         | TAAAAAAAAA/TAAAAAAAAA                                         | TTTTGACCAATCCATCA<br>GTTTTT     | TGCAGTTGAGTAGATA<br>TGCCAAA | 59.7                             | 883                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2725_P4_1078  | scaffold2725                            | 1078                          | CAA/CAAA                                                      | GGAGGACGAAAATGAC<br>CAAA        | TTGCATTTGCATCATTG<br>GAT    | 59.9                             | 345                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2726_P4_4506  | scaffold2726                            | 4506                          | G/GA                                                          | CAAACACCCCTATTGG<br>ATGC        | AGGTCATTTTCGTCCTC<br>CCT    | 60.2                             | 380                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2728_P4_11268 | scaffold2728                            | 11268                         | ATTTTTTTTT/ATTTTTTTTTT                                        | TGGCATCCGGAGTCTA<br>TTTT        | TGATAAACATGATTTTC<br>CGTCA  | 59.5                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold273_P4_104238 | scaffold273                             | 104238                        | TA/T                                                          | CGTTTTGTAGTTGTACT<br>TATAACGAAG | TTTCGGACTTGAAGAT<br>GGCT    | 57.1                             | 548                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold273_P4_49066  | scaffold273                             | 49066                         | TAAAAAAAAA/TAAAAAAAAA                                         | TTTCAGGCGAAAATCG<br>TACC   | ATAACCCGAACCTCAAA<br>CCC        | 60.1                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2734_P4_606   | scaffold2734                            | 606                           | TGCAAG/TGCAAGCAAG                                             | TTTCTTTTCCCTCCAA<br>GCA    | GGGGGAGAGAACAAT<br>CCAT         | 59.8                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2736_P4_3536  | scaffold2736                            | 3536                          | GAAAAA/GAAAAA                                                 | TTCAAGGAAATGCC<br>AGTC     | TGTTGCGACAACACA<br>ACAA         | 60.1                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2737_P4_9534  | scaffold2737                            | 9534                          | TAAA/TAA                                                      | TCTTCGTTTACGGTT<br>TATTTCA | AACATATAACAAAATTG<br>AGTTGTCAAA | 59.2                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2738_P4_27122 | scaffold2738                            | 27122                         | GTTTTT/GTTTTTTTTT                                             | TACCCTGTGGATGGGA<br>ATGT   | CAAAAGATGTGTAACG<br>GCCC        | 60.1                             | 441                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2738_P4_27897 | scaffold2738                            | 27897                         | ATATGAACTTAATGTTATGAACTT<br>AA/ATATGAACTTAA                   | GGAGAAGGCATGGATG<br>TTGT   | TTGCATCGTACCACTT<br>GGA         | 59.9                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2738_P4_31131 | scaffold2738                            | 31131                         | TTTCTTTCTTCTTCTTCTTCTT/TT<br>TCTTTCTTCTTCTTCTTCTTCTT<br>CTT   | TCCTAGAACATGCATC<br>ACGC   | AAACGCAATCCTTGAG<br>TTCG        | 59.8                             | 379                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2738_P4_31449 | scaffold2738                            | 31449                         | T/TCCTTTA                                                     | ATTTTGGAGGACTTTC<br>GGG    | ATTTGTACTGCCAAA<br>CGC          | 60.3                             | 856                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2738_P4_5256  | scaffold2738                            | 5256                          | A/ACTTCTTT                                                    | AATATCATGCCTCGTG<br>GCTC   | GCAAAAACACATTG<br>GCCT          | 60.1                             | 480                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2744_P4_48855 | scaffold2744                            | 48855                         | T/TCG                                                         | ACCCAAATGCATCAGA<br>CTCC   | TGTGTGTTTGTGGA<br>GGGA          | 59.9                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold275_P4_112169 | scaffold275                             | 112169                        | TAGA/TAGAGA                                                   | TGCCTGAGCACAAATT<br>TCAG  | TCTCACGGTTGTGAGG<br>ACTG | 60.0                             | 266                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_147158 | scaffold275                             | 147158                        | AG/A                                                          | GGAGCAAACGGAAGGT<br>ATGA  | ACATGAGTCTTTGTTGC<br>CCC | 60.1                             | 331                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_162362 | scaffold275                             | 162362                        | TG/TGG                                                        | CGAAGCACAAAGGAGAT<br>GACA | GGTTTGGGCAATCTGC<br>TTTA | 60.0                             | 762                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_187416 | scaffold275                             | 187416                        | CTT/C                                                         | CAGCAGCAGGAAAACA<br>TCAA  | TCTTATCCTTGCGGGA<br>ATTG | 60.0                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_258158 | scaffold275                             | 258158                        | AATATATATATATATATATAT/AAT<br>ATATATATATATATATAT               | TTTTGATAACCCCTTGC<br>GAC  | TGACCGTAATGGTTGG<br>ATGA | 59.9                             | 897                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_355509 | scaffold275                             | 355509                        | GAAAAAAA/GAAAAAA                                              | GCTTAGGCAGCCACAA<br>AATC  | TTGCCCTTGGATAAA<br>CTCA  | 59.9                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_360819 | scaffold275                             | 360819                        | TATTCATTCAATTCATTCAATTC<br>TTCATT/TATTCATTCAATTCATT<br>CATT   | TGAAAACCTGAAAAGG<br>CGAC  | AACATGCGGGTTGTTT<br>TCTC | 60.2                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_377072 | scaffold275                             | 377072                        | AATATATATATATATATATATAT/A<br>ATATATATATATATATATATAT           | TCAAGATACCCAGTGC<br>ACCA  | AGCGACATGTGAACAA<br>CAGC | 60.1                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_377314 | scaffold275                             | 377314                        | TAAAAAAA/TAAAAAAA                                             | TCATCGCAGGTGTACC<br>ATGT  | CGCCTTTGGCTATTCAT<br>CAT | 60.0                             | 825                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_377587 | scaffold275                             | 377587                        | TAAAAA/TAAAA                                                  | GCTGTTGTTACATGT<br>CGCT   | CAATTCCACAGGTAC<br>GCTT  | 59.9                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold275_P4_377615  | scaffold275                             | 377615                        | T/TATCAAAATCC                                                 | GCTGTTGTTACATGT<br>CGCT   | CAATTCCACAGGTAC<br>GCTT    | 59.9                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_380162  | scaffold275                             | 380162                        | GTTTTTTTTTTTTT/GTTTTTTTTT<br>TTTTTT                           | TATCACGCGCATCTGT<br>CTTC  | GGTCAAGTGCGGAACA<br>AAAT   | 60.0                             | 899                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_452515  | scaffold275                             | 452515                        | TAAAAAAAAA/TAAAAAAAAA                                         | TTTCGCAGACAACTG<br>AACG   | ATGGAAGGAGGTCACA<br>CCTG   | 60.0                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_629282  | scaffold275                             | 629282                        | TAAAA/TAAAAA                                                  | TTGGATGCACAACATT<br>GGTT  | TCCTCCCAGGCTTAT<br>TCTT    | 59.8                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_67453   | scaffold275                             | 67453                         | AG/A                                                          | CGTACTTGCATCCATG<br>AAACA | CATCGCCGTAGTCAAA<br>CTCA   | 59.6                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_760546  | scaffold275                             | 760546                        | TAACAA/TAA                                                    | CTTGGCATCCAGGAAT<br>CAAT  | TATGCCACAGCCAGTT<br>CTCA   | 59.9                             | 422                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_812219  | scaffold275                             | 812219                        | AAATTTAATTTAATTTA/AAATTTAAT<br>TTA                            | AGTCCCATGTAATTG<br>TCACG  | TCCTCATAGTTTCGAG<br>GACGA  | 59.7                             | 227                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold275_P4_812654  | scaffold275                             | 812654                        | TAAAAA/TAAAAA                                                 | TTAAGGCAAACCAATG<br>AGCA  | TTGCTTTGTCGGATTCT<br>ATTCT | 59.3                             | 227                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2763_P4_142691 | scaffold2763                            | 142691                        | ACCCC/ACCC                                                    | TCTGCCTGAGTGACCT<br>TCCT  | ATGCTGCAGTTTTGGC<br>TTCT   | 60.0                             | 387                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2763_P4_183619 | scaffold2763                            | 183619                        | TC/TCC                                                        | GCACTGAAAGCAACAA<br>CCAA  | ACCAGGTTATGAATAG<br>CCGC   | 59.9                             | 422                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold277_P4_211251 | scaffold277                             | 211251                        | TATT/TATTGAGAATT                                              | GGAGTACCATAGGCCA<br>ACGA    | GAGCGCTACCTCCAAG<br>TCAC   | 60.0                             | 216                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold277_P4_219153 | scaffold277                             | 219153                        | A/AT                                                          | GGGTGTTACAATTCTC<br>CCCTC   | CACTACAAATGTCGAG<br>GACGAA | 59.7                             | 218                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold277_P4_252454 | scaffold277                             | 252454                        | CTCTT/CT                                                      | CCCATTGCATTGCCTT<br>CTAT    | TAAAGGACCATGTCGG<br>GAAG   | 59.9                             | 329                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold277_P4_4447   | scaffold277                             | 4447                          | TACTGA/TA                                                     | TAAAGGAGCATCCGTG<br>GAAT    | TGCATGTATCATAGAC<br>CGCC   | 59.5                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold277_P4_4861   | scaffold277                             | 4861                          | AATATATAT/AATATAT                                             | TGGAGAAACCTTGTGA<br>ACCA    | GAAACGGAAAGGGGAA<br>CAAT   | 59.1                             | 316                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2777_P4_2240  | scaffold2777                            | 2240                          | ATT/ATTT                                                      | GACTTTTGCAC TTATTG<br>GACGA | CATTGCGGTTCAAAAT<br>CCAT   | 59.3                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2777_P4_4052  | scaffold2777                            | 4052                          | GTTAAC/G                                                      | CATTGATTAAGAACGC<br>AAATGG  | AGTTGGTCCCAAAAGT<br>GCAA   | 59.5                             | 199                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2777_P4_5110  | scaffold2777                            | 5110                          | A/AT                                                          | TGCGAGTTAAATGCCA<br>AAAA    | GTGACGTCGCTTCGAA<br>AAAT   | 59.3                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2779_P4_6967  | scaffold2779                            | 6967                          | GTT/GTGTGTTT                                                  | AGGTCATTTTCGCCT<br>CCCT     | TCGAAATGTTTCATCCAA<br>CGA  | 59.9                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2782_P4_27408 | scaffold2782                            | 27408                         | GAAAAAAAA/GAAAAAAAAA                                          | CTCGAAACCCGAAACA<br>CAAT    | CGAATTCGTTGTCAAC<br>TCAT   | 60.0                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2782_P4_6224  | scaffold2782                            | 6224                          | AGG/AGGG                                                      | CTTTTCGGGCGATTTT<br>CATA  | GATGAAATCGAGGACT<br>GGGA  | 60.0                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2783_P4_1246  | scaffold2783                            | 1246                          | TATCCAATCTTGCGCATCCAAT/TAT<br>CCAAT                           | AACCAATGTTGTGCAT<br>CCAA  | TAAGCAGAGGGAGGAC<br>GAAA  | 59.8                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2784_P4_2578  | scaffold2784                            | 2578                          | A/ACTTTTC                                                     | TGACAACTCAAATCGA<br>TGCC  | CGGGTTTCACGTCAGA<br>TTTT  | 59.7                             | 205                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2792_P4_13253 | scaffold2792                            | 13253                         | G/GTCATTTTCGTCCT                                              | AGGTCATTTTCGTCCT<br>CCCT  | TTCGTCCAATGACCAAA<br>ACA  | 59.9                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2792_P4_14181 | scaffold2792                            | 14181                         | GTTTTT/GTTTT                                                  | AGGTTCAATTTGGGTCA<br>TTGG | AACCTTGGGAGGACGA<br>AAAT  | 59.6                             | 973                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2799_P4_34751 | scaffold2799                            | 34751                         | AAAA/AAAAA                                                    | AATCGATTTGGCCATA<br>CAGG  | GAGGGAAAAGCCCAGA<br>TTTC  | 59.8                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold280_P4_103565 | scaffold280                             | 103565                        | G/GT                                                          | AAATCCCAAACCCTAAA<br>CCC  | TCGTCAATAAGTGCA<br>AAAGTG | 59.0                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold280_P4_107582 | scaffold280                             | 107582                        | C/CCTCTGGGG                                                   | AGCTCCTGCTCAAGCA<br>GTTC  | AAAATGACCCCTGATT<br>TCC   | 59.9                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold280_P4_118373 | scaffold280                             | 118373                        | A/AG                                                          | AAACGCATTGGCTTTC<br>AATC  | AACAAATTGGAACCGC<br>TCAC  | 60.1                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold280_P4_118918 | scaffold280                             | 118918                        | CGTT/CGTTTGTT                                                 | GTGAGCGGTTCCAATT<br>TGTT  | GGGTGCTCCTAGGTGT<br>GTGT  | 60.0                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                           |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold280_P4_128741 | scaffold280                             | 128741                        | CAA/CAAA                                                                                  | ATTCCAAACCAAAACC<br>CTCC   | TGATTTTGGGGGAAAA<br>TGAA  | 60.0                             | 943                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold280_P4_13318  | scaffold280                             | 13318                         | AAAACCCCTAAACCCTAAACCCTAAA<br>CCCTAAACCCCTAAACC/AAAACCCCTA<br>AACCCCTAAACCCCTAAACCCTAAACC | TGTCTTTTGTCTTATT<br>GCACGA | GTGGTTTAGGGTTTGG<br>GGTT  | 59.8                             | 269                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold280_P4_13470  | scaffold280                             | 13470                         | GTAACCCCTAAAC/GTAAACCCTAAA<br>CCCTAAAC                                                    | TGTCTTTTGTCTTATT<br>GCACGA | CGGTTGCGGTTTATGG<br>TTTA  | 59.8                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold280_P4_266135 | scaffold280                             | 266135                        | TAATAATAA/TAATAATAAAATAATA<br>A                                                           | TCTTCGTTATGCAGTC<br>AAACCT | TTTCAGGCGATTTTCGT<br>ACC  | 58.9                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold280_P4_302193 | scaffold280                             | 302193                        | CAA/CAAA                                                                                  | TCACCTATCACGGGTC<br>AACA   | TCATCGTATTTTCGCGT<br>GTTC | 60.0                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold280_P4_52649  | scaffold280                             | 52649                         | CTCAAT/CTCAATTGATTATCAAT                                                                  | TGGTCATGCAGAACT<br>CAGC    | ACTCTCATCTGAGGGC<br>GAAG  | 60.0                             | 330                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold280_P4_70492  | scaffold280                             | 70492                         | ATGTGTGTGTGTGTGTGTGTGTGT<br>GT/ATATATATGTGTGTGTGTGTGT<br>GTGTGTGTGTGTGTGTGTGTGT           | CAATAGTACCGTTGGC<br>ACGTT  | AGCATGCATCTGCACA<br>CAAT  | 59.9                             | 920                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2803_P4_1840  | scaffold2803                            | 1840                          | TAAAAAA/TAAAAAAA                                                                          | AGCCAGGTAGGACGA<br>AAAT    | TGCATCCAATAGGTGT<br>GTTTG | 60.0                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold281_P4_1263   | scaffold281                             | 1263                          | CAA/CAATTAA                                                                               | TGTTGACACTCAGTC<br>TTACGG  | TGCATGCCCTTTGATT<br>ACA   | 60.3                             | 287                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold281_P4_1388   | scaffold281                             | 1388                          | GAAAAAAAAA/GAAAAAAAAA                                                                     | TGTTGACACTCAGTC<br>TTACGG  | TGCATGCCCTTTGATT<br>ACA   | 60.3                             | 287                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs    | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|---------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                     |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold281_P4_1467 | scaffold281                             | 1467                          | GGCATGCATG/GGCATG                                             | TGTTCGACACTCAGTC<br>TTACGG | ATCGGAAAAGTGACAT<br>TGGG  | 60.3                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold281_P4_2224 | scaffold281                             | 2224                          | CT/C                                                          | TGGGCAGATTTGTAAC<br>ACGA   | GCGAAACCCGATTCTA<br>TTGT  | 60.1                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold281_P4_3002 | scaffold281                             | 3002                          | TAAAAA/TAAAAA                                                 | ACAATAGAATCGGGTT<br>TCGC   | AGGACTATTTTGGTCT<br>CCCA  | 59.0                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold281_P4_3090 | scaffold281                             | 3090                          | AATATATATATAT/AATATATAT                                       | ACAATAGAATCGGGTT<br>TCGC   | AGGACTATTTTGGTCT<br>CCCA  | 59.0                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold281_P4_3313 | scaffold281                             | 3313                          | GAA/GAAATAA                                                   | AGACATTGCTCTTTCG<br>GTCAA  | CGTTGACCATTTTAAGC<br>TTGG | 59.9                             | 911                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold281_P4_3414 | scaffold281                             | 3414                          | GAAAAGAAAA/GAAAAGAAAAAGAAA<br>A                               | TGGGAGACCAAAAATA<br>GTCCT  | CGTTGACCATTTTAAGC<br>TTGG | 57.7                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold281_P4_3735 | scaffold281                             | 3735                          | A/AATT                                                        | TGGGAGACCAAAAATA<br>GTCCT  | CAAGAGGGGTTGCAAG<br>TGTT  | 57.7                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold281_P4_4125 | scaffold281                             | 4125                          | TGG/TG                                                        | AACACTTGCAACCCCT<br>CTTG   | ATGATGATTTTCTCCCC<br>GTG  | 60.1                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold281_P4_4227 | scaffold281                             | 4227                          | AG/AGGAATTATG                                                 | AACACTTGCAACCCCT<br>CTTG   | ATGATGATTTTCTCCC<br>GTG   | 60.1                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold281_P4_4869 | scaffold281                             | 4869                          | TGCCGGCCG/TGCCG                                               | ACACGGGGAGAAAATC<br>ATCA   | GACGCGCTATAGAACT<br>TCGC  | 60.3                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)        | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                      |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold281_P4_5058   | scaffold281                             | 5058                          | TATAAT/TAT                                                           | CAATTGCAGTCAGTT<br>GTGC    | GACGCGCTATAGAACT<br>TCGC  | 60.3                             | 297                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2812_P4_16756 | scaffold2812                            | 16756                         | TAAAAA/TAAAAAA                                                       | CAATTGTTGTTGTTGAC<br>ATTGG | GGTTGATGCGTCAATG<br>TTGT  | 60.2                             | 871                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2812_P4_43005 | scaffold2812                            | 43005                         | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATAT                    | TCACACGAGAATCATG<br>TCAAG  | TTGCGAATTTGTTTGCA<br>AGT  | 57.2                             | 837                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2812_P4_46737 | scaffold2812                            | 46737                         | CATATA/CATATATA                                                      | CGATTTCTTCACCATT<br>TTCA   | CCTGAGCCTGTAGCTG<br>AACC  | 59.9                             | 728                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2812_P4_58880 | scaffold2812                            | 58880                         | TAAAAA/TAAAAAA                                                       | TTGCTCCCAAAACAAG<br>CTCT   | TACTTTGTGGCTGTTTC<br>CCC  | 60.0                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2812_P4_75007 | scaffold2812                            | 75007                         | AAAATAAATAAATAAATAAATAAATA<br>AATAAA/AAAATAAATAAATAAATAA<br>TAAATAAA | CTGATAGCTGTTATCG<br>CCCG   | ATCGTGTCTAACCCCTG<br>TCGG | 60.8                             | 223                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2815_P4_71273 | scaffold2815                            | 71273                         | TC/T                                                                 | CGGTGCTAGTGGACCA<br>ATTT   | GTTATTCATAGCCTCC<br>GCCA  | 60.0                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2819_P4_18668 | scaffold2819                            | 18668                         | GAAA/GAAAA                                                           | CGACAAAAGTGGACCG<br>AAAT   | TTGTACCGAACTCGTA<br>GGGG  | 60.0                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2823_P4_8578  | scaffold2823                            | 8578                          | CAAAA/CAAA                                                           | TGGATAATTGCCATGC<br>AAGA   | GGCTCACAAATTTTGG<br>CAAT  | 60.0                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold283_P4_26078  | scaffold283                             | 26078                         | GTT/GTTT                                                             | CCGATTTTCATCTGGAC<br>GTTT  | ACTAACCATCGTTTGG<br>CCTG  | 59.9                             | 336                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                  | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold284_P4_14484  | scaffold284                             | 14484                         | ATTTT/ATTTT                                                                                                                    | TTTGCCTCATTGCTTT<br>TCC    | CCCCTTCTCCTAGAA<br>CGC    | 60.2                             | 294                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold284_P4_15317  | scaffold284                             | 15317                         | ATTTTTTTTTCTGCGTTTTTTTTC/A<br>TTTTTTTTTC                                                                                       | CCAGAATCGGACTTGT<br>TTCG   | TTCTTGTGTGGAGTG<br>TGGC   | 60.6                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold284_P4_21461  | scaffold284                             | 21461                         | AT/A                                                                                                                           | AATGTTGTGGTTGGGT<br>TGCT   | ACAAGGCTAACTCAAG<br>GCCA  | 60.0                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold284_P4_3250   | scaffold284                             | 3250                          | AGAATGAATGAATGAA/AGAATGAAT<br>GAATGAATGAA                                                                                      | TCACAATGGGCACAAG<br>AAAA   | TTTCCCATGCAACTTGA<br>ACA  | 60.1                             | 146                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold284_P4_334828 | scaffold284                             | 334828                        | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATT/TTTATTATTATTATTAT<br>TATTATTATTATTATTATTATT<br>TATTATTATTATTATT | TCCTCATACCAATCCAA<br>CATTT | TTGAGAATAAGAGCGC<br>TCGAT | 58.3                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold284_P4_4461   | scaffold284                             | 4461                          | CTC/CTCCTCCTCCTCCTCATC                                                                                                         | TACGATGATGAACAGT<br>CGGC   | TTGGTTTCAAGACCTG<br>CATCT | 59.7                             | 424                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold284_P4_477291 | scaffold284                             | 477291                        | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAA/A<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAA              | TTTATGTGCCCTTGAC<br>CGAT   | GTTTTGGCGTTGTTT<br>CACT   | 60.3                             | 847                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold284_P4_702931 | scaffold284                             | 702931                        | ATTTTTTTTT/ATTTTTTTT                                                                                                           | CATTTTGCCTCTATCT<br>GCCA   | TTGCGATGCTTGATC<br>GTTA   | 60.2                             | 766                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold284_P4_823425 | scaffold284                             | 823425                        | AATATATATA/AATATATATATA                                                                                                        | TAAACCACTTCATCCA<br>GCC    | ATCCAACATGGCTTC<br>GTCG   | 59.9                             | 716                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2845_P4_17944 | scaffold2845                            | 17944                         | AGGG/AGGGG                                                                                                                     | AAACTGCTTCAATGG<br>CGTT    | CTCCAAGTGCTACGGA<br>AAGC  | 59.8                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                          | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                                                        |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2848_P4_7405  | scaffold2848                            | 7405                          | ATTTTTTTTT/ATTTTTTTTT                                                                                                                                                  | CTAGCTTGACCATGCG<br>TTTG   | AACAAGTAGCTCAAGG<br>CCGA  | 59.5                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2850_P4_28403 | scaffold2850                            | 28403                         | CAAAAA/CAAAA                                                                                                                                                           | AAAAAGGAAAGGAACC<br>AACG   | GTCTTGGGTGATGGCA<br>AAGT  | 58.2                             | 129                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2853_P4_12080 | scaffold2853                            | 12080                         | CTTTTTTTTT/CTTTTTTTTT                                                                                                                                                  | GGGTTTGGGATTAGG<br>ATTGA   | GGGTGCATTTTACAGC<br>GTTT  | 60.0                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2853_P4_6530  | scaffold2853                            | 6530                          | CTTTTTTT/CTTTTTTT                                                                                                                                                      | CCATTTCGGTTTTAAC<br>AATGTA | GATTGATGCACTAATTC<br>GACG | 60.0                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2869_P4_34891 | scaffold2869                            | 34891                         | TTT/TTTATTATT                                                                                                                                                          | TTGCATGGTTAAATGC<br>AGGA   | TCATGGATGTTTGGAT<br>GTTTG | 60.1                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold287_P4_180880 | scaffold287                             | 180880                        | TTATATATATATATATATATA/TTA<br>TATATATATATATATATATATA                                                                                                                    | CGGGAATACTCAAAGG<br>TTGC   | CATTGAGACCGACGCT<br>GTAA  | 59.6                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold287_P4_238271 | scaffold287                             | 238271                        | GAAAAAAAAA/GAAAAAAAAA                                                                                                                                                  | ATGGCACTGAATGAGG<br>CTCT   | TATTGTCATGTCGGGG<br>TTGA  | 59.8                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold287_P4_296050 | scaffold287                             | 296050                        | GTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTACTATTACTATTAATACTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT | AGATTGCAACAGTTG<br>GGTC    | TCCGAAAAATAACTAT<br>GGGG  | 60.0                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2871_P4_30418 | scaffold2871                            | 30418                         | AGT/AGTGT                                                                                                                                                              | GGTTTTGGATTGGGC<br>TACA    | GGGTTATGGCTTTGAT<br>CATGT | 59.8                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2887_P4_7283  | scaffold2887                            | 7283                          | CTG/C                                                                                                                                                                  | TGGTGCCTCTTAATGT<br>GGAA   | TTTGCCATGACCTTTT<br>GTTC  | 60.1                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                  |                               |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2893_P4_10683 | scaffold2893                            | 10683                         | AGG/AGGG                                                         | GCCAGATCTTCGATT<br>CAGC       | CCTTCAATGGAACCGC<br>ATAC  | 59.9                             | 255                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2893_P4_11811 | scaffold2893                            | 11811                         | CTTTTT/CTTTT                                                     | GCCAATCGATTATCGC<br>AAGT      | TGGCACTCCGATTAAAC<br>ATGA | 60.1                             | 344                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold29_P4_100652  | scaffold29                              | 100652                        | C/CA                                                             | TCCCGATCTTCGATTT<br>CATC      | CCATCGTTCAGTCCGA<br>AAAT  | 60.0                             | 254                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_101714 | scaffold290                             | 101714                        | GTTTTTTTTTTTT/GTTTTTTTTTT                                        | TCGTATTGACCCGTG<br>TTTG       | CCCGTTCTCAGCGAGA<br>TTAG  | 59.4                             | 322                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_157987 | scaffold290                             | 157987                        | CT/CTTTT                                                         | GGAGGAAGAAATGTGA<br>CGGT      | CGCGCGGACCATTATC<br>TAGT  | 59.0                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_250722 | scaffold290                             | 250722                        | AGGGG/AGGG                                                       | TGCAAGCTACGATGAT<br>TTCG      | GTGAGAGGCCCCACAA<br>TCTA  | 60.0                             | 730                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_293241 | scaffold290                             | 293241                        | ATTATTTATTTATTTATTTATTTATT/<br>ATTATTTATTTATTTATTTATTTATT<br>ATT | TTGCTCTTAATTTTCC<br>TCGAA     | GTGAGTCTGCGACCAC<br>TTGA  | 58.2                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_293476 | scaffold290                             | 293476                        | ATTTTTTTT/ATTTTTTTTT                                             | TTGCTCTTAATTTTCC<br>TCGAA     | GTGAGTCTGCGACCAC<br>TTGA  | 58.2                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_293534 | scaffold290                             | 293534                        | GAAAAAAAA/GAAAAAAAAA                                             | TCGAAGAAAAATTAGG<br>AAGAAGTTG | GTGAGTCTGCGACCAC<br>TTGA  | 59.4                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_308610 | scaffold290                             | 308610                        | CTTTTTTTTT/CTTTTTTTTT                                            | CATATTTGCCTTGTA<br>CCCC       | CGGTTGAGTAACTGTG<br>CCAA  | 60.2                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold290_P4_312602 | scaffold290                             | 312602                        | TAA/TA                                                        | TTCCCGAATATGTGCA<br>ATGA    | GAGCCAACATACGATC<br>CACC    | 59.9                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_315176 | scaffold290                             | 315176                        | AATTATTATTATTATTATT/AATTATT<br>ATTATTATT                      | TTCTTTGGTTGTTGAAT<br>TTTGTT | ACTAGATGGTCGCATC<br>CTGG    | 57.8                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_392260 | scaffold290                             | 392260                        | TAAAAAAAA/TAAAAAAAA                                           | TGGGGTAGCTAGTCCC<br>TCCT    | TGCGAAATGATGAGTG<br>ATGC    | 60.1                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_400824 | scaffold290                             | 400824                        | TAAAAAAAA/TAAAAAAAAAAAA                                       | TTGTGTTGCATTGTGG<br>ATTCT   | CACAGCCCTCTAAAC<br>CAAC     | 59.0                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_434453 | scaffold290                             | 434453                        | ATTATTTTTATTTTTATT/ATTATTTT<br>ATTTTTATTTTTATT                | GGTTCGCATATTTGCC<br>TTGT    | TGCGGTAGAGTAAATG<br>TGACAAA | 60.0                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_435572 | scaffold290                             | 435572                        | GTATATATATATATA/GTATATATATA<br>TATATATA                       | CAGGTTGAGTTGAGGG<br>GTGT    | ATCTGCATTGCACAAA<br>CCA     | 60.0                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_452067 | scaffold290                             | 452067                        | GAAA/GAA                                                      | GAAAAATTCACCACCG<br>ATTAGG  | TACAATCAGGATGCGT<br>CCAA    | 59.7                             | 632                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_470901 | scaffold290                             | 470901                        | ATTTTTTTTTTTTT/ATTTTTTTTTTT<br>TTTT                           | TTCGAATCGAGACATT<br>GCAG    | ACCACTCAATTGGGCA<br>AAAG    | 59.9                             | 877                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_604189 | scaffold290                             | 604189                        | T/TG                                                          | CAGCACAGTCACAAGG<br>TTGG    | GCGTTGTTGTATCCTC<br>CGTT    | 60.3                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_700099 | scaffold290                             | 700099                        | GAAA/GAAAA                                                    | CATGCAAAAATGACCA<br>CCAG    | TTTGCTCCAGCTTCCTC<br>AAT    | 60.0                             | 819                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold290_P4_705643 | scaffold290                             | 705643                        | CAAAAAAAAA/CAAAAAAAAA                                         | CGCCTCCTCAAAGATC<br>TCAC | TGCCATTGAACCTTGT<br>CAAA  | 60.0                             | 896                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_720833 | scaffold290                             | 720833                        | CTTTTTTTTT/CTTTTTTTTT                                         | AACTCCAACAACCCGT<br>TGAG | ATGGGCCAATTACCCA<br>ACTT  | 60.0                             | 341                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_820202 | scaffold290                             | 820202                        | ATT/ATTT                                                      | ACCAAGCCTTTTGGAC<br>AATG | TCTTCGGTTGGAATTT<br>GGTT  | 60.0                             | 879                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_859147 | scaffold290                             | 859147                        | TAAAAA/TAAAAA                                                 | TTCCCTCTCCCATTTT<br>CTT  | GCATTTGGGTTGAAAA<br>TTGC  | 59.9                             | 442                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_860082 | scaffold290                             | 860082                        | GAAAAAAAA/GAAAAAAAAA                                          | ATCTCATGTCCCAAG<br>CCAG  | TGTTGAAAAATTGGA<br>AAACCT | 60.1                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_861782 | scaffold290                             | 861782                        | ATTTTTTTTT/ATTTTTTTTT                                         | AACTGGGGTTCTTAGC<br>CCAT | CGGCCTCTTGCAAATA<br>TGAT  | 59.8                             | 340                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_867556 | scaffold290                             | 867556                        | AGGCCTACG/AGGCCTACGCCTGG<br>CCTACG                            | TGCATTTTGAGTCTTG<br>CTCG | GCCGAAGAAAAAGCCT<br>ATGA  | 60.1                             | 132                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_892920 | scaffold290                             | 892920                        | GAAAATAAAAAATAAAAAATA/GA<br>AAATAAAAAATA                      | ACCCGGGTATAAGGTT<br>CCAC | TTCCCTACGCATAATC<br>GGTC  | 59.9                             | 467                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_893328 | scaffold290                             | 893328                        | GAAAAAAAA/GAAAAAAAAA                                          | GACCGATTATGCGTAG<br>GGAA | TGCATTACATTTTCTC<br>CCA   | 59.9                             | 298                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold290_P4_97167  | scaffold290                             | 97167                         | TGGGGG/TGGGGGG                                                | CCGTCGGCACTAACAA<br>TCTT | GCATTTGGTTTTGCCA<br>GAAT  | 60.1                             | 691                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2900_P4_7979  | scaffold2900                            | 7979                          | ATT/AT                                                        | TATGAAAATCGCCGA<br>AAAG  | GGTCCTCGATTTCATCT<br>GGA | 60.0                             | 355                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2916_P4_15794 | scaffold2916                            | 15794                         | TAAAAAAAAA/TAAAAAAAAA                                         | TGCACCTTTTAGAGCA<br>CCGT | GCAGACTCGGATTTC<br>CTAA  | 60.8                             | 773                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2919_P4_8998  | scaffold2919                            | 8998                          | GTTTT/GTTTT                                                   | TCATTTTCGTCCTTCCT<br>TGG | TGGACGCACAAGATTG<br>GTTA | 60.0                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2922_P4_7477  | scaffold2922                            | 7477                          | CGG/CG                                                        | TTTCATCTGGACTTTTC<br>GGG | TAACACGTTTCGGGTT<br>CCG  | 60.0                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2922_P4_8355  | scaffold2922                            | 8355                          | GAAAAA/GAAAAA                                                 | GACTTTTCGGGCGATA<br>TTCA | ATATGCAACCGAAGAC<br>CAGG | 60.0                             | 647                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2924_P4_11718 | scaffold2924                            | 11718                         | G/GC                                                          | GATCTATGAGGACAGG<br>GCCA | CCTTATCCCCGGTATC<br>ACCT | 60.0                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2924_P4_8200  | scaffold2924                            | 8200                          | ATTTTT/ATTTTT                                                 | TTGCTTCATGGAACCT<br>GAGG | CGTCCTCGAAATTGA<br>CGTG  | 58.8                             | 295                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2928_P4_18293 | scaffold2928                            | 18293                         | A/AT                                                          | TTGGATGCACAAGATT<br>GGTT | GTGTGTCTGGTCATTG<br>GACG | 59.0                             | 196                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2928_P4_22766 | scaffold2928                            | 22766                         | ATTTT/ATTTT                                                   | AACCAATGATGTGCAT<br>CCAA | AGGGAGGACGAAAATG<br>ACCT | 59.8                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2928_P4_23701 | scaffold2928                            | 23701                         | TTGT/TT                                                       | AGACCTCGCTTGGCTG<br>ATTA | ACGGAGGAGGAAAATG<br>ACCT | 60.0                             | 210                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold293_P4_27947  | scaffold293                             | 27947                         | CTTT/CTT                                                      | GCATCACGCTACCATA<br>GGCT | TTGGTCGTTTGAGCCT<br>TTCT   | 60.3                             | 511                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2931_P4_1404  | scaffold2931                            | 1404                          | CTTTTTTT/CTTTTTTTTT                                           | GCCCTCAGATGAGAGT<br>CAGG | GGAGGGTTTTGGTTTG<br>GAAT   | 59.9                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2932_P4_2304  | scaffold2932                            | 2304                          | GTTTT/GTTTTT                                                  | ATTGTCGTCCTCCCTA<br>GGCT | ACACCTATTGGATGCC<br>CAAG   | 60.1                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2940_P4_1242  | scaffold2940                            | 1242                          | TC/T                                                          | TGTGCACCGAATAGGT<br>GTGT | TCCTTCGGAGGATGAA<br>AATG   | 60.0                             | 266                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2950_P4_1436  | scaffold2950                            | 1436                          | ATTTT/ATTTT                                                   | GTCCTCTGAAACCTCC<br>CACA | TTTTGGGTCGTGACAC<br>TTGA   | 60.1                             | 337                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2950_P4_671   | scaffold2950                            | 671                           | CTTTTTTTTTT/CTTTTTTTTTT                                       | TAACGGTCTCCAAATC<br>CCTG | TTGTGTTGGGTTTGCCTT<br>ACC  | 59.9                             | 846                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2950_P4_6843  | scaffold2950                            | 6843                          | A/AG                                                          | CCAAATTACAACCGAC<br>CCAC | AAAGGCGCTCCTCTAT<br>CACA   | 60.1                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2950_P4_6903  | scaffold2950                            | 6903                          | AAA/AAATAA                                                    | CCAAATTACAACCGAC<br>CCAC | AAAGGCGCTCCTCTAT<br>CACA   | 60.1                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2955_P4_10080 | scaffold2955                            | 10080                         | CT/CTT                                                        | AGAGTGGACGGAAT<br>GGTG   | AACTTGGTGCCCTGA<br>CTTG    | 60.0                             | 621                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2955_P4_11713 | scaffold2955                            | 11713                         | GTTTT/GTT                                                     | TGAAAGAGAAAGGGCT<br>TGGA | AACTCGTTTGTTTCATTG<br>GTGA | 59.9                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                         | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                       |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2955_P4_927   | scaffold2955                            | 927                           | ATTTTTTT/ATTTTTTTT                                                                                    | CCCAAATGCCCTACTC<br>TGAA  | CAGGAAACGACCCCT<br>ATTA  | 60.1                             | 129                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2955_P4_9708  | scaffold2955                            | 9708                          | T/TCTAC                                                                                               | ACTATGCAAAGGTGCA<br>AGGC  | CACCATTTTCCGTCCA<br>CTCT | 60.3                             | 374                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2957_P4_10516 | scaffold2957                            | 10516                         | A/AC                                                                                                  | TGCGTCATTGGATTCA<br>CATT  | GCGAGGACGAAAATGA<br>CCTA | 59.9                             | 819                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_11136  | scaffold296                             | 11136                         | GTTTT/GTTT                                                                                            | TTGAATCCTTTTCTGG<br>GTGG  | CTTGTGCTTCGGTTAC<br>AGCA | 59.9                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_11327  | scaffold296                             | 11327                         | TCC/TCCC                                                                                              | TGGACGTAGTCCGAGT<br>TGGT  | CTTGTGCTTCGGTTAC<br>AGCA | 60.6                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_144489 | scaffold296                             | 144489                        | AAATAATAATAATAATAATA<br>ATAATAATATTAATAATAATA<br>ATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATA<br>TA | TCCATTCAACCGAATC<br>ACAA  | TCACCCATCAAAGCAT<br>CAAA | 59.9                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_15393  | scaffold296                             | 15393                         | AAAGAA/AAA                                                                                            | CAGTGTAGCCAGCCAA<br>GACA  | AGTTCAGGCCTTTGCA<br>AGAA | 60.0                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_17248  | scaffold296                             | 17248                         | AATATATATATATATATATAT<br>ATATATAT/AATATATATATAT<br>TATATATATATATATATATAT                              | AGGAGGAGGGATCTG<br>GAAAA  | TTGCTCCTACGTATCTC<br>CCG | 60.0                             | 965                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_233039 | scaffold296                             | 233039                        | AATATATATATATATATATAT<br>ATATATATATATATATATAT                                                         | TTGAGTTGCGACGAGA<br>GTACA | GAAACATGGAGGTTTG<br>CGTT | 59.6                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_250245 | scaffold296                             | 250245                        | TT/TTGGT                                                                                              | TGGTGTTTTTTGTTAC<br>CACG  | CCCGTTACAAATTTGC<br>GAGT | 60.4                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                             | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                           |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold296_P4_261040 | scaffold296                             | 261040                        | ATTTTTTTT/ATTTTTTTTTT                                                                                                                     | TCATGCCGACCTCATA<br>ACTTT | TGGCTTCAAGCTCAAC<br>CTCT   | 59.6                             | 596                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_261415 | scaffold296                             | 261415                        | AGAGGGAG/AGAG                                                                                                                             | CATTGTGGGAGCGTAA<br>GACA  | TCGCAACTCTCATGTG<br>TATGG  | 59.7                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_261628 | scaffold296                             | 261628                        | TACACACACAC/TACACACACAC                                                                                                                   | CATTGTGGGAGCGTAA<br>GACA  | TCGCAACTCTCATGTG<br>TATGG  | 59.7                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_305443 | scaffold296                             | 305443                        | TT/TTTAAAT                                                                                                                                | AGCTTCAAGGCAATGG<br>GATA  | TGGTGCCATTGAAGAT<br>GAAA   | 59.7                             | 672                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_337650 | scaffold296                             | 337650                        | AATTATTATTATTATTATTATTAT<br>TATTATTA/AATTATTATTATTATTAT<br>TATTATTATTATTA                                                                 | ACGAAAATTCACGTCG<br>AACA  | GGAGAATGATACGAGG<br>GTGG   | 59.2                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_382732 | scaffold296                             | 382732                        | A/ACTG                                                                                                                                    | TCTTGCGTCTCCCTC<br>TAAA   | TGCTAGACACAACACG<br>AACAAA | 59.9                             | 270                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_384155 | scaffold296                             | 384155                        | GATATATATATATATATATATATA/<br>GATATATATATATATATATATA                                                                                       | TCATCAATAACATTGAG<br>CGGA | AACACTTTGCTTGCT<br>GACA    | 59.1                             | 272                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_387866 | scaffold296                             | 387866                        | AATATATATATATATATATAT/AAAT<br>ATATATATATATATATAT                                                                                          | AAAGACCGGTGTTGGA<br>GTCA  | ACCTAAGGCCGACACA<br>AATG   | 60.5                             | 317                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_406805 | scaffold296                             | 406805                        | GTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTAATTATT<br>ATTAT/GTTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTAATTATTATTATTAT | AGTTATTACGACGCA<br>CGGG   | GGCACGACATCATCAT<br>CATC   | 60.0                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold296_P4_439780 | scaffold296                             | 439780                        | CAAAA/CAAA                                                                                                                                | AAAAGGCGACCTAGGG<br>AAAA  | GATTCGTGTGTTATGC<br>ACCG   | 60.1                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold296_P4_454518 | scaffold296                             | 454518                        | CTTTTTTTTTTT/CTTTTTTTTTT                                      | GCACGCCAAGAAGTAG<br>TCGT | TTGAAAAATTCAAAATC<br>TCGCA | 60.5                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold2969_P4_32761 | scaffold2969                            | 32761                         | CA/CAA                                                        | GTCATGGACCCACTT<br>TCCA  | TCCAGATAAAGTGAGG<br>ACAGCA | 60.8                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold298_P4_14439  | scaffold298                             | 14439                         | ATTT/ATT                                                      | TTACACCAAATCCTTTG<br>CCC | GAGCCCAACAGTTCCA<br>TGAT   | 59.8                             | 792                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold298_P4_156072 | scaffold298                             | 156072                        | GTTTTTT/GTTTTT                                                | ACCCAATTACTGGAGA<br>TGCG | AGTCAGTGGCAAAAC<br>AGCA    | 60.0                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold298_P4_208119 | scaffold298                             | 208119                        | GTTTTTTTT/GTTTTTTTT                                           | AGTCGGAGGTTCTAG<br>CACA  | ATTGTTGGGCTTGTC<br>GTCC    | 59.9                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold298_P4_208171 | scaffold298                             | 208171                        | TTATATATATATA/TTATATATATATA<br>TATATA                         | AGTCGGAGGTTCTAG<br>CACA  | ATTGTTGGGCTTGTC<br>GTCC    | 59.9                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold298_P4_2633   | scaffold298                             | 2633                          | AAT/ATAT                                                      | CATCCACCCCTCTAAA<br>CCAA | TCGATTGATAGACCTT<br>GCATTT | 59.8                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold298_P4_3669   | scaffold298                             | 3669                          | TAAAAAA/TAAAAAA                                               | AACCGACACTCAACCC<br>ACTC | TGTTGGCGAAATCGTT<br>GTTA   | 60.0                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold298_P4_76407  | scaffold298                             | 76407                         | ATTTTTTTTT/ATTTTTTTTT                                         | GTTCAAACAACACGCT<br>CACG | GATTGGACTTGTCGCT<br>TGCT   | 60.3                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold298_P4_8123   | scaffold298                             | 8123                          | TGA/T                                                         | AAATGAAAAGTGGCGA<br>GGAC | AGTTACCCATTTGTGG<br>CAGC   | 59.2                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)        | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                       |                           |                          |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| scaffold298_P4_8968   | scaffold298                             | 8968                          | ATT/ATTTT                                                             | GCTGCCACAAATGGGT<br>AACT  | CCAAAAACGGTGACGA<br>AACT | 60.0                             | 771                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold298_P4_9591   | scaffold298                             | 9591                          | TAAAA/TAAA                                                            | AGTTTCGTCACCGTTTT<br>TGG  | CTCAAAGGGGCTAGCA<br>AATG | 60.0                             | 672                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold299_P4_112757 | scaffold299                             | 112757                        | GATATATATATATATATATATATA<br>TATATAT/GATATATATATATATAT<br>ATATATATATAT | AAAAACATTCGGGTT<br>GCTG   | CCGATAAAATCTCTGCT<br>CGC | 60.0                             | 628                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold299_P4_27346  | scaffold299                             | 27346                         | GATAATAATAATAATAATAATAA<br>TAATAA/GATAATAATAATAATAA<br>TAATAA         | CTACC GCGATCAAATA<br>CGGT | CCCTTTTGCTTCTTGT<br>GGC  | 60.0                             | 977                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold299_P4_53102  | scaffold299                             | 53102                         | CAAAAAAAAA/CAAAAAAAAA                                                 | TGAAGGGTGTCACAAA<br>CCAA  | ATTCATGGTGCTTTCTT<br>GGC | 60.0                             | 313                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold299_P4_62956  | scaffold299                             | 62956                         | TTATATATATATATATATATA/TTATA<br>TATATATATATATATATA                     | TAACTAGCATCGCAGC<br>ATGG  | AATTGCGGCAGAGAA<br>GATA  | 60.0                             | 362                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold299_P4_63392  | scaffold299                             | 63392                         | AATATATATATATATATATATAT<br>ATATA/AATATATATATATATATAT<br>ATATATATATATA | AAATATCTTCTCTGCC<br>GCA   | CTGAGATGCAGCGTTT<br>TTCA | 59.9                             | 528                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold2998_P4_2970  | scaffold2998                            | 2970                          | TAAAAAAA/TAAAAA                                                       | TTGGATGCACAAATT<br>GGTT   | GAAAAACAAGACCCGC<br>GATA | 58.9                             | 521                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold30_P4_120537  | scaffold30                              | 120537                        | C/CAAAAGAT                                                            | GCCTAGGGAGGAGGA<br>AAATG  | TAACCAATCTTGTGCAC<br>CCA | 60.0                             | 769                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold300_P4_101499 | scaffold300                             | 101499                        | AC/A                                                                  | CGATTGTGTTTGTAC<br>AGGG   | GCACCCTGTTTTGAG<br>GGTA  | 60.0                             | 193                                           | INTERGENIC                                  | --                               | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome:<br>CDC Frontier/PII)                                                   | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                 |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold300_P4_74648  | scaffold300                             | 74648                         | TG/T                                                                                                            | AAAACACGCCTATTGG<br>ATGC     | AGGTCATTTTCGTCCTC<br>CCT   | 60.0                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3015_P4_73264 | scaffold3015                            | 73264                         | TGGCATAG/TG                                                                                                     | TTTGTGTTTGCGATGA<br>CGAT     | TAAGAGCGGAGTTTCT<br>CCCA   | 60.1                             | 792                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3015_P4_73454 | scaffold3015                            | 73454                         | TTTTGACTTTGACTTT/TTTTGACTTT<br>GACTTTGACTTT                                                                     | GTCTCGCGTTGAGTTA<br>AGGG     | TAAGAGCGGAGTTTCT<br>CCCA   | 59.9                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3015_P4_73940 | scaffold3015                            | 73940                         | TG/T                                                                                                            | TGGGAGAAACTCCGCT<br>CTTA     | TGATGGCTCCAAGGTG<br>TATG   | 59.9                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3015_P4_74020 | scaffold3015                            | 74020                         | AAAATCATA/AA                                                                                                    | TGGGAGAAACTCCGCT<br>CTTA     | TGATGGCTCCAAGGTG<br>TATG   | 59.9                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3015_P4_74169 | scaffold3015                            | 74169                         | TTT/TTTCTT                                                                                                      | TTTGGAAATTTAGGGTG<br>TCACG   | TGATGGCTCCAAGGTG<br>TATG   | 59.0                             | 221                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3015_P4_76583 | scaffold3015                            | 76583                         | CTTTTTTTT/CTTTTTTTTTT                                                                                           | GGCTAAATTACATCTGT<br>GGTCCTT | TGAAAGAGAAAGGGCT<br>TGGA   | 59.8                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3015_P4_76843 | scaffold3015                            | 76843                         | CAAAA/CAA                                                                                                       | TTTCCCGACTTGGTCC<br>TTTA     | TGAAAGAGAAAGGGCT<br>TGGA   | 59.5                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3016_P4_84878 | scaffold3016                            | 84878                         | AATATATATATATATATATATATAT<br>ATATATATATATATATATAT/AATATA<br>TATATATATATATATATATATATAT<br>ATATATATATATATATATATAT | CTGTTGCGTAAGGAAA<br>AGGC     | TTAAACATTTTCAACT<br>TGTCCC | 59.9                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3021_P4_2998  | scaffold3021                            | 2998                          | ATTTTTTTT/ATTTTTTTT                                                                                             | TGGTTTGTGCGATGAG<br>AGAG     | TCACGCAGAAAGCAAA<br>ACAC   | 60.0                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3029_P4_14921 | scaffold3029                            | 14921                         | AGG/AGGG                                                      | GCGTTCAATTGGTGTG<br>TTTG  | GTCCTACCGTTTCGTA<br>CCCT     | 60.0                             | 721                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3033_P4_861   | scaffold3033                            | 861                           | ACC/ACCC                                                      | AGTCTAGGGTGGGCGA<br>AAAT  | AGGTTGGTTTCAATGC<br>GAAG     | 60.0                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3046_P4_14446 | scaffold3046                            | 14446                         | AGGG/AGG                                                      | TTGGATGAACATTTCG<br>GTCA  | AAGCCTAGGGAGGACG<br>AAAA     | 59.9                             | 240                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold305_P4_53694  | scaffold305                             | 53694                         | GTAAAAAATTAAAAATTAAAAATT<br>AAAA/GTAAAAAATTAAAAATTAAA<br>AA   | GGTCAATTTAACATTG<br>GGTCG | TTTTTCCGAAATCAAA<br>TCA      | 59.2                             | 822                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3051_P4_18903 | scaffold3051                            | 18903                         | CAAA/CAA                                                      | TGCTTAGGTTGCTGTT<br>GTGC  | CAGTGTTGACAAGGGG<br>TGTG     | 60.1                             | 332                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold306_P4_126424 | scaffold306                             | 126424                        | CA/CAGAAAA                                                    | TGCCTTTGTTTCTCGTT<br>CAA  | TTTCTCATATGGACTTG<br>TTTTGC  | 59.4                             | 219                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold306_P4_128535 | scaffold306                             | 128535                        | TA/T                                                          | ACCGAAAGGAGAACAC<br>ATGG  | TGCAAAATGAAAGTTTAA<br>AGACCA | 60.0                             | 240                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold306_P4_130271 | scaffold306                             | 130271                        | GAAAAAAAAA/GAAAAAAAAA                                         | TGCAAAATTCATCAAAT<br>CCA  | CGTAGCCTTTGTTTGT<br>GCTG     | 57.5                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold306_P4_166393 | scaffold306                             | 166393                        | TAAATCGATTG/TAAATCGATTGGGA<br>AATCGATTG                       | TGCACAAGTCAGTAGC<br>ACCC  | GCCAATCGATTACCCT<br>CAAA     | 59.9                             | 138                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold306_P4_224431 | scaffold306                             | 224431                        | TAAAAAAAAA/TAAAAAAAAA                                         | TGCAGACGTAACAAGC<br>AACC  | TTTGATTTCCTTCA<br>ACC        | 59.9                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)                                            | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                          |                                  | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------|----------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                           |                               |                           |                                  |                                               | Sequence components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| scaffold306_P4_227906 | scaffold306                             | 227906                        | TTATATATATATATATATATATATA<br>TAT/TTATATATATATATATATATATA<br>TATATATATATATATATATATATAT                     | CACCGAAATCATAATG<br>CAAGAA    | TGTGAGACGCAAAAAT<br>AACCC | 60.0                             | 688                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold306_P4_292591 | scaffold306                             | 292591                        | AAGAGAGAGAG/AAGAGAGAG                                                                                     | GAATTGGTGGGGAGGA<br>ATTT      | CGACGCACGAGTTACA<br>CACT  | 60.0                             | 479                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold306_P4_325539 | scaffold306                             | 325539                        | AA/AATATATATA                                                                                             | CAATGCTTGATGTTAG<br>ATCGGA    | TGATGAATCCAACAAC<br>CACG  | 60.1                             | 699                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold306_P4_325934 | scaffold306                             | 325934                        | TG/TGAAG                                                                                                  | AGCGTGGTTGTTGGAT<br>TCAT      | AGGACGGACCTTTTTTC<br>TCGT | 60.4                             | 396                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold306_P4_336722 | scaffold306                             | 336722                        | CTATTA/C                                                                                                  | TTGGAATTCGATGAT<br>CCATT      | AAAGGCATT CATCTCCA<br>TCG | 59.2                             | 438                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold306_P4_423378 | scaffold306                             | 423378                        | TACAACAAC/TACAAC                                                                                          | GCTCGACACACTATGC<br>GAAA      | TTTAGCGTCCCAAATT<br>GCT   | 60.0                             | 572                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold306_P4_45035  | scaffold306                             | 45035                         | CTTTGATTTTTG/CTTTG                                                                                        | TGATGATGTCTCACA<br>ACTGAAAA   | GGCAATAAATTTGCT<br>CATCC  | 59.7                             | 552                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold306_P4_46960  | scaffold306                             | 46960                         | CTAATATA/CTA                                                                                              | AATACCCGTCCCCATA<br>CTCC      | CATCTGGCCTAGACCA<br>AGTCA | 59.9                             | 880                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold306_P4_481879 | scaffold306                             | 481879                        | A/AT                                                                                                      | CGGAATTTAAATCAAA<br>GTTTTCTCA | ACAAGCGAGGCATATG<br>AAGA  | 59.9                             | 249                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold306_P4_485459 | scaffold306                             | 485459                        | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAAA/AAATAAT<br>AATAATAATAATAATAATAATAAA<br>TAATAATAATAATAATAA | GGAATCCCGTGTTTT<br>GAGA       | AGAGGCCAACAAAGAAC<br>CGAA | 59.9                             | 553                                           | INTERGENIC                                     | --                               | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold306_P4_56215  | scaffold306                             | 56215                         | AC/A                                                          | GAATGTGCCACTTCCA<br>ACCT    | AAAATGTCCTTTGGTGT<br>GGC | 60.0                             | 946                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold306_P4_56884  | scaffold306                             | 56884                         | A/AC                                                          | GTCCAACGGATGCTTT<br>CAAT    | CTTTTTCGAATTTCCTC<br>ACA | 59.9                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold306_P4_60490  | scaffold306                             | 60490                         | CAA/CAAA                                                      | TGCTTCAACACTGACTT<br>GGC    | ATTCCCAATTGTTCCCT<br>TCC | 60.0                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold306_P4_64257  | scaffold306                             | 64257                         | GT/GTT                                                        | CTGGTCAATTTTGGC<br>ATGA     | TATGTTAAGCAACCCC<br>CTGG | 59.5                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold306_P4_6432   | scaffold306                             | 6432                          | TAATAAATAAATAAATA/TAATAAATA<br>AATAAATAAATA                   | TCAAACCCGGGTGTCT<br>TAAT    | CGCATAATCGACTCCC<br>AAAT | 59.3                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3061_P4_604   | scaffold3061                            | 604                           | GTA/GTATAGTTAATACATA                                          | AGGCAACAAGATATGT<br>GGGC    | TCTTGTGGAAGGAAGC<br>TCGT | 60.0                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3082_P4_10375 | scaffold3082                            | 10375                         | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                 | GCCCTCAGATGAGAGT<br>CAGG    | CCATCAGCATAACCCC<br>ACAT | 59.9                             | 716                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3092_P4_1124  | scaffold3092                            | 1124                          | TAAAAAAA/TAAAAAAA                                             | GAGGTATTTTACAGCG<br>CTCTTTC | TTGGGTCTGAAGAATG<br>GCTC | 58.7                             | 117                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3093_P4_19732 | scaffold3093                            | 19732                         | GATATATATATATAT/GATATATATAT<br>ATATAT                         | GAACCTCACAATCAC<br>ACGA     | GAGCGCTGTAAACAC<br>CTCC  | 59.5                             | 863                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold310_P4_39808  | scaffold310                             | 39808                         | TGGG/TGG                                                      | TGTTCCCTTGACTG<br>ATTG      | AAGCCTAGGGAGGACG<br>AAAA | 59.9                             | 216                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                          | Forward primers (5'-3')        | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------|--------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                        |                                |                             |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold311_P4_23991  | scaffold311                             | 23991                         | TG/T                                                                                                                                   | TTTTCGTCTCCCTAG<br>GCTT        | GCCAATGACACAAACA<br>CACC    | 60.2                             | 455                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold311_P4_91768  | scaffold311                             | 91768                         | CAAAAA/CAAAA                                                                                                                           | TGGGCAAGAAAAAGCC<br>TATG       | AGGTCATTTTCGTCTC<br>CCT     | 60.2                             | 836                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold3115_P4_46887 | scaffold3115                            | 46887                         | TC/T                                                                                                                                   | TGTCTACATTTCTCTT<br>TTCATCTTGA | TTTCTAAATCGTTTCT<br>TGCCCC  | 59.7                             | 600                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold3115_P4_49667 | scaffold3115                            | 49667                         | AATATATATATATATATATATAT/A<br>ATATATATATATATATATATATAT                                                                                  | GAATCTTACCATCGAG<br>GGGC       | TGACTTTGTAATGAAG<br>GTGAGGC | 60.8                             | 233                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold3115_P4_55767 | scaffold3115                            | 55767                         | TATACATACATACATACATACAT/A<br>ATACATACATACATACATACAT<br>A                                                                               | TGCATGTCCCTCAAAG<br>GTAA       | TCATTTGCTTACAAAG<br>CCC     | 59.1                             | 830                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold3115_P4_62578 | scaffold3115                            | 62578                         | ATTTTTTTTTTT/ATTTTTTTTTTT<br>T                                                                                                         | CTTGGTGGTCCACTAT<br>GTGC       | GGAGGTCAAATACTA<br>ACTGCGA  | 59.0                             | 594                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold3115_P4_62639 | scaffold3115                            | 62639                         | CTTTTTTT/CTTTTTTTT                                                                                                                     | CTTGGTGGTCCACTAT<br>GTGC       | TTCATAGGAGGCTGCC<br>ATTG    | 59.0                             | 632                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold3115_P4_62933 | scaffold3115                            | 62933                         | TTTATTATTATTATTATTATTATT<br>ATTTTATTATTATTATTATAATT<br>ATTATTATTA/TTTATTATTATTATTA<br>TTATTATTATTTTATTATTATTATTA<br>TTATAATTATTATTATTA | CTTGGTGGTCCACTAT<br>GTGC       | TTCATAGGAGGCTGCC<br>ATTG    | 59.0                             | 632                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold3115_P4_63986 | scaffold3115                            | 63986                         | AATATATATATATATATATATATATA<br>ATA/AATATATATATATATATATAT<br>ATATATATA                                                                   | TGAAGCATATGCCGTG<br>AGAG       | GCGTCAATGAACTTTA<br>CATGC   | 60.0                             | 559                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold3115_P4_69161 | scaffold3115                            | 69161                         | CTATA/CTA                                                                                                                              | GGGCAGGCTAGATTGA<br>AAGTC      | TGTTTTGGCGATACAC<br>CTCA    | 60.2                             | 699                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)            | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                          |                             |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3115_P4_7166   | scaffold3115                            | 7166                          | AATATATATATATATATATATATATATATATATATAT/AATATATATATATATATATATATATATATAT    | AAAACATGAATTGATTG<br>TCACGA | GTGGATTGCACACGTT<br>TTTC | 59.4                             | 335                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3118_P4_5186   | scaffold3118                            | 5186                          | ATTT/ATT                                                                 | AGGGAGGTGGAATG<br>ACCT      | TGCGTCATTGGATGAA<br>CATT | 59.8                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3121_P4_6428   | scaffold3121                            | 6428                          | ATTT/ATT                                                                 | AACTTTTCCGCTGCTT<br>GAA     | ATATGCTTGAGGGGCA<br>TCAG | 60.0                             | 160                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3127_P4_10029  | scaffold3127                            | 10029                         | TGAT/TGATCCACAAGATTGGAT                                                  | AGGGAGGACGAAATG<br>ACCT     | TGTGCGTCCAATAGGT<br>GTGT | 59.9                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3127_P4_2181   | scaffold3127                            | 2181                          | AC/A                                                                     | GGAAGCACAAGATGGG<br>GTAA    | CGGTCATTTTCTCCTC<br>CCT  | 59.9                             | 265                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3127_P4_8863   | scaffold3127                            | 8863                          | A/AT                                                                     | AATCCAATGGCACAAA<br>CACA    | GGACATTTTCGTCCTG<br>CCTA | 59.8                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold313_P4_10968   | scaffold313                             | 10968                         | TGGTTTAGGGTTTAGGGTTTAGGG<br>TTTAGGGTTTA/TGGTTTAGGGTTTA<br>GGGTTTAGGGTTTA | GCTTCGGTGCTTGGTT<br>TTAG    | ACCCGAAACGCAAAAC<br>ACTA | 59.9                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold313_P4_511     | scaffold313                             | 511                           | GTTTAGGCTTTAG/GTTTAGGCTTTA<br>GGCTTTAG                                   | TTAGGGTTTAGGGCTT<br>GGGT    | AACCATAATACCGAAC<br>GCA  | 59.8                             | 177                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3134_P4_109334 | scaffold3134                            | 109334                        | AATATATATATATATATATATAT/AAT<br>ATATATATATATAT                            | AGGAAGAGTGGAGTTG<br>CGAA    | TTAATGTGTTGCGGGT<br>GAAA | 60.0                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3134_P4_4696   | scaffold3134                            | 4696                          | TGAAAC/TGAAACGAAAC                                                       | TGTTAGGAGGATCTCA<br>CGGG    | TCGATCGATTCCCAAA<br>CTC  | 60.1                             | 805                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                  | Forward primers (5'-3')  | Reverse primers (5'-3') | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------|--------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                |                          |                         |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| scaffold3135_P4_4161  | scaffold3135                            | 4161                          | TCC/TC                                                                                         | TCCAGATGAAATCGAG GACC    | CCCCAAAAGTCCAGAT GAAA   | 60.0                             | 882                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold314_P4_127594 | scaffold314                             | 127594                        | ATTTTTTTTTTT/ATTTTTTTTTTTT                                                                     | GGCATTTGTTAACGAA CTAAAAA | CAGAAACTGAACCAAC CCGT   | 57.6                             | 872                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold314_P4_131593 | scaffold314                             | 131593                        | AATATATATATATATATATATATATAT ATATATATATATATATAT/AATATATA TATATATATATATATATATATATATAT ATATATAT   | AGCAATTTGGGTTGTT GAGG    | TCACAACCTCATGCAT AAATC  | 60.0                             | 620                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold314_P4_1870   | scaffold314                             | 1870                          | GAAAAAAAA/GAAAAAAAAAAAAA A                                                                     | GCCCTCAGATGAGAGT CAGG    | AAACGCAATCCTTGAG TTCG   | 59.9                             | 509                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold314_P4_233208 | scaffold314                             | 233208                        | ATATATATATATATATATATATATATA TATATATATATATAT/ATATATATATA TATATATATATATATATATATATATAT ATATATATAT | CTTTCAGAATGAAGGG TC GG   | GGGAATGTCTTCATCC AAGG   | 59.7                             | 625                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold314_P4_272639 | scaffold314                             | 272639                        | CTATATATATATATATATATAT/CTAT ATATATATATATATAT                                                   | CCTATGGCCTGGCCTA CATA    | CCTGATGTGTAATAGG GCAATG | 59.9                             | 223                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold314_P4_273842 | scaffold314                             | 273842                        | TTA/T                                                                                          | AAACCTTGAAAACCTA ATTGTT  | GCCTGGCCTGTAAGCC TATT   | 57.3                             | 822                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold314_P4_294507 | scaffold314                             | 294507                        | AATATATATATATATATATATATATAT ATATATA/AATATATATATATATATAT ATATATATATATATATATATATATA              | ATACAAGGGTGATTGG CGAG    | AGAGTGTGATGGAGGG TTGG   | 60.0                             | 675                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold314_P4_512009 | scaffold314                             | 512009                        | CAGA/CA                                                                                        | GCAAACAAGCACAAACC ATTG   | CATGCATGGCTAAAGC AAGT   | 60.2                             | 379                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold314_P4_512200 | scaffold314                             | 512200                        | GA/G                                                                                           | GCAAACAAGCACAAACC ATTG   | TGGCTGTTGCCACACT CTTA   | 60.2                             | 862                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3149_P4_9644  | scaffold3149                            | 9644                          | TAG/TAGGAG                                                    | TTTCATCTGGACTTTTC<br>GGG    | ATCGTCGATGGGTACG<br>AAAG  | 60.0                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3155_P4_5924  | scaffold3155                            | 5924                          | CTT/CTTATT                                                    | AATTGGCATCTCACGG<br>GTAG    | CTCAATGTAGTCACGC<br>CACG  | 60.0                             | 310                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3160_P4_10108 | scaffold3160                            | 10108                         | GTTTTTTTTTTT/GTTTTTTTTT                                       | ATCACACAAATCACCA<br>GCCA    | TCTTCAGTCCAAGTCAA<br>ATCG | 60.0                             | 335                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3160_P4_10499 | scaffold3160                            | 10499                         | AG/AGG                                                        | TGGCTTTTGTAGTTAGA<br>GCACCA | GCAAACAAAGGAAACG<br>GAAA  | 59.1                             | 629                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3160_P4_7888  | scaffold3160                            | 7888                          | ATTTTTTTT/ATTTTTTTTTTT                                        | AACGGACGATGTAAGG<br>TGGT    | GTCTGCGAAAAAGGAG<br>CAAC  | 59.3                             | 141                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3160_P4_9833  | scaffold3160                            | 9833                          | TGG/TG                                                        | AACCAGTCACTCAAGC<br>GTCC    | TGGCTGGTGATTTGTG<br>TGAT  | 60.3                             | 165                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3163_P4_1133  | scaffold3163                            | 1133                          | CG/CGG                                                        | GCCTGTGATAGGCGGT<br>ACAT    | ATTCCAAACCAAAACCC<br>TCC  | 60.0                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3164_P4_2274  | scaffold3164                            | 2274                          | ACC/AC                                                        | CGTATTTTCGGGGAAGA<br>GTCA   | TCGAGATTGTGTGCAA<br>GGAG  | 60.1                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3168_P4_514   | scaffold3168                            | 514                           | CAGTAG/CAG                                                    | AGTGAAACCAACGCCA<br>AAAC    | ATTCCCCACCCAAATAC<br>CTC  | 60.0                             | 761                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold317_P4_102437 | scaffold317                             | 102437                        | ATT/AT                                                        | TGTCTCATGGCAAATA<br>CCGA    | TGCCTATGTACCAATT<br>CCA   | 60.1                             | 826                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold317_P4_181016  | scaffold317                             | 181016                        | CT/C                                                          | TCTTGCATGGCAACTA<br>TCCA  | CAGCCCCTAGAACTCC<br>ACAG  | 60.2                             | 730                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold317_P4_203820  | scaffold317                             | 203820                        | AATATATATATATATATATA/AATA<br>TATATATATATATATATATA             | GAAATTTTGACGGAAA<br>CGGA  | AACGACTGTAAACACGC<br>CAAA | 59.9                             | 974                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold317_P4_209733  | scaffold317                             | 209733                        | T/TC                                                          | TGTTGTTGTGATTGTG<br>CCCT  | CAGGATGTCAGCAGCA<br>AAAA  | 60.0                             | 243                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold317_P4_80876   | scaffold317                             | 80876                         | TAA/TAAA                                                      | ACACAATTCCCTCAGG<br>AACG  | GTGGCACCTCGGTAAA<br>CAGT  | 60.0                             | 320                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3170_P4_106196 | scaffold3170                            | 106196                        | CTATATATATATATATAT/CTATAT<br>ATATATATATATATAT                 | GGAATAAGGCGGGTGT<br>ATCA  | TCACAATGAAACAAG<br>GGCA   | 59.8                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3170_P4_130115 | scaffold3170                            | 130115                        | CAA/CAAA                                                      | CACCCTCGCTTAGAGA<br>AACG  | TTTACCTCAGCCATGT<br>GGG   | 60.0                             | 321                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3170_P4_15363  | scaffold3170                            | 15363                         | CATATATATATATATATATAT/CAT<br>ATATATATATATATATATAT             | AAAGGCATATGCGGAC<br>TGAT  | ACACATTCTTCCAAGC<br>ACC   | 59.6                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3170_P4_63184  | scaffold3170                            | 63184                         | GAAAAAAAA/GAAAAAAAAA                                          | CCATTATTTTCATGGGG<br>CCTA | AAACAAGAAAGGGAAG<br>GGGA  | 59.6                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3170_P4_90840  | scaffold3170                            | 90840                         | TTTATTATTATTATTATTATTATT<br>/TTTATTATTATTATTATTATT            | TGGTTTAACCGGTCGA<br>AAAG  | CCTCCAAACTCCCAAA<br>CAAA  | 60.0                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3171_P4_2201   | scaffold3171                            | 2201                          | CTTCTTCTCAATT/CTTCTTCTCAAT<br>TTCATTTCTTCTCAATT               | TATGTGGATGCATCAA<br>TGCC  | CCTTCTCTCAATCCTCCA<br>TCA | 60.3                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3171_P4_2398 | scaffold3171                            | 2398                          | C/CTA                                                         | TGATGGAGGATTGAGG<br>AAGG   | GTTGACAAATGCAAAAT<br>GCG  | 60.0                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3171_P4_2647 | scaffold3171                            | 2647                          | ATTTTTTT/ATTTT                                                | TGATGGAGGATTGAGG<br>AAGG   | GTTGACAAATGCAAAAT<br>GCG  | 60.0                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold319_P4_5560  | scaffold319                             | 5560                          | ATTTTTTT/ATTTTTTT                                             | ATAACCCGAACCTCAA<br>ACCC   | GGTCCTCGATTTCATCT<br>GGA  | 60.1                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold321_P4_36107 | scaffold321                             | 36107                         | AC/A                                                          | AGGGAGGACGAAAATG<br>ACCT   | CTTGGCGTCCAATAG<br>ATGT   | 59.9                             | 862                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3212_P4_1519 | scaffold3212                            | 1519                          | GAAAAAAAA/GAAAAAAAAA                                          | AATGACATTTGTCCCC<br>GTAGA  | ATCGGTGGCATGTCTCT<br>TACT | 59.3                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3212_P4_1828 | scaffold3212                            | 1828                          | TAATCTAA/TA                                                   | GCAGAAATTAATGA<br>GTGGTGTG | TGGAAGGTGGAGGTTT<br>AGAG  | 59.9                             | 715                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3212_P4_2564 | scaffold3212                            | 2564                          | A/AC                                                          | TGAACCTCCACCTTCC<br>ATTC   | CAACAAATGAGTGGC<br>GATG   | 59.9                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3212_P4_3813 | scaffold3212                            | 3813                          | GTT/GTTT                                                      | GTGGCCATTGTTCCAA<br>GAGT   | GTATGCATGAATTACG<br>GGGG  | 60.0                             | 728                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3212_P4_6334 | scaffold3212                            | 6334                          | ATTTTTTTT/ATTTTTTT                                            | GAGCACATGATCTCGC<br>AGAA   | CACTGCTGAAGCGGAA<br>TACA  | 60.1                             | 213                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3212_P4_725  | scaffold3212                            | 725                           | CTT/CTTTT                                                     | CGAGTCGTGCTTGAT<br>AATGGA  | CCCATTAGTGGTGATG<br>CTCC  | 60.1                             | 125                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3217_P4_4318  | scaffold3217                            | 4318                          | ATATATATTTA/ATA                                               | CTAGCAGAAGCAAGGC<br>ATCA   | ATCCCCATCAATTTGG<br>ACA   | 59.3                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3217_P4_4699  | scaffold3217                            | 4699                          | TTA/TTACTATA                                                  | CGCTTTGCCCTTAGTT<br>TGAG   | ATCCCCATCAATTTGG<br>ACA   | 60.0                             | 298                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold322_P4_54117  | scaffold322                             | 54117                         | AC/A                                                          | AGAAGATTAGCATGGC<br>CCCT   | TGCATTTTAACAATGTT<br>GGCA | 60.1                             | 295                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold322_P4_54129  | scaffold322                             | 54129                         | CTTTTTTTTT/CTTTTTTTTTTT                                       | AGAAGATTAGCATGGC<br>CCCT   | TGCATTTTAACAATGTT<br>GGCA | 60.1                             | 295                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold322_P4_77924  | scaffold322                             | 77924                         | GTTGATATTTTG/GTTGATATTTGA<br>TATTTTG                          | TTAGGAATCGAACCCG<br>TGTC   | TCCTTGAAGACAAGCA<br>ACCA  | 59.9                             | 346                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3225_P4_24908 | scaffold3225                            | 24908                         | ACC/ACCC                                                      | ACTGCCAGCAACAAAG<br>GTTC   | AAGGAAGCTCTGGGACA<br>CCCT | 60.3                             | 338                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3228_P4_1858  | scaffold3228                            | 1858                          | CATA/CATATA                                                   | TCAGCTTTTTGGCTGA<br>TGTG   | CTTGTGGATTGGGTCT<br>TGTG  | 60.0                             | 247                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3228_P4_619   | scaffold3228                            | 619                           | TCCCCC/TCCCCC                                                 | GGCTTAATTGCAGTTTT<br>GGTTC | GCAGTTTTGGTCCCC<br>TATT   | 60.0                             | 339                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3229_P4_5378  | scaffold3229                            | 5378                          | TA/TATTGCA                                                    | AGCTGAAATCCACAA<br>GGCA    | GATAATGGCCGCATGA<br>AAAG  | 60.8                             | 366                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3229_P4_6703  | scaffold3229                            | 6703                          | GAAAAAAA/GAAAAA                                               | CAACGATTAGCCATT<br>GTTGA   | TTGATGCCTCTTGGCT<br>CTTT  | 58.7                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')         | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|---------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                   |                                 |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3229_P4_8934  | scaffold3229                            | 8934                          | GATATATATATATATATATATATATATATATATAT/GATATATATATATATATATATATATATAT | TGAAGCACAAATGTTGG<br>TTTTG      | TGTAAAGTGCAACACC<br>CGTC      | 59.6                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3234_P4_11746 | scaffold3234                            | 11746                         | CAAAA/CAAAA                                                       | CATGCACCTTGAAAGG<br>GTTT        | TTGGCAAGTGTGGATG<br>TTGT      | 60.0                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold324_P4_144840 | scaffold324                             | 144840                        | AT/A                                                              | CGTTGAACTGTAAAC<br>GGTGA        | GGGACTTTCGTACCAC<br>CAGA      | 58.7                             | 765                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold324_P4_161480 | scaffold324                             | 161480                        | C/CAA                                                             | TTTGACAACTCAATTTT<br>GTTATATGTT | CGTTTTATGGTTTACT<br>ACACAACGA | 57.5                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold324_P4_22984  | scaffold324                             | 22984                         | T/TAC                                                             | CGGAACCCGAAACAAA<br>GTTA        | TGCATAACGAATACAGT<br>AAAAGCA  | 60.0                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold324_P4_350218 | scaffold324                             | 350218                        | CAAAA/CAAAA                                                       | GTACGAAAATTGCCCG<br>AAAA        | AGTTTCGAACCAAACG<br>ATGG      | 59.9                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold324_P4_63390  | scaffold324                             | 63390                         | TAAA/TAA                                                          | CGCGTGTCTTGTTTTT<br>CTTG        | TGCATAATCGATTGGC<br>ACAT      | 59.5                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3242_P4_3411  | scaffold3242                            | 3411                          | GAAAA/GAAAA                                                       | GCTGTGGTGCCTTTGG<br>TTAT        | CCCGCCTGACAGTTAA<br>TCAT      | 60.0                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3243_P4_21197 | scaffold3243                            | 21197                         | CAGA/CA                                                           | CCACCACAAGACAATT<br>GTTGA       | GCACATGTCATAGTTC<br>GTTGG     | 59.5                             | 418                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3258_P4_41416 | scaffold3258                            | 41416                         | AT/A                                                              | TTTTTGTGTTGAATAC<br>ACGGTT      | TTTTTCCTCGAGTGCA<br>GCTT      | 58.5                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')    | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                   |                            |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3258_P4_46908 | scaffold3258                            | 46908                         | GAC/GACCGGCTACGTAC                                                                | ATGGCCCCATTATTGA<br>GGTT   | TGCACGAGTCTAATGA<br>GGGA       | 60.4                             | 696                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3258_P4_48852 | scaffold3258                            | 48852                         | TTATGT/TT                                                                         | ATGACACGGCTGAATG<br>TCAA   | ACGCACGTATGTTGTC<br>CAAA       | 60.1                             | 374                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3258_P4_48984 | scaffold3258                            | 48984                         | TG/T                                                                              | GATGAATGTGCCAACA<br>AACG   | TTCATCATGTTTGCAGC<br>CTC       | 60.0                             | 369                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3258_P4_52201 | scaffold3258                            | 52201                         | TA/T                                                                              | TTTTTGGGTCCCTATCA<br>ACTAA | TCCAACAATAATTTAAA<br>ACCTTACAA | 57.7                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3258_P4_66747 | scaffold3258                            | 66747                         | TACA/TA                                                                           | GAAAGCGCTGTAAAAG<br>GTGC   | TGATTTGCTGGGAAAT<br>GACA       | 60.0                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3258_P4_71440 | scaffold3258                            | 71440                         | CTATATATATATATATATATATAT<br>ATATATATAT/CTATATATATATAT<br>ATATATATATATATATATATATAT | GCAAGCGATATGTGAC<br>CCTT   | GATTCAACTGGCGATG<br>GTTT       | 60.1                             | 836                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3258_P4_74031 | scaffold3258                            | 74031                         | ATTTTTTT/ATTTTTT                                                                  | AACTTCCACACCTGTC<br>TCCG   | AATTCAAAAGAATGTCG<br>GCG       | 60.2                             | 726                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3258_P4_74657 | scaffold3258                            | 74657                         | CTTTTTTTTTTT/CTTTTTTTTTT                                                          | AATGCAATCGTCAGGA<br>CACA   | TATGGACCGGAAATGG<br>ATGT       | 60.1                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3258_P4_77550 | scaffold3258                            | 77550                         | CTTTTTT/CTTTTTT                                                                   | TGCATGCATGAAAGGA<br>AAAT   | GAAAGAAAAGAAAGAG<br>GGGAAA     | 59.1                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3258_P4_77609 | scaffold3258                            | 77609                         | CTTT/CTTTTTT                                                                      | TGCATGCATGAAAGGA<br>AAAT   | TCCCTCTTTAGCAAAA<br>TAATTGG    | 59.1                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                              | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                            |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3258_P4_77639 | scaffold3258                            | 77639                         | TATAAT/TAT                                                                                 | TGCATGCATGAAAGGA<br>AAAT     | TCCTCTTTAGCAAAA<br>TAATTGG | 59.1                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3258_P4_78313 | scaffold3258                            | 78313                         | GAAAAAAAAA/GAAAAAAAAAAA<br>AA                                                              | GATGAAGAGTTAGTTG<br>CACCTTGA | TCACATGATCGTTTTGG<br>CAT   | 59.8                             | 280                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3258_P4_81448 | scaffold3258                            | 81448                         | GTTTTTTTT/GTTTTTTTTT                                                                       | CCATATTGAATGCACAT<br>GGTC    | AAGGTCCAACCTCCAA<br>CGAA   | 58.7                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3283_P4_5175  | scaffold3283                            | 5175                          | CATATATATATATATATATATATA<br>TATATATATATA/CATATATATATATA<br>TATATATATATATATATATATATA<br>ATA | GTTGGTCCCTAGCAC<br>CGTA      | AGAAGGCCGAGTGAA<br>CAAA    | 60.0                             | 836                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold330_P4_10729  | scaffold330                             | 10729                         | AC/A                                                                                       | TTCCCTCATTCACTAT<br>GGC      | GTGCTCGAAATTTTGT<br>TCG    | 59.9                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold330_P4_8164   | scaffold330                             | 8164                          | TAAAA/TAAAA                                                                                | AGGAAGAGTGGAGTTG<br>CGAA     | AACAATCTCCCTCACA<br>ACAA   | 60.0                             | 775                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold331_P4_19367  | scaffold331                             | 19367                         | ATT/AT                                                                                     | ACATTCCCATCCACAG<br>GGTA     | AAAAACATGCAGGGAA<br>ATCG   | 60.1                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold331_P4_44264  | scaffold331                             | 44264                         | AAATTAA/AAA                                                                                | AAAACAAGTTTGCTCC<br>CCCT     | AGGACCAGCCCTGTTT<br>AGGT   | 60.0                             | 243                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3317_P4_3339  | scaffold3317                            | 3339                          | TGACGAC/TGAC                                                                               | GCATCTGTGTAGCCAT<br>CCA      | TAGTCAATTTTCGTCT<br>CCG    | 59.7                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold332_P4_194682 | scaffold332                             | 194682                        | GTTTTTTTT/GTTTTTTTTT                                                                       | TGTTACCCAATCGTTT<br>TGA      | TGTCGTGGGGGTGTG<br>ATAA    | 59.9                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                   | Forward primers (5'-3')        | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------|--------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                 |                                |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3321_P4_69689 | scaffold3321                            | 69689                         | TAA/TA                                                                                                                          | TCTTGCAGGAGCTTGG<br>ATT        | TGTGCCGACAATTAAC<br>CAAA    | 60.0                             | 681                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3321_P4_69753 | scaffold3321                            | 69753                         | AAAAAGAGAAAAGAGA/AAAAAGAG<br>A                                                                                                  | TCTTGCAGGAGCTTGG<br>ATT        | TGTGCCGACAATTAAC<br>CAAA    | 60.0                             | 681                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold333_P4_21781  | scaffold333                             | 21781                         | TGGG/TGG                                                                                                                        | GGTACGAAAATCGCCA<br>GAAA       | GACGTGGAACCCAAA<br>GAAA     | 60.1                             | 585                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold333_P4_39892  | scaffold333                             | 39892                         | T/TA                                                                                                                            | GTGTTTTCGGACCAGA<br>CGAT       | TTCGAAAATCACCCGA<br>AAAG    | 60.0                             | 298                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold333_P4_8945   | scaffold333                             | 8945                          | TCC/TC                                                                                                                          | GATGAAATCGAGGACC<br>AGGA       | GACTTTTCGAGCGATT<br>TCG     | 60.0                             | 299                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold333_P4_91813  | scaffold333                             | 91813                         | GAACAACAAC/GAACAAC                                                                                                              | GATGAAATCGAGGACC<br>AGGA       | GTGCCAGTCGATTGCC<br>TAAT    | 60.0                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3336_P4_39173 | scaffold3336                            | 39173                         | TAAAAAAAA/TAAAAAAAA                                                                                                             | TGAGATTGAATTGATAT<br>TGTGTTTGA | TCTCTTTCTCCTGCCCT<br>TCA    | 59.8                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3336_P4_718   | scaffold3336                            | 718                           | ATTT/ATT                                                                                                                        | TTGGAAGGAGCCCTTA<br>CCTT       | GCCAATTCCTCCTTT<br>CTC      | 60.1                             | 307                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3336_P4_8274  | scaffold3336                            | 8274                          | GATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATT/GATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATT | CGGCCGTTTCTAACAT<br>CATT       | TTGCTTTTGAAACCAAT<br>TTAGGA | 60.0                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3337_P4_21791 | scaffold3337                            | 21791                         | C/CA                                                                                                                            | AACCGCAAAACACTAA<br>AGCC       | TTGCGTTTCGGGTATA<br>TGGT    | 59.3                             | 300                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                             |                           |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold334_P4_58371  | scaffold334                             | 58371                         | CTATATATATATATA/CTATATATA<br>TATATATATA                                     | ACCTTGCTCCCTTACC<br>CACT  | TATTTTGATTTTGGCT<br>CGG      | 60.0                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold334_P4_94530  | scaffold334                             | 94530                         | CAA/CA                                                                      | TCAGAAAGCCATCCAG<br>CTCT  | TTTTCTGGTTTTGGGG<br>ACTG     | 60.1                             | 158                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3347_P4_1135  | scaffold3347                            | 1135                          | C/CA                                                                        | AATTCCAAACCAACC<br>CTCC   | GATGGGCCACAAGATG<br>ATTG     | 60.0                             | 300                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold335_P4_161368 | scaffold335                             | 161368                        | GA/GAA                                                                      | GCCTGTGTGGCTGGTT<br>TAAT  | TGCACCAATCAAACGT<br>CATT     | 60.0                             | 387                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold335_P4_191468 | scaffold335                             | 191468                        | ATT/AT                                                                      | ACTCGAGTCGTTTCGC<br>AAGT  | GGAATAAAAGTCCAAT<br>GCCG     | 60.1                             | 730                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold335_P4_38013  | scaffold335                             | 38013                         | TTATATATATATATATATATATATA<br>TAT/TTATATATATATATATATATA<br>TATATATATATAT     | AAAAACCAGGACGGAG<br>ACAT  | TTTCCAACAAACCACCA<br>ACA     | 58.5                             | 879                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold335_P4_88156  | scaffold335                             | 88156                         | GTTATTATTATTATTATTATTATT<br>ATTATT/GTTATTATTATTATTATTAT<br>TATTATTATTATTATT | TTGTCCTTCTGTGGCC<br>GACT  | TTTACAGGCGATTTC<br>GAGC      | 60.8                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3354_P4_665   | scaffold3354                            | 665                           | T/TA                                                                        | CAACACAATTGAGCTG<br>TCAAA | TCGTAAGTACAACCTC<br>AAAACGAA | 57.4                             | 585                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3354_P4_678   | scaffold3354                            | 678                           | ATTT/ATTTT                                                                  | CAACACAATTGAGCTG<br>TCAAA | TCGTAAGTACAACCTC<br>AAAACGAA | 57.4                             | 585                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold336_P4_186479 | scaffold336                             | 186479                        | AT/ATATATGT                                                                 | CGCGTTAACAGAGGAA<br>GAGG  | GCGGTGAATCTTTTAC<br>GAGG     | 60.0                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                         | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                       |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold336_P4_187063 | scaffold336                             | 187063                        | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATAT                                                                 | CCTCGTAAAAGATTCA<br>CCGC    | GAAGAAGAGTGAAGGT<br>GGCG | 59.7                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold336_P4_292805 | scaffold336                             | 292805                        | A/AT                                                                                                                  | TTCATCTTTTATCTTCA<br>TTCGGC | GCGCTGTTGTATCCTC<br>CATT | 59.6                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold336_P4_323635 | scaffold336                             | 323635                        | GAAAAAAA/GAAAAAA                                                                                                      | CCTCTGTGAGATTTTG<br>AGCCTT  | AAGGTTATAACGGGGC<br>CAAG | 59.9                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold336_P4_360914 | scaffold336                             | 360914                        | AG/ATTATGGG                                                                                                           | TGCACATTTTACAGCG<br>CTTC    | CTGGGCAAGGGATCTG<br>AATA | 60.0                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold336_P4_399884 | scaffold336                             | 399884                        | TG/T                                                                                                                  | GATCATCGAGTTTCCC<br>GTGT    | ACCATGCAAAGACATC<br>CACA | 59.9                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold336_P4_450339 | scaffold336                             | 450339                        | TT/TTATTATTAT                                                                                                         | GGCATTTTGGGATAGT<br>GGAC    | CAATTTTGTGTCGGTTC<br>GTG | 59.2                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold336_P4_617875 | scaffold336                             | 617875                        | AATATATATATATATA/AATATATA<br>TATATATATATA                                                                             | GGCAACGTGCATAAAC<br>AAAA    | TGTGAGTGTGGGAAAC<br>GGTA | 59.6                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold336_P4_633921 | scaffold336                             | 633921                        | A/AC                                                                                                                  | GAGAAAGGCAAGACCA<br>GTGC    | TTGCAATTCAACTGATG<br>GGA | 60.0                             | 365                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3362_P4_60804 | scaffold3362                            | 60804                         | AATATATATATATATATATATATAT<br>ATATATATATATATATATATA/AAT<br>ATATATATATATATATATATATATA<br>TATATATATATATATATATATATAT<br>A | CAGCAACAAAGAAGGG<br>GGTA    | CGCTCAAGGATTCTTC<br>CCTT | 60.1                             | 844                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3364_P4_43644 | scaffold3364                            | 43644                         | T/TG                                                                                                                  | AGCCAAGGGAGGATGA<br>AAAT    | CGTCCACCCCTTGATTA<br>TCC | 59.9                             | 214                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                               | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                             |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3369_P4_17145 | scaffold3369                            | 17145                         | CTTTTTTTTTTTTT/CTTTTTTTTT<br>T                                                                                                              | TCGTAGTCGATCCCCT<br>TCTG  | CGGACTCAAGTTGTGA<br>TGGAA  | 60.2                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3369_P4_18856 | scaffold3369                            | 18856                         | T/TA                                                                                                                                        | TTCAACGTGACCTGCT<br>CATC  | ATGGGTCCAGGTCATC<br>TCAG   | 59.8                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold338_P4_76520  | scaffold338                             | 76520                         | GTATATATATATATATAT/ATATATAT<br>ATATATATATAT                                                                                                 | CTTGCCATAAAATCG<br>GAAA   | AGGATGCATGGGATGA<br>AAAG   | 59.9                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3396_P4_4608  | scaffold3396                            | 4608                          | GC/G                                                                                                                                        | TGGACAAAAACCAAAA<br>TGACG | GGGTTGAGGTTTAGG<br>GTTT    | 60.7                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3397_P4_20637 | scaffold3397                            | 20637                         | CT/CTT                                                                                                                                      | GAGAGAACGTGAGGAA<br>ACGC  | AGATCATGTGCAAAAA<br>GGGG   | 60.0                             | 512                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3397_P4_55203 | scaffold3397                            | 55203                         | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTAT/ATATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT | TTACTCACTTGCAACAC<br>GCC  | GGGAAGCAATGTTTTG<br>ATCC   | 59.9                             | 859                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3397_P4_66509 | scaffold3397                            | 66509                         | CAAAAA/CAAAAAA                                                                                                                              | AGAGCCACGTGTTGTC<br>ATTG  | TGTGAGTTTGCTCCCA<br>TCAC   | 59.8                             | 845                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3397_P4_67850 | scaffold3397                            | 67850                         | ATTTTTTTT/ATTTTTTT                                                                                                                          | TCATCGAGGGAATATC<br>GATTG | CACACAGCGAAAAATA<br>GTTTGG | 59.9                             | 750                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3397_P4_88653 | scaffold3397                            | 88653                         | GTTATTATTATTATTATTATTATT<br>TATTATTATTATTATTATT                                                                                             | CGGCAAAATATCAGAA<br>ACACG | AGGATGCGACCATTTA<br>CTGC   | 60.5                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_110171 | scaffold340                             | 110171                        | GTTTT/GTTTTT                                                                                                                                | TTTGATTGAAACCAATG<br>CCA  | ACTGATGAAATTGCGC<br>TCCT   | 59.9                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                         | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                       |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold340_P4_146001 | scaffold340                             | 146001                        | A/AT                                                                                  | CAACTTGGTCGCTAAG<br>CACA   | CAACCGCTAATCAGGT<br>CAAAA | 60.1                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_161360 | scaffold340                             | 161360                        | ATTTTTTT/ATTTTTTTT                                                                    | GCGGATATCGTAGGGT<br>GCTA   | TACATCCAGAAGGCTA<br>CCGC  | 60.1                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_161643 | scaffold340                             | 161643                        | TTTTATTTATTTATTT/TTTTATTTATT<br>TATTTATTT                                             | GCGGATATCGTAGGGT<br>GCTA   | TCACAAGGGAGGCTCT<br>ATGG  | 60.1                             | 694                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_164421 | scaffold340                             | 164421                        | TAAAAAAAAA/TAAAAAAAAA                                                                 | GATTCCCAACATCCA<br>AATG    | TTGGGGTTGACGACT<br>AAAG   | 60.0                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_192447 | scaffold340                             | 192447                        | AATATATATATATATATATATATATAT<br>ATATATAT/AATATATATATATATATA<br>TATATATATATATATATATATAT | ACAATGATCCTCCAAG<br>CACC   | GAAGAGGAACCTCTGT<br>TGCG  | 59.9                             | 562                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_194683 | scaffold340                             | 194683                        | GAAAAAAAAA/GAAAAAAAAA                                                                 | AGGTCGGAGGGGATA<br>GTTTG   | TTCAAGGTGGCATGAT<br>GAAA  | 60.3                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_216073 | scaffold340                             | 216073                        | TAGAGA/TAGA                                                                           | AAGCCAAACCAAGAGA<br>AGCA   | AAAATATCAAAGGGCC<br>CCAC  | 60.0                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_216811 | scaffold340                             | 216811                        | TAAAAAAAAAAAAAAAAA/TAAAAA<br>AAAAA                                                    | TGGGACACAAATTTG<br>ACACTAA | TATTTGCCACGACAA<br>GTGA   | 59.4                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_225242 | scaffold340                             | 225242                        | TAAAAAAA/TAAAAAA                                                                      | TCACCTTGAAAAAGTC<br>TGCC   | TATCCCCCAAGATTTG<br>GTCA  | 60.2                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_249861 | scaffold340                             | 249861                        | A/AAT                                                                                 | AACAATTGCCGATGAA<br>TCTTG  | AAAAGTCTCCACCAAC<br>ACCA  | 60.0                             | 224                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold340_P4_251725 | scaffold340                             | 251725                        | AC/A                                                          | TCTCCCGCATATCATC<br>ATCA | TTCGCAATTTTCGTACC<br>CAT  | 60.0                             | 787                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_259875 | scaffold340                             | 259875                        | CT/CTTTTTATTT                                                 | TAAAGGACCAAGTCGG<br>GAAA | GAAAGAGCTTTTGATT<br>GGACG | 59.5                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_284291 | scaffold340                             | 284291                        | AA/AATA                                                       | AACCTTTGCACTCCGA<br>GAAA | TGATCCAATCTTGGGG<br>GATA  | 59.9                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_287968 | scaffold340                             | 287968                        | ATTTTTTTTT/ATTTTTTTT                                          | GTCACAGAGGGAACGG<br>ATGT | TTGGAAAAGCCACCT<br>ACAC   | 60.0                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_287997 | scaffold340                             | 287997                        | ATTATTTATTTATTTATTT/ATT<br>ATTTATTTATTTATTT                   | GTCACAGAGGGAACGG<br>ATGT | TTGGAAAAGCCACCT<br>ACAC   | 60.0                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_299058 | scaffold340                             | 299058                        | ATTTTTTTTTTTTT/ATTTTTTTTTT<br>TTT                             | TGACATTGACTCTTGG<br>AGCG | TTGGACACACCTGACT<br>GGAG  | 60.0                             | 773                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_316742 | scaffold340                             | 316742                        | ATTTTTTT/ATTTTTTTTT                                           | CGGGAATTAAGTGAAG<br>GCCA | TGTTTCATGGATGCAA<br>GTACG | 60.1                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_317389 | scaffold340                             | 317389                        | ACG/ACGGCG                                                    | CCGTAAAAAGGTGGCG<br>ATAA | CCACAACGATCGCTCA<br>ACTA  | 60.0                             | 154                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_58349  | scaffold340                             | 58349                         | TA/T                                                          | ACGTCCATGTCCATT<br>CCAT  | CAATCCGATGCATGA<br>GACA   | 60.1                             | 855                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_60037  | scaffold340                             | 60037                         | TAAAAAAAA/TAAAAAAAAA                                          | ACATGATGAATGCGCT<br>TGAG | TCACATCCTCGCCTTAT<br>TCC  | 59.8                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome:<br>CDC Frontier/PII)                         | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                       |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold340_P4_60281  | scaffold340                             | 60281                         | AGG/AG                                                                                | ACATGATGAATGCGCT<br>TGAG   | TCACATCCTCGCCTTAT<br>TCC    | 59.8                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold340_P4_60721  | scaffold340                             | 60721                         | CTTTTTTTTT/CTTTTTTTTTTT                                                               | TGCTACGCACTAGATG<br>GCAC   | TTGCAGCATTGTCTTTG<br>TCC    | 60.0                             | 803                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold341_P4_116765 | scaffold341                             | 116765                        | CAA/CA                                                                                | TTGTGTTTGTCACAGG<br>CCAT   | TTTCTGATTCAACCCC<br>CAG     | 60.0                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold341_P4_132249 | scaffold341                             | 132249                        | GATATATATATATATATATATATA<br>TATATATATATATAT/GATATATATAT<br>ATATATATATATATATATATATATAT | TTTGATGCCCCGTTTA<br>AAAT   | ATGAGCCATTACCTCC<br>GTTG    | 59.3                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold341_P4_135211 | scaffold341                             | 135211                        | TATATATATAGAAA/TA                                                                     | AATGGAGTTGCGACGA<br>GAGT   | TCTCCGTAAAGGATTC<br>ACCG    | 59.9                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold341_P4_135303 | scaffold341                             | 135303                        | GAAAA/GAAAAA                                                                          | AATGGAGTTGCGACGA<br>GAGT   | TCTCCGTAAAGGATTC<br>ACCG    | 59.9                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold341_P4_159739 | scaffold341                             | 159739                        | AT/ATGT                                                                               | GTTGGTTCCCTAGCAC<br>CGTA   | TTGGACGAGCTACAAA<br>GCCT    | 60.0                             | 872                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold342_P4_164779 | scaffold342                             | 164779                        | TTATATATATATATATAT/TTATAT<br>ATATATATATAT                                             | TTCCAACATGCTTGAA<br>CTCA   | GGCCGAAATTCATTC<br>AACA     | 59.3                             | 703                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold342_P4_249187 | scaffold342                             | 249187                        | ATTTTTTTTT/ATTTTTTTTT                                                                 | CAACGGTGAAGCCCAT<br>AACT   | TGGGTGTTAAAATTCTC<br>CTCTTG | 60.0                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold342_P4_310549 | scaffold342                             | 310549                        | CATATATAT/CATAT                                                                       | TTGTGACATTTTCATCA<br>ACACA | CAACCGACGTTGAAGA<br>ACAA    | 57.5                             | 933                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold342_P4_340574  | scaffold342                             | 340574                        | TC/T                                                          | TGTTCCAGCATACCA<br>ATGC    | AGCAAAATCCGAGGAG<br>GAAT    | 59.5                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold342_P4_370625  | scaffold342                             | 370625                        | TTATCAT/TT                                                    | TGGGGTCCTTTCTCTT<br>CTCC   | TATGCCCATGAGTTG<br>GACA     | 60.6                             | 387                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3422_P4_131072 | scaffold3422                            | 131072                        | ATT/A                                                         | CCGAAATCATGTAATT<br>GACCA  | TGTGTTGCACTTGACA<br>CGAA    | 59.7                             | 668                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3422_P4_56233  | scaffold3422                            | 56233                         | CAAA/CAAAA                                                    | GAGATCCAAGCCCTTG<br>ATGA   | ATGGGCTGCAATTGA<br>AAAA     | 60.2                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3432_P4_23969  | scaffold3432                            | 23969                         | CAATAAT/CAAT                                                  | CCTGAATCCGAGACAA<br>GACG   | TCATGGGTTGTATGGA<br>AGCA    | 60.8                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3432_P4_35439  | scaffold3432                            | 35439                         | TTTATATT/TTTATATTATATT                                        | TGATTGATTTTGCGGT<br>TACG   | AAAGAGATCGGTTCTA<br>CCCAAA  | 59.6                             | 278                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3432_P4_43962  | scaffold3432                            | 43962                         | T/TTTGA                                                       | TGAATGCTTTCTATGAT<br>GTGCT | AGTTATTGATCGTCGG<br>TGCC    | 57.5                             | 872                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3432_P4_56454  | scaffold3432                            | 56454                         | GAAAAAA/GAAAAAAA                                              | TTTGAGGGAAGTTTTC<br>CACG   | CGTCAGATTTATCTGC<br>GGGT    | 60.1                             | 368                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3434_P4_7567   | scaffold3434                            | 7567                          | GAAAAAA/GAAAAAAA                                              | CGACATTCGTCATGGT<br>TTTG   | CATAGCAATCCAACAAC<br>AAGAAA | 60.0                             | 876                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3434_P4_8209   | scaffold3434                            | 8209                          | TAAA/TAAAA                                                    | TCAGACGTTCTAAGTG<br>TTGGGA | CGCCACAACCTCTACT<br>CCTT    | 59.8                             | 218                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                                                       | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                                                                                     |                               |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3436_P4_13785 | scaffold3436                            | 13785                         | TGAGGA/TGA                                                                                                                                                                                          | GCGCTACATTTTACGG<br>CTCT      | TTCGTCCTCGAAATTCA<br>ACC    | 59.5                             | 757                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3436_P4_9281  | scaffold3436                            | 9281                          | GAGACTTAT/G                                                                                                                                                                                         | GGCCATGAATTCACAA<br>ACAA      | TTGCCAAATACAAAAG<br>AAATGAA | 59.4                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3436_P4_9348  | scaffold3436                            | 9348                          | GTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAGTAATAATA<br>ATAA/GTAATAATAATAATAATAAA<br>TAATAATAATAATAATAATAATAA<br>ATAATAATAATAATAATAATAATAA<br>ATAATAATAATAATAATAATAATAA | TTTCACCATTTTGCATT<br>TCG      | CAGGTTTACGTTATTTT<br>GTTTCA | 59.5                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3436_P4_9959  | scaffold3436                            | 9959                          | TAATA/TTAATAATATACAAATA                                                                                                                                                                             | TGGAGTTCGGGCTAAG<br>TACAG     | CGTGCTTGCAGAAAA<br>CAAA     | 59.4                             | 309                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3438_P4_22632 | scaffold3438                            | 22632                         | TA/T                                                                                                                                                                                                | GTGCTGTTGAACCCCA<br>AACT      | TGAATACCCTCCCTTG<br>AACG    | 60.0                             | 711                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3453_P4_1173  | scaffold3453                            | 1173                          | CA/CAAA                                                                                                                                                                                             | ATATGCCTCTACCGTG<br>CAGC      | TCGTGAAAGCAAACAA<br>AGGA    | 60.3                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3470_P4_6060  | scaffold3470                            | 6060                          | ATT/ATTT                                                                                                                                                                                            | TTTCGGGTTTTTGTCC<br>ACTC      | TGGATGCACAAGATCG<br>GTTA    | 59.9                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3472_P4_51384 | scaffold3472                            | 51384                         | TAAAAAAAA/TAAAAAAAAA                                                                                                                                                                                | GAAATCCATGTTAGAA<br>ATTTTGTGA | TTGTGTTGTTTTGCCT<br>TCA     | 59.7                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3472_P4_6763  | scaffold3472                            | 6763                          | GTATATATATATATATATATATAT<br>ATATA/GTATATATATATATATATA<br>TATATATA                                                                                                                                   | CAAGCATGATCCAGGG<br>AGAT      | CTCGCGAGTTTGTGT<br>GTAA     | 60.0                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3472_P4_7007  | scaffold3472                            | 7007                          | CAATAATAATAATAATAATAATA<br>ATAATAATAATA/CAATAATAATAAT<br>AATAATAATAATAATAATAATAA                                                                                                                    | CAAGCATGATCCAGGG<br>AGAT      | CTCGCGAGTTTGTGT<br>GTAA     | 60.0                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3472_P4_71251 | scaffold3472                            | 71251                         | CTACAGCGCTT/CTACAGCGCTGT<br>TTTACAGCGCTT                      | GAAAGCGCTTCCGTT<br>ACAG   | GACATTTAACAGCGCC<br>CATT    | 60.0                             | 159                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3472_P4_7148  | scaffold3472                            | 7148                          | TATTAATAATT/TATTAATAATTAA<br>ATAATT                           | CAGGCTAGCTAAATGC<br>CTCG  | ACCATGGTTGTTGCAA<br>GTGA    | 60.1                             | 720                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3472_P4_9063  | scaffold3472                            | 9063                          | CAA/CAA                                                       | GCTCCATGTGCTTCAC<br>ACAC  | GTGACACGTGACAATC<br>CCAC    | 60.3                             | 107                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3472_P4_9396  | scaffold3472                            | 9396                          | TC/TCC                                                        | TTTTCAGAGAGAAACC<br>CGCT  | CTGTGAGAGCGAAGA<br>TGGT     | 59.9                             | 223                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3475_P4_1316  | scaffold3475                            | 1316                          | TA/TAA                                                        | CCATCCAACAAAAATG<br>GACC  | TCTTCGTTATCCAGTCA<br>AACATC | 60.0                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3475_P4_31282 | scaffold3475                            | 31282                         | TG/TGG                                                        | GCTATTTTCGTACCAC<br>CCGA  | GCCCAAAAAGTCCAGA<br>TGAA    | 60.0                             | 326                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3475_P4_33409 | scaffold3475                            | 33409                         | GATAATAATAA/GATAATAATAATAA                                    | TTCATTGGGACTTTTCA<br>GGC  | TTTCAGGCGATTTTCGT<br>ACC    | 60.1                             | 792                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3475_P4_6139  | scaffold3475                            | 6139                          | AG/A                                                          | GGCCTGGAGACCCCTTA<br>TAGC | ACCACTCGACGAAAAT<br>GGAC    | 60.1                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3475_P4_6197  | scaffold3475                            | 6197                          | AT/ATT                                                        | GGCCTGGAGACCCCTTA<br>TAGC | ACCACTCGACGAAAAT<br>GGAC    | 60.1                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3475_P4_7484  | scaffold3475                            | 7484                          | AATTTTGTCTATTTTGTGTC/AATTTT<br>TGTC                           | GGGTACGAAAATCGCC<br>TGTA  | GAACCTAAAAGGGTCT<br>CCCG    | 60.0                             | 414                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                      | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                                                                                                    |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3489_P4_1552   | scaffold3489                            | 1552                          | GTTT/GTT                                                                                                                           | ACTATCCATCGTCTGG<br>TCCG | GAAAGGGTCCAACAGA<br>ACGA | 60.0                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3489_P4_2052   | scaffold3489                            | 2052                          | TAATAAAAAATAAAAAATAAAAAATA<br>AAAAA/TAATAAAAAATAAAAAATAAA<br>AAA                                                                   | TCGTTCTGTTGGACCC<br>TTTC | AGTGGAATAATGCCG<br>TTGC  | 60.1                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3489_P4_2491   | scaffold3489                            | 2491                          | CTTTTTTTTT/CTTTTTTTTTTT                                                                                                            | CGTTACCGTGAACCAC<br>CTCT | TATGCCCTTAGGAAT<br>GTGC  | 60.0                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold349_P4_186710  | scaffold349                             | 186710                        | TTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAA/TTAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAA | GCAACAACCCCTGCT<br>TAGA  | TTTCTTTTGGTGGTT<br>GGC   | 60.2                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold349_P4_335267  | scaffold349                             | 335267                        | ATT/ATTT                                                                                                                           | TTGGTCAATGTGGCTT<br>CTCA | CTGAGCTTGTGACCA<br>ATCG  | 60.2                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3497_P4_13567  | scaffold3497                            | 13567                         | TAAA/TAAAA                                                                                                                         | CATGCATGCACCAACA<br>ATAA | CACACCAACACCTA<br>CACG   | 59.0                             | 284                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold350_P4_165550  | scaffold350                             | 165550                        | ATGTGTG/ATGTGTGTG                                                                                                                  | CAATTCCATGGCTCCA<br>AAGT | CAATGCCTCCCATAA<br>CAAT  | 59.9                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3500_P4_111838 | scaffold3500                            | 111838                        | ACC/ACCC                                                                                                                           | ACCCAGATATCAAAAC<br>CCCA | CATCCGAACAAAAGG<br>GAAA  | 59.1                             | 632                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3500_P4_6141   | scaffold3500                            | 6141                          | CAA/CTGTAA                                                                                                                         | GCGTTCGATTCCACAT<br>CTTT | TCATTATGCGTGTTC<br>GCTA  | 60.1                             | 434                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3514_P4_12548  | scaffold3514                            | 12548                         | CAAAAAAAAA/CAAAAAAAAAAA                                                                                                            | CTCTTTAAGACGTTTC<br>GCGG | TTGGTGCCCACTGAT<br>TCAA  | 60.0                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3514_P4_19067 | scaffold3514                            | 19067                         | ATTTTTTTTT/ATTTTTTTTT                                         | TGACACCCTTAATTAAC<br>CCCA  | TTAATTGTGAGCGTGT<br>GGGA | 59.2                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3514_P4_21266 | scaffold3514                            | 21266                         | TAAAAAAAA/TAAAAAAAA                                           | CCGAGACACGACGGAT<br>AAAT   | TTGGACCCCAAACTTC<br>AGTC | 60.0                             | 310                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3514_P4_40711 | scaffold3514                            | 40711                         | GAAA/GAAA                                                     | TGACCAAATCGGAATT<br>GATTTT | CATTTCGAATCTTCCC<br>GTA  | 60.5                             | 723                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold352_P4_133593 | scaffold352                             | 133593                        | AAAGA/AA                                                      | TTTTGAGTTCGGGAGT<br>CGAT   | TTTCTTGAGTTTGGGA<br>CACA | 59.7                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold352_P4_177986 | scaffold352                             | 177986                        | TAAAAA/TAAAAA                                                 | AACGCATCTTTTACCC<br>ACG    | GGCCTGAATCTCATCC<br>AAGA | 60.0                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold352_P4_178010 | scaffold352                             | 178010                        | ATTT/ATT                                                      | AACGCATCTTTTACCC<br>ACG    | GGCCTGAATCTCATCC<br>AAGA | 60.0                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold352_P4_178511 | scaffold352                             | 178511                        | ATGAGTTGAGTTGAGTT/ATGAGTT<br>GAGTT                            | TCGCAATGCAACATCT<br>CTTT   | GCTTGTGAGTGTGTGT<br>GCCT | 59.4                             | 823                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold352_P4_179458 | scaffold352                             | 179458                        | CGTAGTA/CGTA                                                  | ATGAGCTGATGAGCGT<br>GTTG   | GCATTCTAGCTTTGCCT<br>TGC | 60.0                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold352_P4_179520 | scaffold352                             | 179520                        | AAT/AATTATAT                                                  | TTTGCATGTGATGTG<br>AGGT    | AGGAAGGAGAACAAGC<br>CCAT | 60.1                             | 196                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3529_P4_11975 | scaffold3529                            | 11975                         | G/GA                                                          | TGACCGAAATGTTTCAT<br>CCAA  | TTTTCGTCCTCCCTAG<br>GCTT | 59.9                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3542_P4_24046 | scaffold3542                            | 24046                         | T/TTCAAAACAAA                                                 | AGCATTGAATTGAACC<br>ACCA | AAAATCGTGGTTGGGA<br>AGGT  | 59.0                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3542_P4_24348 | scaffold3542                            | 24348                         | AT/ATCCGTT                                                    | AAAATAACGAGGGAAT<br>GGGC | TCAATGAAGGAAATGG<br>CTCC  | 60.2                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3542_P4_25608 | scaffold3542                            | 25608                         | C/CGGCGCAT                                                    | CAGGTTAGGAAGCAAG<br>CAGG | TACAGCGCTCATTCC<br>ACAG   | 60.0                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3542_P4_26037 | scaffold3542                            | 26037                         | TT/TCAGATTAT                                                  | CTGTGGAATGAGCGC<br>TGTA  | AGACCTTGACACGTA<br>ACGG   | 60.0                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3542_P4_507   | scaffold3542                            | 507                           | AGGGGGGG/AGGGGGG                                              | GAAGAGTTACGCGGAC<br>AAGC | CCGAGCCAAAATCCAA<br>AATA  | 60.0                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold355_P4_1384   | scaffold355                             | 1384                          | GTTTTT/GTTTT                                                  | GGGGCGTTACATGTGG<br>TATC | CAGATTCACGAAGTGC<br>ACACA | 60.1                             | 314                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold355_P4_740    | scaffold355                             | 740                           | AT/A                                                          | GTTGTGGGATGAACTG<br>ACCC | CCCACAAGGTCCGAGA<br>ATTA  | 60.2                             | 571                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3562_P4_1038  | scaffold3562                            | 1038                          | ATTT/ATT                                                      | AGGGAGGACGAAAATG<br>ACCT | CCAATTGGTGTTTG<br>CATC    | 59.9                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3594_P4_1839  | scaffold3594                            | 1839                          | CCTAT/CCTATCTAT                                               | AAACCCGAAACGCTTA<br>ACCT | TTTCGGATTTGGGTTT<br>TTG   | 60.0                             | 115                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3594_P4_6118  | scaffold3594                            | 6118                          | CAAAA/CAAA                                                    | AATCCCGACACCCTAA<br>ACCT | GCGTTACGGATTCCGT<br>TTTA  | 59.7                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                 | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3594_P4_716  | scaffold3594                            | 716                           | TAAGAAGA/TAAGA                                                                                                | CGAACTGGGCTCAGAG<br>AAAC   | ACGATCTCGTTTGAAC<br>GCT      | 60.0                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3594_P4_965  | scaffold3594                            | 965                           | GAGCTAAAAAGCTAAAAAGCT/GAG<br>CTAAAAAGCTAAAAAGCTAAAAAGC<br>T                                                   | CGTTCAAAACGAGATC<br>GTCA   | TACAATGCCGAGCAAA<br>TCAA     | 59.8                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold36_P4_105612 | scaffold36                              | 105612                        | ATATTATTATTATTATTATTATTA<br>TTATTATT/ATATTATTATTATTATTA<br>TTATTATTATTATTATTATT                               | GGAGCATGTTGAGGTG<br>GTTT   | GCTCCCAAAATCTTCA<br>CCA      | 60.0                             | 988                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold36_P4_159165 | scaffold36                              | 159165                        | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATT/TTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATT     | GTTCCGCTGAAAAATC<br>CGTA   | GGTGGTATGTTGGATA<br>ACTTGGGA | 60.1                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold36_P4_209632 | scaffold36                              | 209632                        | TTATATATATATATATATATATATA<br>TATATATATATATATATATAT/TTATA<br>TATATATATATATATATATATATAT<br>ATATATATATATATATATAT | CAAAGGGAGAATTGTA<br>ACACCC | GAAATTTGGACGAAAA<br>CGGA     | 59.7                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold36_P4_236312 | scaffold36                              | 236312                        | ATTTTTTTTT/ATTTTTTTTTT                                                                                        | TAGGTCTCATAGCCCC<br>GATG   | GCCCTCAGATGAGAGT<br>CAGG     | 60.1                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold36_P4_297435 | scaffold36                              | 297435                        | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATT/TTTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATT                | AAACCAAGGCTGAATG<br>GTTG   | GGCTTGAATCAAAATG<br>AGTGC    | 60.0                             | 614                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold36_P4_298635 | scaffold36                              | 298635                        | TATAATAATAATAATAATAATAAA<br>TATTAATAATAATAA/TATAATAATAA<br>TAATAATAATAATAATAATATTA<br>ATAATAATAA              | GCTAATTGGCGGCACT<br>TCTA   | TCATATTTCTTGTGTG<br>TTTGGTT  | 60.4                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold36_P4_327089 | scaffold36                              | 327089                        | TTATATATATATATATATAT/TTAT<br>ATATATATATATATAT                                                                 | TTTCGAGCCGACTCTC<br>AAAT   | ACCGATGCCAAACGAT<br>AGAC     | 60.0                             | 929                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold36_P4_53553  | scaffold36                              | 53553                         | G/GTGTAAGTTAGGGAA                                                                                             | TACCTGAAGCTCCTGG<br>CACT   | GGAGCCAAATCCAAC<br>TCCT      | 60.0                             | 371                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')         | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|---------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                 |                                 |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold36_P4_72840   | scaffold36                              | 72840                         | TAAAAAAAAA/TAAAAAAAAA                                           | ATCATGGGATCTCAAG<br>TGGG        | GCGCATGCCTTGTCTA<br>TGTA     | 59.7                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold362_P4_131241 | scaffold362                             | 131241                        | TAA/TAAAA                                                       | TTTTGCACAACCTGAA<br>CCTG        | GCCCATTAGTAGCCCA<br>TGAA     | 59.7                             | 978                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold362_P4_267543 | scaffold362                             | 267543                        | A/AC                                                            | TATCTTGTTCGACCC<br>AACC         | CTTGAATCCATGCGT<br>CCTT      | 59.8                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold362_P4_82815  | scaffold362                             | 82815                         | C/CCGCT                                                         | CCCAACTTGAAACGCT<br>TGAT        | CTCGGAGAAAGTGAA<br>TCCG      | 60.1                             | 291                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold363_P4_83340  | scaffold363                             | 83340                         | CTGT/CT                                                         | AGGTTCTCTACGCCG<br>TTCT         | CTATCCATTGTGACG<br>GCCT      | 60.3                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3637_P4_13149 | scaffold3637                            | 13149                         | GATATATATATATATA/GATATATA<br>TATATATATATA                       | AATGTGAATCCCACCA<br>GGAA        | CAAGCGCTATGTGACC<br>CTTT     | 60.2                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3643_P4_22623 | scaffold3643                            | 22623                         | TAAAAAAAAA/TAAAAAAAAA                                           | CAAGCACACGTATTGG<br>ATGG        | TTTGTGCGTGACATTG<br>GATT     | 60.0                             | 111                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3659_P4_2503  | scaffold3659                            | 2503                          | AT/ATT                                                          | GCCATTAATTATGTTAA<br>CGTTTGG    | CAGAACATTTAACGTGA<br>GCAAGA  | 58.8                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold366_P4_104824 | scaffold366                             | 104824                        | CTATATATATATATATATATATAT<br>ATATATAT/CTATATATATATATAT<br>ATATAT | TGCAAGCGTTATGTGA<br>CCTC        | ATGTGAATCCCACCAG<br>GAAA     | 59.9                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3663_P4_4120  | scaffold3663                            | 4120                          | T/TG                                                            | TTTTATTGTTTTACTAC<br>ATAACGACGA | AAGTTTGACTGCATAAC<br>AATGACA | 57.7                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                              | Forward primers (5'-3')       | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                            |                               |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3663_P4_4430  | scaffold3663                            | 4430                          | TAAA/TAAAA                                                                                                                                 | TGTCATTGTTATGCAGT<br>CAAACCT  | TCTTCGTTTTATGGTTT<br>TATTCA | 58.7                             | 280                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3666_P4_1070  | scaffold3666                            | 1070                          | AACA/AA                                                                                                                                    | AAATGCAACAAAGGAC<br>TGCAT     | CGTCGGTTGAGAACAA<br>CACTT   | 59.6                             | 409                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold367_P4_158238 | scaffold367                             | 158238                        | A/AG                                                                                                                                       | TTGAGTAAAATGTCGTT<br>GATTAGCA | ACCACCCAACCTACCAT<br>GTGA   | 60.1                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold367_P4_6421   | scaffold367                             | 6421                          | A/AAAT                                                                                                                                     | GTTGGCTGAAAGGAAC<br>TTCG      | TAGATTGGGTGGATTG<br>GCTC    | 59.9                             | 261                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3673_P4_1322  | scaffold3673                            | 1322                          | ATTTTT/ATTTTT                                                                                                                              | AGGTCGGTCTAGCCG<br>TTTT       | CCGAGCCAAAATCCAA<br>AATA    | 60.1                             | 632                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3687_P4_82563 | scaffold3687                            | 82563                         | G/GTAA                                                                                                                                     | GAGTTTCCTCTACCAC<br>CCCC      | GGGACTATGTTAGTGG<br>CGGA    | 59.8                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3687_P4_85224 | scaffold3687                            | 85224                         | CTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATT/CTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATT | TTTAATGTGTCGCGTC<br>TTCG      | TCACACGGTAGTTGTT<br>AAGGATG | 59.9                             | 292                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3689_P4_16220 | scaffold3689                            | 16220                         | TATTCA/TA                                                                                                                                  | TCCCATCCCTATTTTG<br>GACA      | ACATGGCAAGCCAAAT<br>TTTC    | 60.1                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold369_P4_125737 | scaffold369                             | 125737                        | ATTTTTTTTTTT/ATTTTTTTTTTT                                                                                                                  | CGGAAGCTCGGATTAC<br>ACAT      | GGGTCGTGGGACTTTG<br>ATAG    | 60.1                             | 771                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold369_P4_133769 | scaffold369                             | 133769                        | ATTTTTTTTTTT/ATTTTTTTTTTT                                                                                                                  | TGCGAACAACTCGAAC<br>TTTG      | CATCCCCATCACCTAAA<br>TGC    | 60.0                             | 769                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold369_P4_65702  | scaffold369                             | 65702                         | AATATATATATATATATA/AATATA<br>TATATATATATATA                   | AAAAGTACGGCTTTCC<br>CGTT   | GAATCTGCCAAATCCTT<br>CCA  | 60.0                             | 785                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold370_P4_164080 | scaffold370                             | 164080                        | TG/T                                                          | GCCAAGGGTTACAACC<br>AAGA   | TGCATCCAGCAAAATC<br>AAAA  | 60.0                             | 864                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold370_P4_176953 | scaffold370                             | 176953                        | TAAA/TAA                                                      | ATGGCCTGTGACAAAC<br>ACAA   | GTTAATCGGAGTGCCA<br>ATCG  | 60.0                             | 157                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold370_P4_56126  | scaffold370                             | 56126                         | T/TA                                                          | AAAGGAAAACACATT<br>GCGAAGA | TGTTCAAAATATGACGC<br>GAAA | 59.3                             | 615                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold370_P4_58169  | scaffold370                             | 58169                         | TC/T                                                          | CCCTCGTCGTGTTTGA<br>AAAT   | TTTTGGGCACTTTTCGT<br>ACC  | 60.0                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold370_P4_74830  | scaffold370                             | 74830                         | ACCCC/ACCC                                                    | GGTCCTCGATTTCATC<br>TGGA   | CGAAATCGCTCGAAA<br>AGTC   | 60.0                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold370_P4_75163  | scaffold370                             | 75163                         | AC/A                                                          | GATTTTCGTACCCCTC<br>GTCA   | AGTCGCTCGAAAAGTC<br>CAAA  | 59.9                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold370_P4_83329  | scaffold370                             | 83329                         | ATTTTTTTTT/ATTTTTTTT                                          | AAAAGCGTTGTAAACG<br>GTGC   | GCGCTTTCTAAACAAAT<br>GCC  | 60.2                             | 340                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3705_P4_4075  | scaffold3705                            | 4075                          | T/TGGGCTAAACC                                                 | CAATAACCCCTCAATG<br>GCTCA  | GCTTTGCTTCCCTTCC<br>TCT   | 59.9                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold373_P4_25857  | scaffold373                             | 25857                         | ACTTC/ACTTCTTC                                                | AGCCACGAATTTAAGC<br>TCCA   | AGGGACAAAGGGCAAG<br>AAAT  | 59.8                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold374_P4_13002  | scaffold374                             | 13002                         | AC/ACC                                                        | CAAATTCAACGAGGTC<br>ACACA   | ATTTGGAGCGTTACATT<br>GGG   | 59.6                             | 184                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold374_P4_142006 | scaffold374                             | 142006                        | TAAA/TAA                                                      | AATTCCTTCCACACAA<br>CCA     | AGCGGAGATTTTACCG<br>GAAT   | 60.2                             | 128                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold374_P4_154680 | scaffold374                             | 154680                        | TAAAAAAAAAAAAA/TAAAAAAAAA                                     | GATTGATGTTGGGAC<br>CGTT     | TCAAATGCTTCAACTTG<br>TGCTT | 59.7                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold374_P4_158468 | scaffold374                             | 158468                        | ACACGATCAGCACGA/ACACGA                                        | CCTATCACAGGTCAGC<br>ACGA    | GGTGTGGATGGAATT<br>GGAG    | 59.9                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3742_P4_3802  | scaffold3742                            | 3802                          | TTAT/TTATAT                                                   | CGATAGACTCAAGTTG<br>GACCTG  | GTGTCTGCTTGTTGC<br>CTGA    | 58.9                             | 632                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3757_P4_3479  | scaffold3757                            | 3479                          | C/CT                                                          | GGTCTCGATTTCATC<br>TGGA     | TTGTGCGAGGGGTACG<br>AAAC   | 60.0                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3765_P4_4174  | scaffold3765                            | 4174                          | TCCCC/TCCC                                                    | TTCTCCCTGGGCTTA<br>TTCT     | AGGGAGGACGAAAATG<br>ACCT   | 60.0                             | 901                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold377_P4_146742 | scaffold377                             | 146742                        | GAAAAAAAAA/GAAAAAAAAA                                         | TCATGAGCCTTACATG<br>AACTGAA | CGGCCATTCACTTAAC<br>CCTA   | 59.8                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold377_P4_251352 | scaffold377                             | 251352                        | A/AGGAAAC                                                     | TTAGCCTTGTGGAATG<br>GGTC    | TGGGGTTTAGGGTGTC<br>ACAT   | 59.9                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold377_P4_263808 | scaffold377                             | 263808                        | GTATATATATATATATATATATAT<br>AT/GTATATATATATATATATATAT         | GTGTGTAGAAGCCTAG<br>CCGC    | TGCACTTTGCTCTCAA<br>TCG    | 60.0                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                     | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                   |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold377_P4_75306  | scaffold377                             | 75306                         | C/CAT                                                                                             | TCACGGGTCGACACAA<br>TTTA   | AACTGGACGTTGAGAA<br>TGGG  | 60.0                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3780_P4_7994  | scaffold3780                            | 7994                          | C/CT                                                                                              | TCATTTCGTGAAATTAGC<br>CCC  | CCCAATTCCCCCAACTT<br>AAC  | 59.9                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3789_P4_2620  | scaffold3789                            | 2620                          | AGG/AGGG                                                                                          | AATGGTTCCTGGACAG<br>TGGC   | GGCTGGTGGTTTGTAT<br>AGGA  | 60.0                             | 548                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold379_P4_136180 | scaffold379                             | 136180                        | GTTTTTTTTTTT/GTTTTTTTTT                                                                           | TGATCGAGTGAGAGAA<br>CAAAAA | CCACGGTAAACAACA<br>AATCAA | 57.6                             | 173                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold379_P4_194523 | scaffold379                             | 194523                        | AATATATATATATATATATA/ATA<br>TATATATATATATA                                                        | CCGAACCTTACTGGGC<br>CTAA   | ACCGTTTTGGTGTCTTCT<br>TGC | 59.2                             | 602                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold379_P4_81972  | scaffold379                             | 81972                         | CTATTATTATTATTATTATTATTA<br>TTATTATTATTATTA/CTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTA | GAAGTGAGAAACGTGG<br>CATT   | ACTTGCAATCAAAGTTG<br>GGG  | 60.1                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3794_P4_34380 | scaffold3794                            | 34380                         | GTAT/GTATTTCAATTATATTAT                                                                           | TGTGAGAGGGACACTT<br>GGCT   | CAGTGTCGTGGTGGAT<br>TTTG  | 60.9                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3794_P4_41745 | scaffold3794                            | 41745                         | TGG/TG                                                                                            | ACCCATCATGGAATGG<br>AAAA   | CATTGGTTGTGCGTG<br>TTTC   | 60.0                             | 192                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3794_P4_45335 | scaffold3794                            | 45335                         | G/GTTTTGAT                                                                                        | CAACGGCCAAACGTTA<br>TTTT   | TGACATGTTTTAGTCCC<br>CCA  | 59.9                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3794_P4_49295 | scaffold3794                            | 49295                         | CA/CAAA                                                                                           | ACAAGAACATTGGCTC<br>CCAC   | TAGGGCTTCAGATGCT<br>CGTT  | 60.0                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3794_P4_58392 | scaffold3794                            | 58392                         | GTTTTTTTTT/GTTTTTTTTT                                         | GCCTTGAGACCGAGTT<br>TTGA  | GAGCGCGACAACATA<br>ACAA     | 60.4                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3794_P4_82476 | scaffold3794                            | 82476                         | CCAC/CC                                                       | CAAAGGGACCACACCT<br>CTTT  | TTGGCCCCTTTAGTGT<br>ATCG    | 59.0                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_135300  | scaffold38                              | 135300                        | GTTTTTT/GTTTTTTT                                              | TGGTTGAAATTAAGC<br>CAAGG  | TCACATCAGGAAAAAT<br>GGCA    | 59.1                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_204585  | scaffold38                              | 204585                        | GTTGTTTCT/GTTGTTTCTTGTTC<br>T                                 | CATCATTTCTTGCACAT<br>GCC  | CAAAACAAATCAATCC<br>CCC     | 60.1                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_268644  | scaffold38                              | 268644                        | ACC/ACCC                                                      | AACCGAACCAGATCAA<br>CCAG  | TTGGGTTTGCATGCTTT<br>TCA    | 60.0                             | 374                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_281889  | scaffold38                              | 281889                        | TAAAAAAAAA/TAAAAAAAAA                                         | ATCACCATTGTGGCAT<br>TGAC  | TTGCAATAATGCGAAC<br>CAAA    | 59.2                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_3173    | scaffold38                              | 3173                          | ATT/ATTT                                                      | AGTGTGGGATCGGTTT<br>TTGA  | CATCAAAAGGGGGAA<br>ATTG     | 58.1                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_320899  | scaffold38                              | 320899                        | A/AT                                                          | CCCAAAGAAAAACAAT<br>CAGGA | TCTCCATCAATGACATT<br>TCAACA | 59.1                             | 285                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_324967  | scaffold38                              | 324967                        | CTATA/CTATATATA                                               | TGGCGTGAGAGCAACA<br>AATA  | ACCTTGGCCATACTG<br>CATC     | 60.4                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_335590  | scaffold38                              | 335590                        | GAAAAAAAAAAAAA/GAAAAAAAAA<br>AAAA                             | TACGCTTTCAGATCAT<br>GCCA  | GGCCTGAGTCTCACCT<br>ACGA    | 60.4                             | 122                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold38_P4_351192 | scaffold38                              | 351192                        | TTAT/TTATAT                                                   | CTCTTGGTTTGATTT<br>GGG   | GTGGCTCCACCTAACG<br>GATA  | 59.4                             | 810                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_359185 | scaffold38                              | 359185                        | ATTTTTTTT/ATTTTTTTT                                           | TGCATCTGACTCAGCA<br>AACC | CATCACACGCGCTTCA<br>CTAT  | 60.0                             | 843                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_377863 | scaffold38                              | 377863                        | GT/G                                                          | TTGCCTACCTCAACAC<br>CCTC | TGGTGCTTAGGTGTCA<br>ACGA  | 60.1                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_383150 | scaffold38                              | 383150                        | AATATATATATATATATATATAT/A<br>ATATATATATATATATATATATATA<br>TAT | TGTCGGTTAACTGGCC<br>CTAC | AAATTTTGGGAAGCCC<br>AAGT  | 60.0                             | 331                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_393971 | scaffold38                              | 393971                        | T/TGACACAAGG                                                  | AGTGCATGTCCGAAAA<br>CCAT | AACTGATTGGGAGCAT<br>TTCA  | 60.4                             | 758                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_413791 | scaffold38                              | 413791                        | ATTTT/ATTTT                                                   | CTTCGCTGCAAAATTC<br>CTC  | TTGATGTCGGGTAGTG<br>TCTGA | 60.0                             | 755                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_425721 | scaffold38                              | 425721                        | CTTTTTTTTTT/CTTTTTTTTTT                                       | TTTAGGGACATGTTGG<br>GTGG | TGCTTAGAAGGAGAGA<br>CCCC  | 60.6                             | 597                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_451899 | scaffold38                              | 451899                        | TTCTCT/TTCT                                                   | TGAGGAAGGCAGCCAC<br>TACT | ATGACGTGCTTCCCTC<br>AATC  | 60.0                             | 191                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_474073 | scaffold38                              | 474073                        | TAAAAAAAAAAAAA/TAAAAAAAAAAA                                   | TGTGTCAGAAGGATCT<br>TGCG | TGAGATTCGCCAGTTA<br>ACCC  | 60.0                             | 652                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold38_P4_499478 | scaffold38                              | 499478                        | ATTTTTTTTTT/ATTTTTTTTTT                                       | AACACTTTCCTCCAAA<br>GGCA | TCACACAACCTCAAAAT<br>CCCA | 59.7                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                              |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold38_P4_73302   | scaffold38                              | 73302                         | GTTTTTTTTTTT/GTTTTTTTTTTT                                                    | TTTGTGTGCGTTTGA<br>CTGA   | AACATGCATAGAAGTC<br>GGGG  | 58.9                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold381_P4_6157   | scaffold381                             | 6157                          | CGTTTTAGGTTTTAGGTTTTAGGTT<br>TTAGG/CGTTTTAGGTTTTAGGTTTT<br>AGGTTTTAGGTTTTAGG | GTTGATGGTTTCGGGT<br>TGAT  | AACGCAAAACACTAAAC<br>CGC  | 59.7                             | 304                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold381_P4_6830   | scaffold381                             | 6830                          | AAG/A                                                                        | TGCAAAAGGGTCACTT<br>GATTT | CCCCAAACCCTAAACC<br>CTAA  | 59.6                             | 355                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold381_P4_8177   | scaffold381                             | 8177                          | GGGTTTA/GGGTTTATGGTTTA                                                       | GTTTGGATTTAGGTT<br>TGCG   | AAAACCAACGTCGAA<br>GACCT  | 59.5                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3810_P4_21944 | scaffold3810                            | 21944                         | AAATAATATATAATAATAT/AAATAAT<br>AT                                            | GACCATCTCCAAGGT<br>ACCAA  | CATTGTGCCACATTAGT<br>TGGA | 58.9                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3811_P4_21005 | scaffold3811                            | 21005                         | CCCATTCAATCCATT/CCCATTCAAT<br>CCATTCAATCCATT                                 | GATGCATCCATGTGAG<br>ATCCT | ACGCCATTTGTCAACAT<br>CAA  | 59.9                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3824_P4_11386 | scaffold3824                            | 11386                         | ATTTTTTTTTT/ATTTTTTTTTT                                                      | CCCTCTATGGCTGATG<br>AGGA  | CCCCATCAAGGTAAC<br>CCAA   | 60.2                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold383_P4_81337  | scaffold383                             | 81337                         | ATTT/ATTTT                                                                   | GATGCTCGGGTTTGAT<br>GTTT  | TGGATGCAAATTGGAC<br>AGAA  | 59.9                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3837_P4_2371  | scaffold3837                            | 2371                          | ATTTTTTTTTTTT/ATTTTTTTTTT                                                    | CTTCTTGGTGGCATGG<br>TTTT  | TACCCTGTGGATGGGA<br>ATGT  | 60.0                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3837_P4_2435  | scaffold3837                            | 2435                          | T/TTA                                                                        | CTTCTTGGTGGCATGG<br>TTTT  | TACCCTGTGGATGGGA<br>ATGT  | 60.0                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3837_P4_5661  | scaffold3837                            | 5661                          | AT/ATT                                                        | GCCTCCGAGTCAATAC<br>CAAA    | ATTGAGGGTAGGGAG<br>CAGT    | 60.1                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3856_P4_5075  | scaffold3856                            | 5075                          | ATTTTTTTTTTT/ATTTTTTTTTTT                                     | AATTCCTCCTGTTGTG<br>TTTG    | CGGGGGAAAATGAGAC<br>TTTT   | 59.7                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold387_P4_113674 | scaffold387                             | 113674                        | GTATATATATATATATATATAT/GTAT<br>ATATATATATATAT                 | GTTGGTCCCTAGCAC<br>CGTA     | ACCCAATTACTGGAGA<br>TGCG   | 60.0                             | 797                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold387_P4_16023  | scaffold387                             | 16023                         | CAT/C                                                         | CACACCCCTTGTC AAC<br>ACTG   | TTAAGCTGAGAGCCTT<br>CCCA   | 60.0                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold387_P4_160969 | scaffold387                             | 160969                        | TTA/TTACTA                                                    | AGCTCCAAATCCAGAG<br>CAAA    | GGGATATGATCTTCTA<br>CCCCA  | 60.0                             | 835                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold387_P4_161414 | scaffold387                             | 161414                        | ATTTTTTT/ATTTTTTTTTTT                                         | CCACCCCACTGGTACT<br>GTTC    | TGCGACTATTGCAATTT<br>TG TG | 60.3                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold387_P4_161432 | scaffold387                             | 161432                        | ATAAAA/ATAAAGTAAAA                                            | TGGTACTCACATGAAA<br>ATCGAAA | GCGACTATTGCAATTTT<br>GTGAA | 59.5                             | 281                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold387_P4_22975  | scaffold387                             | 22975                         | AATC/AATCATC                                                  | CGCAATCTGAACAAAT<br>GACAA   | TCCACTAACCACCTTGA<br>CCC   | 59.7                             | 338                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold387_P4_23363  | scaffold387                             | 23363                         | ATGT/ATGTGT                                                   | GGGTCAAGGTGGTTAG<br>TGGA    | TCCTCTGCCTTTCATGT<br>GTG   | 59.8                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold387_P4_23485  | scaffold387                             | 23485                         | ATTTTT/ATTTTTTT                                               | GGGTCAAGGTGGTTAG<br>TGGA    | TCCTCTGCCTTTCATGT<br>GTG   | 59.8                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold387_P4_23589 | scaffold387                             | 23589                         | ATGTGTGTG/ATGTGTGTGTG                                         | GGGTCAAGGTGGTTAG<br>TGA      | TCCTCTGCCTTTCATGT<br>GTG   | 59.8                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold387_P4_2684  | scaffold387                             | 2684                          | CAAAAAAAAAAAAA/CAAAAAAAAA<br>AAA                              | TTCACATGGCATCATCT<br>CGT     | TTGTGAGGGTTTTATTCT<br>GGC  | 60.1                             | 797                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold388_P4_8749  | scaffold388                             | 8749                          | C/CCTATA                                                      | GCCCCAGAATTCAAAG<br>TTCA     | GCAGGAATCCTCTGTAC<br>CTCA  | 60.1                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3885_P4_621  | scaffold3885                            | 621                           | AAAA/AAAATAAA                                                 | CAAAGGACAATCACC<br>ACCA      | GCTTCCAATGGGACTC<br>AGAA   | 59.4                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold39_P4_39921  | scaffold39                              | 39921                         | TTATATATATATATATATAT/TTATAT<br>ATATATATATATATAT               | CGGCCATCTACGTTGT<br>CTTT     | AACAACTCCTTCGCTC<br>CAA    | 60.1                             | 316                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold39_P4_40229  | scaffold39                              | 40229                         | GAAAAAAAA/GAAAAAAAAA                                          | CGGCCATCTACGTTGT<br>CTTT     | GACATTGCATTTTGA<br>CACG    | 60.1                             | 924                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3900_P4_4432 | scaffold3900                            | 4432                          | CG/CAG                                                        | TTCTGAATCAATGTAGT<br>TCGTCTG | AAACCTTAATCCCAAA<br>CCC    | 59.3                             | 294                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3900_P4_4684 | scaffold3900                            | 4684                          | T/TC                                                          | GGGTTTGGGATTTAGG<br>GTTT     | CCTAGGAAAGACGAAA<br>ATGACC | 59.0                             | 250                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3900_P4_6679 | scaffold3900                            | 6679                          | AATTGGT/A                                                     | GGGTTTGGGATTTAGG<br>GTTT     | TGGACAACAACAAAAAT<br>TGACA | 59.0                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3907_P4_5333 | scaffold3907                            | 5333                          | AGGG/AGG                                                      | TGGAATTGGTGACATA<br>GGCA     | TCTCCACTACCCCATTT<br>TGC   | 59.9                             | 770                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3917_P4_4350  | scaffold3917                            | 4350                          | ATTT/ATTTT                                                    | TGAGGCGTATCATGTG<br>TTGA   | CAACTTTGGTGAGGCC<br>ATT   | 58.6                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3918_P4_4292  | scaffold3918                            | 4292                          | TAAAAAAAA/TAAAAAAAAA                                          | ATGCCCTTCGTCCTCTC<br>CTTT  | ACATTGAACTGCCCAT<br>TCC   | 60.2                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3918_P4_4537  | scaffold3918                            | 4537                          | CTTAATT/CTT                                                   | ATGCCCTTCGTCCTCTC<br>CTTT  | CGAGTGAAGGCATGGG<br>TATT  | 60.2                             | 914                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3923_P4_3230  | scaffold3923                            | 3230                          | GA/GAA                                                        | TGCTGCAACTTCTACAT<br>CCG   | AGAAAGCGTGAAACT<br>CCGA   | 60.0                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3927_P4_1574  | scaffold3927                            | 1574                          | ATTTTT/ATTTTTTT                                               | GAATCCTGGGCTGAA<br>TCAA    | CGTGGTAATCGCGTAG<br>GAAT  | 60.0                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3932_P4_1321  | scaffold3932                            | 1321                          | CAA/CA                                                        | AGGGAGGACGAAATG<br>ACCT    | GGCATCCAATAGGAGG<br>GTTT  | 59.9                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3934_P4_3831  | scaffold3934                            | 3831                          | CAAAAA/CAAAA                                                  | CATCTTCCCATGCTCC<br>ATT    | CTGGGGTTCCACTGTG<br>ACTT  | 59.9                             | 712                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3934_P4_972   | scaffold3934                            | 972                           | A/AAC                                                         | AAACGTTTTTGGTCCAT<br>CCA   | ACGAGAGAGAAAGCG<br>TGAG   | 60.2                             | 329                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold395_P4_195509 | scaffold395                             | 195509                        | GTATTATTATTATTATTATTATT/<br>GTATTATTATTATTATTATTATT           | AATGCGGTCTTCCCT<br>AAGT    | TTAGGCCCAATAGGAT<br>GTCG  | 60.0                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold395_P4_232446 | scaffold395                             | 232446                        | AAAT/AAATTTCTTCAAT                                            | TTCATTCCTAGCTTCGT<br>CAACA | AAACTCCAAACCGAA<br>GAAAAA | 59.9                             | 789                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                     |                         |                         |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold395_P4_247210 | scaffold395                             | 247210                        | TCCC/TCCCC                                                          | CTCGGTCATGGACCAATCTT    | AGAGGATGGTTGGCTTCCTT    | 59.9                             | 673                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold395_P4_64480  | scaffold395                             | 64480                         | TTTATTATTATTATTATTATTATTATTATT/TTTATTATTATTATTATTATTATTATTATTATTATT | AAATTGCCCAACCAATTACG    | GAAGGTGCGACCAGCTAAAG    | 59.7                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold395_P4_8212   | scaffold395                             | 8212                          | TT/TTAAT                                                            | TTCTGGTGGGATTCAATT      | AGCGATGCATGTCTCAAGTG    | 60.2                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3950_P4_12638 | scaffold3950                            | 12638                         | T/TTCAGCA                                                           | CAAGAGCCTAAGGATGCTGC    | AGCATGAAACGGTGGAAT      | 60.1                             | 919                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3950_P4_6762  | scaffold3950                            | 6762                          | C/CAAGAAGTTTT                                                       | AGTGGCATAGGAGTGCCATC    | ATCGGAGAAACGACATCTGG    | 60.1                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3950_P4_7394  | scaffold3950                            | 7394                          | GTATATATATATATA/GTATATATATATATATA                                   | CCAGATGTCGTTTCTCGAT     | TTGTATGACATCTCGCCACC    | 60.1                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3950_P4_7697  | scaffold3950                            | 7697                          | C/CTT                                                               | TTTCTCTTTTGGTGGTTGCC    | TCCACCAATATGCAAAAGCA    | 60.1                             | 854                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3950_P4_7767  | scaffold3950                            | 7767                          | TAAAA/TAAAA                                                         | GGTGGCGAGATGTCATACAA    | TCCACCAATATGCAAAAGCA    | 59.5                             | 366                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3950_P4_8338  | scaffold3950                            | 8338                          | ATGT/ATGTGTGTGT                                                     | TGCTTTTGCATATTGGTGGA    | AAAACATGGCCTTCAACTGG    | 60.1                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3950_P4_8477  | scaffold3950                            | 8477                          | TAAAAA/TAAAAA                                                       | TGCTTTTGCATATTGGTGGA    | AAAACATGGCCTTCAACTGG    | 60.1                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold3950_P4_8667  | scaffold3950                            | 8667                          | AAATAATAATAATA/AAATAATAA<br>A                                 | CCAGTTGAAGGCCATG<br>TTTT  | TTTTATGGAAGCATGTG<br>GCA   | 60.0                             | 528                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold3950_P4_8791  | scaffold3950                            | 8791                          | TAAAAAAAAA/TAAAAAAAA                                          | CCAGTTGAAGGCCATG<br>TTTT  | TTTTATGGAAGCATGTG<br>GCA   | 60.0                             | 528                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold3952_P4_963   | scaffold3952                            | 963                           | G/GT                                                          | GATGAAATCGAGGACC<br>AGGA  | TTTCATTTGGTCTTTTC<br>GGC   | 60.0                             | 470                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold396_P4_371269 | scaffold396                             | 371269                        | TAAAAAAAAA/TAAAAAAAA                                          | GTTTTGACTGGCCAA<br>AGAG   | GAGCGCTGTAAAAGAC<br>CACC   | 59.7                             | 588                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold396_P4_372299 | scaffold396                             | 372299                        | CATATATATATATATATATATATA/<br>CATATATATATATATATATATA           | TGTATTTCTGCGCATTC<br>TCG  | TTGTTAGTTTGACGAG<br>GGCA   | 60.0                             | 357                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold396_P4_425172 | scaffold396                             | 425172                        | TTTCT/TT                                                      | TGTTTCGTCAAAATGTC<br>CCAA | TCAAGGCGTGCAATC<br>ACAT    | 59.9                             | 535                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold396_P4_478537 | scaffold396                             | 478537                        | GAA/GAAA                                                      | CCACCATTCTTGAAGG<br>AGGA  | TCTCCAAATGATTGGAA<br>GGC   | 60.0                             | 502                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold396_P4_577559 | scaffold396                             | 577559                        | GAA/GA                                                        | TCCCAACCCAAATAAA<br>CCAA  | AAGCTCAACATGCAAAA<br>CCC   | 60.0                             | 538                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold396_P4_577641 | scaffold396                             | 577641                        | ACCC/ACCCC                                                    | TCCCAACCCAAATAAA<br>CCAA  | AAGCTCAACATGCAAAA<br>CCC   | 60.0                             | 538                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold396_P4_78617  | scaffold396                             | 78617                         | TAACA/TAACAACA                                                | CTAGTACGTCGGGTCG<br>GAAG  | TGGACTTTACGAATGC<br>TTGAGA | 59.8                             | 712                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold397_P4_149950 | scaffold397                             | 149950                        | TAAAA/TAAA                                                    | CAATCTGGGTTGTCA<br>GGTT   | GCTCAGCCTTGAGACC<br>AAAC | 59.8                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold397_P4_167388 | scaffold397                             | 167388                        | AATATATATATATATATATAT/AAT<br>ATATATATATATATATATATATAT         | GATTGCTTTGCGTGA<br>CAGA   | CGGTGAATCCTTTACG<br>GAGA | 60.0                             | 279                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold397_P4_191121 | scaffold397                             | 191121                        | AA/AACCA                                                      | GGAGGAGAGGAAGAC<br>CAAAGA | GGGTAGTTGTGGCTTG<br>CATT | 59.8                             | 114                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold397_P4_23238  | scaffold397                             | 23238                         | CATATATATATATAT/CATATATATAT<br>ATATAT                         | TGGAGGCGGCTACTAG<br>TGTT  | ATTGAATTCGCCATAAA<br>CGG | 59.9                             | 411                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold397_P4_23446  | scaffold397                             | 23446                         | A/AT                                                          | TGGAGGCGGCTACTAG<br>TGTT  | ATTGAATTCGCCATAAA<br>CGG | 59.9                             | 411                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold397_P4_28683  | scaffold397                             | 28683                         | AT/ATTT                                                       | CAATGCTCCATGTAAC<br>ACCCT | CAAACCCATTGGTCCC<br>TTTA | 59.9                             | 819                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold397_P4_360330 | scaffold397                             | 360330                        | C/CTCTTTCTA                                                   | AGCTTGACGCCTCAGT<br>CATT  | ACCCATATGAGGTGGT<br>GGAA | 60.0                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold397_P4_421976 | scaffold397                             | 421976                        | AATATATATATATATATATAT/AATAT<br>ATATATATATATATATAT             | TGGGGAATTTTGTGCT<br>GAAT  | TTGAAGGAGCCCTTA<br>CCTT  | 60.3                             | 716                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold397_P4_87352  | scaffold397                             | 87352                         | CATATATATATATATATAT/CATATAT<br>ATATATATATATAT                 | AATGAAGGAGGGAGG<br>GAGAA  | CGTCTCTAGCGCATGT<br>TCAA | 60.0                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_100881 | scaffold398                             | 100881                        | T/TCTGAATTTAGTTTG                                             | CGCGGTTACAATCTAG<br>CACA  | GCTTGCAAACATTTTCG<br>GTT | 59.9                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold398_P4_1047   | scaffold398                             | 1047                          | ATTTTTTTTT/ATTTTTTTTTT                                        | TGGGAGGATTTGCAAC<br>ATT   | CGGTCTATTATGATTGT<br>TTGCG  | 60.3                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_115536 | scaffold398                             | 115536                        | CTTTTTTTTT/CTTTTTTTTT                                         | GAGGTTGGTGCTTGGA<br>CAAT  | TGTCACGTTTTCCCAAC<br>AAA    | 60.0                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_13974  | scaffold398                             | 13974                         | ATTTTTTTTT/ATTTTTTTTT                                         | CCTTGAGTTCGACACT<br>CGGT  | TCCCTCAATCATGCGA<br>CATA    | 60.3                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_203973 | scaffold398                             | 203973                        | TTAT/TTATAT                                                   | GCTCGTCTTCATTTCAT<br>TGGA | CAATGGGAAACACTCT<br>CCGT    | 60.2                             | 133                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_216604 | scaffold398                             | 216604                        | G/GTA                                                         | TGGATGTTGTGTTGCT<br>TGGT  | TGAGGCTTGATGCTCT<br>GGTA    | 60.0                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_21767  | scaffold398                             | 21767                         | GAAAAATAAAAA/GAAATAAAAA                                       | TGTCTCATGGCAAATA<br>CCGA  | CCATGAGTGTTTCGTG<br>GATG    | 60.1                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_268890 | scaffold398                             | 268890                        | GAAAAAAAAA/GAAAAAAAAAAAA                                      | CCATGGAGATTAATGG<br>ACCG  | TGGGATCATCAAATAT<br>GACACG  | 60.1                             | 429                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_269244 | scaffold398                             | 269244                        | TAAA/TAAAA                                                    | CGTGCATATTTGATG<br>ATCCCA | CTCACTTGCCTGCATC<br>ACTC    | 60.6                             | 509                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_269435 | scaffold398                             | 269435                        | TAAAA/TAAA                                                    | CACGAAAACTCACCA<br>TTTTCA | AAAGCAACCTCACTTG<br>CCTG    | 60.0                             | 104                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_269493 | scaffold398                             | 269493                        | GTTTTTTTTT/GTTTTTTTTT                                         | TACTGGAGTGATGCAG<br>GCAA  | CAAAAGTCCAATAAAAT<br>GGAGCA | 60.4                             | 330                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold398_P4_270743 | scaffold398                             | 270743                        | TAAAAAAAAA/TAAAAAAAAA                                         | GTAGTGGTTGAAGTGG<br>CGGT    | CTACTCCATCGGGTCT<br>CCAA  | 60.0                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_270928 | scaffold398                             | 270928                        | TAAAAAAAAA/TAAAAAAAAA                                         | GTAGTGGTTGAAGTGG<br>CGGT    | CTACTCCATCGGGTCT<br>CCAA  | 60.0                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_272524 | scaffold398                             | 272524                        | CTTTT/CTTT                                                    | GGGGTGTGATTAGGG<br>GTCTT    | TGGGTGCAATTCTGAT<br>TCAA  | 60.1                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_291477 | scaffold398                             | 291477                        | CTTT/CTT                                                      | GGGCAAGAAAAGGGA<br>GAATC    | TTGAAAACAGCCTTT<br>TGG    | 60.0                             | 316                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_306564 | scaffold398                             | 306564                        | ATATTATTATTAT/ATATTATTATTAT<br>TAT                            | GTTGTGGGGAATATGG<br>TGCT    | CCCGCCATCTGTACAA<br>AAAC  | 59.7                             | 826                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_309013 | scaffold398                             | 309013                        | T/TC                                                          | TCACTTTGGAGGGTGC<br>TTCT    | TCGCAATAGGTTAGGA<br>TGGG  | 59.8                             | 763                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_318558 | scaffold398                             | 318558                        | CTGTG/CTG                                                     | CAAACTGCCACCATA<br>ACCC     | GCAATGACTGCCATGC<br>TAAA  | 60.2                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_33523  | scaffold398                             | 33523                         | AATTA/AA                                                      | AGTGATCCAACCTCAA<br>CATCG   | GGATTTCCACATTTCAT<br>AGCA | 60.0                             | 912                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_33778  | scaffold398                             | 33778                         | AATAT/AATATAT                                                 | TTTGATTTTGATTGAT<br>TTATTCG | CATGGCCACTCAAAGC<br>ACTA  | 59.3                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_33851  | scaffold398                             | 33851                         | A/ATTTTT                                                      | TTTGATTTTGATTGAT<br>TTATTCG | CATGGCCACTCAAAGC<br>ACTA  | 59.3                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold398_P4_347600 | scaffold398                             | 347600                        | TAAAAA/TAAAAA                                                 | TTTGGTCGGACATACT<br>CGCT   | CCAAGTGCCTCATA<br>ATTT   | 60.7                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_348902 | scaffold398                             | 348902                        | AATGTGACATATA/AA                                              | TTGAAGGTCGGAGACT<br>TTAACC | GGAAGAATGAAATCCG<br>CAAA | 59.6                             | 367                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_375858 | scaffold398                             | 375858                        | C/CA                                                          | CTTCTCCAGGAAGCAA<br>CCAG   | AAGGTCGCTCAAAGAG<br>CAAA | 60.0                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_379143 | scaffold398                             | 379143                        | AGAA/AGAAATTGAA                                               | TCTGAGGAAGAGGAGG<br>ACGA   | AGCGTGGCAGATTTTG<br>AAAG | 60.1                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_390541 | scaffold398                             | 390541                        | GAAAAA/GAAAAA                                                 | TGAAATGAGCATGATG<br>GGTG   | CAGTTTCCCGCTGAAA<br>CATA | 60.5                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_390628 | scaffold398                             | 390628                        | A/AC                                                          | CACGAGTGGAGCATGT<br>CAGT   | CAGTTTCCCGCTGAAA<br>CATA | 59.9                             | 114                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_449721 | scaffold398                             | 449721                        | ATTT/ATT                                                      | ACATGACCACAGTTCC<br>GTGA   | CTCGAGTCTCCAAC<br>GCAT   | 60.0                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_45043  | scaffold398                             | 45043                         | T/TGTA                                                        | CCCTACGACGTCCGTT<br>AAAA   | TCGCTCGTTGCACCAT<br>ATTA | 60.0                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_459574 | scaffold398                             | 459574                        | CAAAAAAAAA/CAAAAAAAAAA                                        | TCGGGTTGTAATGGGG<br>TTTA   | TTGGTCGTTTGAGCCT<br>TTCT | 60.0                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_463323 | scaffold398                             | 463323                        | AGG/AG                                                        | TGAAACTTTTCCCTTG<br>TGG    | AGCATGAGATCGAGCC<br>ACTT | 59.9                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold398_P4_466018 | scaffold398                             | 466018                        | ACCCCC/ACCCC                                                  | TGCATGCAGACAAGAG<br>TCAA | TTGGAAAAGCCACCT<br>ACAC   | 59.1                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_474746 | scaffold398                             | 474746                        | ATTTTTTTTT/ATTTTTTTTT                                         | TGTGGGGCACAAGTTT<br>GTTA | CCATCAAGTGGGAGTG<br>TCCT  | 60.0                             | 192                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_49024  | scaffold398                             | 49024                         | GAAAAAAAA/GAAAAAAAAA                                          | CTTGTGGCTTGTGCGT<br>CTAA | TTTTCTTCACATGCC<br>ATCTT  | 60.1                             | 604                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_492512 | scaffold398                             | 492512                        | ATTTTTTTTT/ATTTTTTTTT                                         | AGCTTCTGAATAGCT<br>GCGG  | CCATTGATTGACCAT<br>GTG    | 59.8                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_494953 | scaffold398                             | 494953                        | GAAAAAAAA/GAAAAAAAAA                                          | TTCCCGAGTTGGTCC<br>TTTA  | CGGGCAGTGTTTACG<br>TTCT   | 59.5                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_51327  | scaffold398                             | 51327                         | CATA/CA                                                       | TTGAAAACATGTGCAT<br>TGCT | GGGGTGTAGAATTCT<br>CCCTTT | 59.2                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_69760  | scaffold398                             | 69760                         | GAAAAA/GAAAAA                                                 | GGCTGTTCATGGTTGG<br>TTTT | AGGGTATTGCCACAAA<br>TGGA  | 59.8                             | 795                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold398_P4_75332  | scaffold398                             | 75332                         | ATTTTTTTTT/ATTTTTTTTT                                         | AAACCCAAATCTCCGC<br>TTTT | CAACCCCAATCTTTGA<br>GGA   | 59.9                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold3985_P4_15896 | scaffold3985                            | 15896                         | C/A/C                                                         | GGGTAGCCAGTCCCTC<br>CTAC | TCGACTTGTCATCGC<br>TTTG   | 60.0                             | 760                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_1009432 | scaffold40                              | 1009432                       | AAAAGAAA/AAAA                                                 | CGTTCATGAGCGGTGG<br>TAA  | GCAACGAAGCCACACC<br>TATT  | 60.7                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                           | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                         |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold40_P4_101065  | scaffold40                              | 101065                        | GAGTGTGGAAA/GAGTGTGGAAA<br>CAAGTGTGGAAA                                                                 | AATAACAACGCTCCCA<br>AACG  | CCTCCCTAGCGTTACA<br>ACCA    | 60.0                             | 648                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_1060709 | scaffold40                              | 1060709                       | C/CT                                                                                                    | CTCAACCTTAATTGC<br>GGGA   | AGGTCAATGACTGGGA<br>GGTG    | 60.1                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_123494  | scaffold40                              | 123494                        | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATT/TTTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATT | TTTGGTCCCCAACAC<br>CTTA   | TTAGTTCACGTGTCCC<br>CCTC    | 60.2                             | 959                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_363147  | scaffold40                              | 363147                        | T/TC                                                                                                    | TCACCTATCACGGTC<br>AACA   | CTGGGTGTTATGTTGC<br>GTTG    | 60.0                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_41230   | scaffold40                              | 41230                         | CTTT/CTTTT                                                                                              | TGGGAGTCATGGATGA<br>GTGA  | CCGAGCCAAAATCCAA<br>AATA    | 60.0                             | 341                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_466805  | scaffold40                              | 466805                        | ATTTTT/ATTTT                                                                                            | GCCTGAAATATGCCGA<br>GGTA  | TCGGCTCTCCATGTCA<br>GATA    | 60.1                             | 420                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_56808   | scaffold40                              | 56808                         | CATA/CATATA                                                                                             | ATTTGCACGGAAAGTC<br>ATCC  | CCTCCACCTCCTCCTC<br>CTAC    | 59.9                             | 810                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_59284   | scaffold40                              | 59284                         | TAAAAAA/TAAAAAA                                                                                         | TCAGCCAAAAGCTGA<br>TG TG  | AGTTGACATTTGATGGT<br>CTATGG | 60.0                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_757293  | scaffold40                              | 757293                        | CTTTTTTTTT/CTTTTTTTTTT                                                                                  | TGGGCCAAATAAATCA<br>AGATG | CAAACCCCATTTCTTG<br>TGT     | 59.8                             | 886                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_812138  | scaffold40                              | 812138                        | TAAAAA/TAAAAA                                                                                           | ACGAAAGGGGTAAGC<br>CTAA   | AATGGTGAGGAACCTT<br>GCTG    | 60.0                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold40_P4_819231 | scaffold40                              | 819231                        | GATATATATATATATATAT/GATAT<br>ATATATATATATATATAT               | TTGTGCCTTCTTCTG<br>CCTT     | TTTTGTGATAGGTTCT<br>GATGC  | 60.0                             | 953                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_829558 | scaffold40                              | 829558                        | TAAAAA/TAAAAA                                                 | CAACAGCTGCCCTCT<br>TTAC     | ACAGATGGACACAACG<br>GTGA   | 59.9                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_850223 | scaffold40                              | 850223                        | TTATATATATATATATATATATAT<br>TATATATATATATATA                  | AAAGAGTTGCCAATA<br>TCCGT    | TAAAGCGGACTCATTG<br>TCCC   | 57.8                             | 496                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_852290 | scaffold40                              | 852290                        | AT/ATGT                                                       | AAAGGGGAAATTGGGA<br>AGTG    | TTGGATGACACGATGA<br>CTTGA  | 60.2                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_854889 | scaffold40                              | 854889                        | CAAA/CAA                                                      | ATTCACCCAAATTCCA<br>TGC     | GCATGTTGGGTTTCCT<br>TATGA  | 59.6                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_855888 | scaffold40                              | 855888                        | TTGGTGACAAT/TT                                                | ACAAACTCGGGAAACA<br>AACG    | TGACGTCTCCATCTCA<br>ACCA   | 60.0                             | 797                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_864935 | scaffold40                              | 864935                        | ATTTTTTTTTTTTT/ATTTTTTTTTT                                    | TGTGGGGGATCAAATA<br>AGGA    | GGCCATAAGTCAGTGT<br>CGGT   | 60.1                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_867619 | scaffold40                              | 867619                        | TTATTCATAT/TTAT                                               | GCACAAATACTCTCCC<br>TCATCC  | TGTGGTTGTTTTGCT<br>GGAC    | 60.0                             | 923                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_894794 | scaffold40                              | 894794                        | TTATATATATATATATATATATATA<br>TATAT/TTATATATATATATATATA<br>T   | AAAATTGGATTTATACA<br>ATGGCG | CGCTTACAAACGCTGT<br>AAAAGA | 59.2                             | 597                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_895179 | scaffold40                              | 895179                        | TAA/TAAA                                                      | TTGATGCCTCAATCTTT<br>CAAAC  | CGCTTACAAACGCTGT<br>AAAAGA | 60.1                             | 263                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                                                                                                              |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold40_P4_901398 | scaffold40                              | 901398                        | A/AG                                                                                                                                         | AATTGTTGTTGCTCCC<br>GTTC  | TGTATTTCCACCCTC<br>GTTT   | 60.0                             | 339                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_924554 | scaffold40                              | 924554                        | ATTTTTTTTT/ATTTTTTTT                                                                                                                         | TTTCCCATTGGTGTGA<br>GTGA  | AACCTAACAGAGCGGG<br>GATT  | 59.9                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_93804  | scaffold40                              | 93804                         | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATT/TTTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTATT | GGAATGGGGTGATGTC<br>CTTA  | TTGTGTGGAGGTTGTG<br>TTGA  | 59.6                             | 254                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_954482 | scaffold40                              | 954482                        | TAAAAAAAAA/TAAAAAAAAA                                                                                                                        | CTTTTAGAGGGGAGG<br>AACG   | TTGCCTCCCATTTTATC<br>TCTG | 60.1                             | 181                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_980769 | scaffold40                              | 980769                        | CA/CAAA                                                                                                                                      | GACGAACCACTAGCAC<br>ACGA  | CGGGGATTGCCATCTA<br>ACTA  | 59.9                             | 174                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold40_P4_990512 | scaffold40                              | 990512                        | AC/ACC                                                                                                                                       | ATAATGGGAGCTTTTG<br>CCCT  | CTCACATCTACGGGC<br>ACTA   | 59.9                             | 745                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold400_P4_12532 | scaffold400                             | 12532                         | AATATATATATATATATATATAT<br>/AATATATATATATATATATATATA<br>TATATAT                                                                              | CTTTTGATGCCCGGAT<br>TAAA  | GTACCGCCTATCACAG<br>GCAT  | 59.9                             | 777                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold400_P4_1544  | scaffold400                             | 1544                          | ATT/A                                                                                                                                        | GAAGAGTTACGCGGAC<br>AAGC  | TCTCCGTAAAGGATTC<br>ACCG  | 60.0                             | 686                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold400_P4_26945 | scaffold400                             | 26945                         | GGAGAGAGAGAGAGAGAGAGAG/<br>GGAGAGAGAGAGAGAGAGAGAGA<br>GA                                                                                     | AAAGATGATGCACGAT<br>TTTCC | TCAAGATGCTGTGACG<br>ATCAG | 59.0                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold400_P4_43610 | scaffold400                             | 43610                         | T/TG                                                                                                                                         | AATGGTGGTGGATTTT<br>GCAT  | ACACGCGTTCGTGAAT<br>CATA  | 60.1                             | 619                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                            | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                          |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold404_P4_237330 | scaffold404                             | 237330                        | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATT/TTTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>T | AGAGGCAAACAAGAAC<br>CGAA   | GCAACCAAAATTGAAACA<br>CCA | 59.9                             | 581                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold404_P4_269302 | scaffold404                             | 269302                        | GAIAAAAAAAAA/GAIAAAAAAAAA                                                                | CCCTCAAATGAGAACC<br>AGGA   | GGGAGAATTGTAACAC<br>CCCA  | 60.0                             | 981                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4041_P4_1126  | scaffold4041                            | 1126                          | TTATATATATATATATATATAT/TTAT<br>ATATATATATATATATATATAT                                    | GGGTTGGGATATGTTA<br>GCAAAA | GTCCAAACCCAGCACA<br>ATCT  | 60.1                             | 192                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4041_P4_15570 | scaffold4041                            | 15570                         | AT/ATGTGTGTGT                                                                            | AGATTGTGCTGGGTTT<br>GGAC   | AAGGAAATGAGGAAAA<br>TGGGA | 60.0                             | 803                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4041_P4_15702 | scaffold4041                            | 15702                         | T/TG                                                                                     | AGGAATTGGATCGGGA<br>GATT   | AAGGAAATGAGGAAAA<br>TGGGA | 59.7                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4041_P4_15753 | scaffold4041                            | 15753                         | TAAAAAAAA/TAAAAAAAAAAAAA                                                                 | AGGAATTGGATCGGGA<br>GATT   | AAGGAAATGAGGAAAA<br>TGGGA | 59.7                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4041_P4_15867 | scaffold4041                            | 15867                         | AT/ATT                                                                                   | GGGTTGGGATATGTTA<br>GCAAAA | GAATGCGAAAGCCACA<br>ATTT  | 60.1                             | 851                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4041_P4_15956 | scaffold4041                            | 15956                         | TAAAAAAAA/TAAAAAAA                                                                       | TCCCATTTTCCTCATTT<br>CCTT  | GAATGCGAAAGCCACA<br>ATTT  | 59.8                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4041_P4_16171 | scaffold4041                            | 16171                         | AAA/AAATTAA                                                                              | GGCACGTCCTATTTT<br>TGAA    | GAATGCGAAAGCCACA<br>ATTT  | 59.9                             | 345                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4041_P4_16422 | scaffold4041                            | 16422                         | A/ATTTAT                                                                                 | GGCACGTCCTATTTT<br>TGAA    | CCGAGAATGCCGCTAT<br>GTAT  | 59.9                             | 754                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')    | Reverse primers (5'-3') | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|----------------------------|-------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                               |                            |                         |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold4041_P4_39114 | scaffold4041                            | 39114                         | A/AAG                                                                         | GTGTGGTGACGAACCTTTT        | CGTGTCTCAAACTCGAGGA     | 59.9                             | 769                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4041_P4_994   | scaffold4041                            | 994                           | CT/CTTT                                                                       | TCATTCTAATTCCTGCC<br>TGATG | GTCCAAACCCAGCACATCT     | 59.2                             | 494                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4045_P4_1604  | scaffold4045                            | 1604                          | GTTT/GTTTT                                                                    | CACAACGCCAAGATGCTAGA       | CCCCCTTTTGCATAAGTGA     | 60.0                             | 779                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4057_P4_31206 | scaffold4057                            | 31206                         | GTTTTTT/GTTTTTTT                                                              | TGGTCGACAAGCAACTGAAG       | CTCCCCCTTTTGGCAT<br>AAT | 60.0                             | 649                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4064_P4_1246  | scaffold4064                            | 1246                          | ATTTT/ATTTT                                                                   | TATGCATGCGGACAAGAGTC       | GTGTTGCACTGCATGCTTTT    | 59.8                             | 277                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4064_P4_1366  | scaffold4064                            | 1366                          | TTAT/TT                                                                       | AAAAGCATGCAGTGCAACAC       | TCCCGTCTGAAAATTATGCG    | 59.9                             | 367                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4064_P4_2033  | scaffold4064                            | 2033                          | ATTTTTTT/ATTTTTTTT                                                            | CTGCAAATGAGTGCCTTGA        | AGGTTTCTTTGGCCC<br>ACTT | 60.0                             | 349                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4064_P4_805   | scaffold4064                            | 805                           | TTATATATATATATATATATATATATATA<br>TATATA/TTATATATATATATATATATATATATATATATATATA | ATGCTCTGCACTTGCA<br>GCTA   | TGACTTGACTCTTGCC<br>GCA | 59.9                             | 581                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold408_P4_130988 | scaffold408                             | 130988                        | T/TG                                                                          | GTGGTGATTTTGGGAGGCC        | TCGTGGTTTTGGTGTTGGTA    | 59.2                             | 662                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold408_P4_131029 | scaffold408                             | 131029                        | A/AAG                                                                         | GTGGTGATTTTGGGAGGCC        | TCGTGGTTTTGGTGTTGGTA    | 59.2                             | 662                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold408_P4_3395  | scaffold408                             | 3395                          | G/GGTAATA                                                     | CAAGGAGGAGCAAGAT<br>CAGG | GGGAAAGCGACGTGT<br>ATTA    | 59.9                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold408_P4_3569  | scaffold408                             | 3569                          | TCCCC/TCCCCC                                                  | TAATACACGTCCGCTTT<br>CCC | CGAACCTGCTGTCCAA<br>AAAT   | 60.0                             | 394                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold408_P4_51701 | scaffold408                             | 51701                         | GTTTTTTTTT/GTTTTTTTTT                                         | CCCGAAAGTCTCCAA<br>AAAT  | GGATCTTAGCGTTTGT<br>TTGC   | 60.3                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4088_P4_5270 | scaffold4088                            | 5270                          | AT/A                                                          | ATCAACTTGCAAGGCA<br>GCTT | TACCATTCAATTGGCG<br>AACA   | 60.0                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold41_P4_113850 | scaffold41                              | 113850                        | CG/C                                                          | ACACCAGTCCCCTAA<br>CCAA  | TCACTTGAAAGTGTGA<br>TGGTTG | 59.3                             | 404                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold41_P4_114200 | scaffold41                              | 114200                        | ATTTTTTTTT/ATTTTTTTTTTT                                       | ACCAGTCCCCTAAAC<br>AACA  | TTGATTGAAACATTGAT<br>TTCCG | 59.3                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold41_P4_116041 | scaffold41                              | 116041                        | ATT/ATTT                                                      | GGACGGACAATTCAAA<br>ATGG | GCACTGCACCAAAACA<br>CAAC   | 60.2                             | 788                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold41_P4_122249 | scaffold41                              | 122249                        | TG/TCCCCGATGG                                                 | TCGCTACGGCTCTAGT<br>GGTT | AAGTCCTGTAGCCGAA<br>AGCA   | 60.0                             | 294                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold41_P4_122306 | scaffold41                              | 122306                        | ATT/ATTT                                                      | TCGCTACGGCTCTAGT<br>GGTT | AAGTCCTGTAGCCGAA<br>AGCA   | 60.0                             | 294                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold41_P4_122382 | scaffold41                              | 122382                        | C/CG                                                          | TCGCTACGGCTCTAGT<br>GGTT | AAGTCCTGTAGCCGAA<br>AGCA   | 60.0                             | 294                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                              |                           |                              |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold41_P4_181968  | scaffold41                              | 181968                        | AATATATATATATATATATATATAT/A<br>ATATATATATATATATATATATATATA<br>TAT                                            | TGCGTTACGTGTGAAA<br>TGGT  | TCCGATAAAATCTCCGT<br>TCG     | 60.0                             | 566                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold41_P4_83801   | scaffold41                              | 83801                         | T/TAATAG                                                                                                     | GAGTGTGGCTGGTTTG<br>GAGT  | CACCTCATTTGCCATTT<br>CTTT    | 60.2                             | 841                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4107_P4_9634  | scaffold4107                            | 9634                          | CT/CTAAATT                                                                                                   | CCTAAACCTAAACCA<br>AAAACC | TCGTCCAATAAGAACAA<br>AAGTCAA | 57.4                             | 127                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4108_P4_4843  | scaffold4108                            | 4843                          | AAAACCTTAAACCTTAAACCTAAA<br>CCTTAAACCTTAAACC/AAAACCTTA<br>AACCTTAAACCTTAAACCTTAAACC<br>CTAAACCTTAAACCTTAAACC | CGAAACCTTAAACCA<br>AACA   | TGATTAAGCGTTCCGG<br>ATTTC    | 59.8                             | 301                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4108_P4_8749  | scaffold4108                            | 8749                          | CTT/CT                                                                                                       | CAAACCGGAAACGCT<br>TAAC   | TTTTGGGCTTCGAGTTT<br>AGG     | 59.6                             | 294                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold411_P4_251051 | scaffold411                             | 251051                        | TTTATTATTATTATTATTATTATT<br>ATTA/TTTATTATTATTATTATTATTA<br>TTATTATTATTA                                      | CCCTTCTCCTTCCGTA<br>GAGC  | TTGACACGGTCTGCGT<br>AGTT     | 60.3                             | 371                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold411_P4_298521 | scaffold411                             | 298521                        | AT/AGATTGT                                                                                                   | CTTGCATGGCAATTAT<br>CCAA  | TTGGGCTGATGCAATA<br>AACA     | 59.5                             | 469                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold411_P4_3049   | scaffold411                             | 3049                          | GTTTTTTTTTTTT/GTTTTTTTTTTTT<br>TT                                                                            | TTGGGTTACGTCCAGT<br>CCTC  | AGATCGAAACTGCACC<br>ATCC     | 60.0                             | 661                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold411_P4_340187 | scaffold411                             | 340187                        | TAAAAA/TAAAA                                                                                                 | ATTGGTGTTGTGCAGG<br>TGAA  | CACGGTTGTGATGACT<br>GGAC     | 60.0                             | 109                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold411_P4_373772 | scaffold411                             | 373772                        | TAAAAAA/TAAAAAA                                                                                              | TGCCCTCAAATTCCTCT<br>CAC  | GAAAAACGATGTCCGA<br>TTTGA    | 60.2                             | 772                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                          | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                                                        |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold411_P4_436040 | scaffold411                             | 436040                        | CATA/CATATA                                                                                                                                                            | ACCCGAATACCTCAAG<br>GGTC | TCGTTTATTCGGATTCTC       | 60.2                             | 922                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4155_P4_7060  | scaffold4155                            | 7060                          | AATATATAT/AATATATATAT                                                                                                                                                  | CGGTTCAACGTAACCG<br>ACTT | TTGGGCAACAATCGAT<br>GTAA | 60.0                             | 402                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4176_P4_8263  | scaffold4176                            | 8263                          | GAAA/GAAAA                                                                                                                                                             | ACTATGTTTCGGGTTTT<br>GCG | TCCTGGTCCTCGATTT<br>CAAC | 60.0                             | 130                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold418_P4_35361  | scaffold418                             | 35361                         | ATTTTTTTTTTT/ATTTTTTTTTT                                                                                                                                               | CCCCTAAACTTTTGTG<br>GGCT | CGTGTCTCATTTGCTTT<br>TGG | 60.3                             | 819                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold418_P4_60007  | scaffold418                             | 60007                         | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>TTATTATTATTATTATTATTATTATT<br>TTATCTATTATTATTATTATTATT | CACATGCACGGATTCA<br>TTGT | TGCATGTGCCAAAAAC<br>AAAT | 60.4                             | 747                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold418_P4_9574   | scaffold418                             | 9574                          | TTATATATATATATATATATATATA<br>TATATA/TTATATATATATATATATAT<br>ATATATATATA                                                                                                | TGAATATGTGGCGGAA<br>AACA | CATGTGTGAGGGTTGT<br>GGAG | 59.9                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold419_P4_134403 | scaffold419                             | 134403                        | GAAAAAAAAA/GAAAAAAAAA                                                                                                                                                  | AGTGGGAGCGATCAAA<br>TCAG | ATTGGTCCATGGGATT<br>TTCA | 60.2                             | 872                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold419_P4_148404 | scaffold419                             | 148404                        | CTATATATATATATATAT/CTATAT<br>ATATATATATATAT                                                                                                                            | GAGCAACGACCTATTC<br>TGCC | GGTGAGGATCTGGTGT<br>GGTT | 59.8                             | 750                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold419_P4_148627 | scaffold419                             | 148627                        | CA/CAA                                                                                                                                                                 | AACAAGCAAGCCATTC<br>AAGC | GGTGAGGATCTGGTGT<br>GGTT | 60.4                             | 657                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold419_P4_167353 | scaffold419                             | 167353                        | CTATATATATATATATATATAT/CT<br>ATATATATATATATATATATATATA<br>T                                                                                                            | CGCATCGATAACCAAT<br>CTGA | GATGAGTGCATGAGGA<br>AGCA | 59.6                             | 430                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                       | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                     |                           |                           |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold419_P4_263511 | scaffold419                             | 263511                        | TTATATATATATATATATATA/TTATA<br>TATATATATATA                                                         | AATAGTGACGAAAAAC<br>CGCA  | GATCTAATGGGGCAGA<br>CGAA  | 58.3                             | 780                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold419_P4_297177 | scaffold419                             | 297177                        | AATAAAAAAT/AATAAAAAATATAAAA<br>AAT                                                                  | GGAGGCGTGAA GTTCT<br>TGAG | TGTTTTGATCCAAAATG<br>GCT  | 60.0                             | 840                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold419_P4_30067  | scaffold419                             | 30067                         | TTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAA/TTAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAA | TTCACAATTTGGCGATT<br>TGA  | GAGGTGGTATTTGCCG<br>AGAA  | 60.1                             | 227                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold419_P4_95800  | scaffold419                             | 95800                         | CATATATATATATATATATATAT/C<br>ATATATATATATATATATATATAT                                               | GGAAGAAGAAGAAGGA<br>CGGG  | CATTGTGGATTGAATG<br>CGA   | 60.2                             | 391                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4192_P4_3668  | scaffold4192                            | 3668                          | T/TC                                                                                                | ATCCAAGTTTGAGGCA<br>ATCG  | CGATTTTCGAGGTCT<br>TGTT   | 60.1                             | 484                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4192_P4_3800  | scaffold4192                            | 3800                          | CAATCGAT/CAATCGATCGACGAAT<br>CGAT                                                                   | ATCCAAGTTTGAGGCA<br>ATCG  | GGGCAATGAATGTTTG<br>TGTG  | 60.1                             | 673                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4197_P4_16348 | scaffold4197                            | 16348                         | GAAA/GAA                                                                                            | AATGGCCACGAATCTG<br>AAAG  | GTGCGGAAGCCATGAG<br>TAAT  | 60.1                             | 483                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4197_P4_29532 | scaffold4197                            | 29532                         | TAAAATCAAATCAAATCAAATCA<br>AAATCAAA/TAAAATCAAATCAAAA<br>TCAAATCAAA                                  | CCATTTTACCCCTGTC<br>CCTT  | GCCTATTTGACATTTGC<br>CTGA | 60.0                             | 559                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold420_P4_210416 | scaffold420                             | 210416                        | T/TAC                                                                                               | GGAAGATCCTCGAGTT<br>TCCC  | ACCATGCAAAGACATC<br>CACA  | 60.0                             | 536                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold420_P4_265273 | scaffold420                             | 265273                        | GAAAAAAA/GAAAAAAA                                                                                   | CGTGATCGTGTTTGGT<br>TGTC  | GGGAATGGCAGCAAT<br>AGAA   | 60.0                             | 587                                           | INTERGENIC                                           | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                           | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                         |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold420_P4_69655  | scaffold420                             | 69655                         | CAA/CAAA                                                                                                                                | ATGGCGAAGAATTATG<br>GTGC | CATGTACCGCCCATCT<br>CTTT   | 59.9                             | 265                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold420_P4_70835  | scaffold420                             | 70835                         | AG/AACATCTG                                                                                                                             | TCCGGAGAAATCAAAA<br>TTGC | ACGTGTTACGCATTGG<br>CATA   | 60.0                             | 380                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold420_P4_85641  | scaffold420                             | 85641                         | AATTATAATTATA/AA                                                                                                                        | ACGCGTTCATGCACTA<br>CAAG | GATGGTGTGAGTGGAG<br>CTGA   | 59.9                             | 982                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4213_P4_2577  | scaffold4213                            | 2577                          | GC/GCC                                                                                                                                  | AGTGCCGGTGCATTTT<br>ATTG | CGCATTCCAATTCAAT<br>TCC    | 60.0                             | 780                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4221_P4_48310 | scaffold4221                            | 48310                         | TGGTTTTG/T                                                                                                                              | CATCCCCGTTTAATAC<br>CACG | GTCCTTCCAAGCAACA<br>CCAT   | 60.1                             | 712                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4221_P4_50496 | scaffold4221                            | 50496                         | AA/AATAATA                                                                                                                              | AAGACCCGCCTTTTTT<br>TAGC | GTCCTTCCAAGCAACA<br>CCAT   | 59.9                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4221_P4_54414 | scaffold4221                            | 54414                         | GTGTTTTTTTTT/GTTTTTTTTT                                                                                                                 | GAGCCCGAATCGTTAT<br>TTTG | TTGTGGTATACCCGAC<br>AAAGAA | 59.5                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4221_P4_54517 | scaffold4221                            | 54517                         | ATTAGGG/ATTAGGGTTAGGG                                                                                                                   | GAGCCCGAATCGTTAT<br>TTTG | TTGTGGTATACCCGAC<br>AAAGAA | 59.5                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4221_P4_54616 | scaffold4221                            | 54616                         | CAATAATAATAATAATAATAATA<br>ATAATAATAATAGTAATAATAATAAT<br>AATA/CAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAATAG<br>TAATAATAATAATAATA | GAGCCCGAATCGTTAT<br>TTTG | TTGTGGTATACCCGAC<br>AAAGAA | 59.5                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4221_P4_569   | scaffold4221                            | 569                           | AAAGAA/AAA                                                                                                                              | ATTGATTTTGAATCGC<br>CCA  | CAGTTTCCTGCCAGCC<br>TTAG   | 60.3                             | 441                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold4221_P4_691   | scaffold4221                            | 691                           | A/AG                                                          | CTAAGGCTGGCAGGAA<br>ACTG  | CGCTTCTTTGGTCATG<br>CAA        | 60.0                             | 443                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4221_P4_7762  | scaffold4221                            | 7762                          | TAAAAA/TAAAA                                                  | TGCCAGAACTGATTTT<br>CTGCT | GAGCGCTGTAAACAC<br>CTCC        | 60.0                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold424_P4_63623  | scaffold424                             | 63623                         | GAAACCCTTA/GA                                                 | AGTTCGATGTAGTCGG<br>GTGG  | GGTCCTCGATTTCATCT<br>GGA       | 60.0                             | 813                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4243_P4_1042  | scaffold4243                            | 1042                          | CGG/CG                                                        | GGTACGGAATTGCCT<br>GAAA   | GGTCCTCGATTTCATCT<br>GGA       | 59.9                             | 204                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4243_P4_14917 | scaffold4243                            | 14917                         | CT/CTT                                                        | TGCTTGATTGCTTGAG<br>TTCC  | GATGAAATCGAGGACT<br>GGGA       | 59.0                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4243_P4_16781 | scaffold4243                            | 16781                         | CTTTTT/CTTTTT                                                 | TTTCATCTGGACTTTTC<br>GGG  | TCGAGGATAGGGAGAC<br>CCTT       | 60.0                             | 964                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4243_P4_17716 | scaffold4243                            | 17716                         | AGG/AGGG                                                      | AGGCGATTTTCGTACC<br>ACAC  | AAACCGTGTTTCGGTTT<br>CTG       | 60.0                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4269_P4_11557 | scaffold4269                            | 11557                         | AAATAATAATAAT/AAATAATAATAAT<br>AAT                            | GGGTTTGAGGTTTCGGG<br>TTAT | TCATCTACGTTTTGTAG<br>TTGTACTCA | 60.1                             | 774                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold429_P4_127972 | scaffold429                             | 127972                        | AACAC/AACACAC                                                 | AATCCAATGACACAAA<br>CGCA  | CCAATTTTGTGCATCCA<br>ATG       | 60.0                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold429_P4_13926  | scaffold429                             | 13926                         | CTTTT/CTTTT                                                   | TAGGCTTCAAGGAAGC<br>TGGA  | GGCTCTTGATGCCAAT<br>TGTT       | 60.1                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold429_P4_69799  | scaffold429                             | 69799                         | TAA/TA                                                        | TGGATGCACGAGATTG<br>GTTA | AGGTCATTTTCGTCTC<br>CCT   | 60.1                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4319_P4_1139  | scaffold4319                            | 1139                          | ATTT/AT                                                       | CGATTTCCTCACGAC<br>AAAT  | TTTGGACAGCTACAA<br>GTGGTT | 59.9                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4319_P4_1189  | scaffold4319                            | 1189                          | A/AGTCAAAT                                                    | CGATTTCCTCACGAC<br>AAAT  | TTTGGACAGCTACAA<br>GTGGTT | 59.9                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4319_P4_1245  | scaffold4319                            | 1245                          | TAAAAA/TAAAA                                                  | CGATTTCCTCACGAC<br>AAAT  | TTTGGACAGCTACAA<br>GTGGTT | 59.9                             | 582                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold433_P4_144085 | scaffold433                             | 144085                        | GAAAAAAAAA/GAAAAAAAAA                                         | TGAAAGGTAGGGTCGA<br>ATGG | TCGCTCATTTTCATTT<br>CCC   | 59.9                             | 225                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold433_P4_144718 | scaffold433                             | 144718                        | GCC/GCCC                                                      | TGGCTAATCGCCAGTT<br>TTCT | AATGATCGTCTTCGGA<br>TTGC  | 59.8                             | 854                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold433_P4_146170 | scaffold433                             | 146170                        | TAAAAAAAAA/TAAAAAAAAA                                         | GTTGCCAAAGCAGGGT<br>AAAA | TGAAACGGATTTTCAAC<br>CAA  | 60.1                             | 434                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold433_P4_146841 | scaffold433                             | 146841                        | AATTATTATTATTATTATTATTAT<br>T/AATTATTATTATTATTATTATT          | TGGTGACAATTGATG<br>GTTCT | CAGTGCGATGGAGAAA<br>TCAA  | 57.9                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold433_P4_157672 | scaffold433                             | 157672                        | GATATATA/GATATA                                               | GCATTCAAGATGGGC<br>AGTT  | AATGATCGTCTTCGGA<br>TTGG  | 60.1                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold433_P4_15776  | scaffold433                             | 15776                         | ATT/ATTGTT                                                    | TACCGTCGTCAGTTCA<br>CACC | ACGTATCCCCAGGTGC<br>AATA  | 59.6                             | 322                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold433_P4_19270 | scaffold433                             | 19270                         | TAAAAAAAAA/TAAAAAAAAA                                         | TGCACACCGTTTGAA<br>AATA  | CCAAATCTTCGAAGGC<br>CATA | 60.0                             | 926                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold433_P4_66257 | scaffold433                             | 66257                         | TATAG/TATAGAAATAG                                             | CCAGCCAACGACCTCA<br>TACT | TGTGTTGATCCGATTG<br>GAAA | 60.1                             | 862                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold433_P4_70798 | scaffold433                             | 70798                         | CGGG/CGG                                                      | GGGTACGTCGGTGAGT<br>GTTT | GAACAAAAGAGAACGG<br>CTGC | 59.9                             | 751                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold433_P4_8392  | scaffold433                             | 8392                          | A/AAT                                                         | ACATGTAAGGCAAGGC<br>CAAC | GCCAGTCACCCCAACT<br>TTTA | 60.0                             | 377                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold433_P4_86247 | scaffold433                             | 86247                         | GTTT/GTT                                                      | GCCCTCAGATGAGAGT<br>CAGG | AGAATTTACGAGCAGC<br>GGAA | 59.9                             | 287                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4349_P4_1831 | scaffold4349                            | 1831                          | GTTTT/GTTT                                                    | AGGTCATTTTCGTCCT<br>CCCT | CAACACACCTGTTGG<br>ATGC  | 59.9                             | 182                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold435_P4_57484 | scaffold435                             | 57484                         | ATTTTTTTTT/ATTTTTTTTT                                         | GCATGTGGGATTCGTA<br>CCTT | ATGTGCTTGACAAGAA<br>TGCG | 59.8                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold435_P4_89652 | scaffold435                             | 89652                         | ATTTTTTTTT/ATTTTTTTTT                                         | TGTTGTCGTCGTCCTT<br>GGTA | CACGTTTTGACGGAGA<br>GTCA | 60.2                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold436_P4_67143 | scaffold436                             | 67143                         | A/AC                                                          | CAAACACCTGTTGG<br>ATGC   | AGGTCATTTTCGTCCTC<br>CCT | 60.0                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold436_P4_68438 | scaffold436                             | 68438                         | A/AT                                                          | GGCCGGATGAAAATGA<br>ACTA | ATTTTCGTCCTCCAAG<br>GCT  | 59.9                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)      | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                    |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold4366_P4_1890  | scaffold4366                            | 1890                          | G/GC                                                               | GGACATGAATAGGGCA<br>ATGG | GGTCATTTTGTCCAC<br>GCTT  | 60.2                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4367_P4_11881 | scaffold4367                            | 11881                         | CTAAAAATTTAAAAATTAA/CTAAAAAT<br>TAA                                | TGGATGCACAAGATGG<br>GTTA | ATTTCATCCTCCCAAG<br>GCT  | 59.9                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4367_P4_29144 | scaffold4367                            | 29144                         | TAAAAA/TAAAA                                                       | GGGGACGAAAATGACG<br>TAAA | GTGCCAGTCGATTGCC<br>TAAT | 59.8                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold437_P4_24485  | scaffold437                             | 24485                         | TAAAAA/TAAAA                                                       | AACGTACTGCCTATCA<br>CGGG | TTGCTCACTACCACGC<br>TACG | 60.0                             | 566                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold437_P4_2817   | scaffold437                             | 2817                          | ACCC/ACC                                                           | CCTGCTTTTCCAAACC<br>ATGT | TGGCACAGTTCCAAGA<br>TCAA | 60.0                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold437_P4_45718  | scaffold437                             | 45718                         | CAATATTTAAAAATATTAAA/CAATAT<br>TAAAAAATATTAAAAATTTAAAAAT<br>ATTAAA | TCGAAGAGGACCATTG<br>ATCA | AGGTCGCACTCCAAAT<br>ATCG | 59.2                             | 777                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold437_P4_63608  | scaffold437                             | 63608                         | AG/A                                                               | CGCTCCAAGAGTCAAT<br>GTCA | TGAGTTGGTCCCATCA<br>ACAA | 60.0                             | 354                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold437_P4_63647  | scaffold437                             | 63647                         | TA/T                                                               | CGCTCCAAGAGTCAAT<br>GTCA | TGAGTTGGTCCCATCA<br>ACAA | 60.0                             | 354                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4371_P4_8554  | scaffold4371                            | 8554                          | T/TTAG                                                             | TAATTTTCGTCTCCGT<br>TGG  | AGACGCATATTGGATG<br>CACA | 59.9                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4374_P4_1159  | scaffold4374                            | 1159                          | CTAAACC/CTAAACCATAAACC                                             | TAAACCCCAATGACC<br>GAAA  | AGGGGTTAGGGGTTAG<br>GGTT | 60.2                             | 444                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                               | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                             |                          |                          |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold4377_P4_10163 | scaffold4377                            | 10163                         | GGTCAATTTTGTCAA/GGTCAATT<br>TTGTCAATTTTGTCAA                                                                | AACAGTGTTTGGATT<br>CCGC  | TCCTGGTCCTCGATT<br>CATC  | 60.0                             | 274                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4377_P4_6572  | scaffold4377                            | 6572                          | AA/AAGA                                                                                                     | TCCAGATGAAATCGAG<br>GACC | AGGCGATTTCGTACC<br>ACAC  | 60.0                             | 319                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold438_P4_60096  | scaffold438                             | 60096                         | AT/ATATATGT                                                                                                 | AGTTTGAAATCGGGG<br>AAGT  | TTCTTTCCTTGGCATT<br>TTG  | 59.8                             | 311                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4387_P4_5432  | scaffold4387                            | 5432                          | AG/AGTGCTTG                                                                                                 | GCACAAAACCTTATC<br>CCCA  | AAATGCTCGCCTCTTT<br>TGA  | 59.8                             | 311                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold4387_P4_5507  | scaffold4387                            | 5507                          | ATAGTATA/ATAGTATAGCTAGTATA                                                                                  | GCACAAAACCTTATC<br>CCCA  | AAATGCTCGCCTCTTT<br>TGA  | 59.8                             | 311                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold44_P4_24154   | scaffold44                              | 24154                         | TAA/TAAAAA                                                                                                  | TTGGAAAAGCCACCT<br>ACAC  | TGCAATGCAATGTCCA<br>TTTT | 60.0                             | 236                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold44_P4_287139  | scaffold44                              | 287139                        | CA/CATGTTTTGAATA                                                                                            | TTAAAATTTGGCGGTT<br>TGG  | AAAAATTCGAAGCGG<br>AAAG  | 59.8                             | 166                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold44_P4_287168  | scaffold44                              | 287168                        | T/TGTTTTGA                                                                                                  | TTAAAATTTGGCGGTT<br>TGG  | AAAAATTCGAAGCGG<br>AAAG  | 59.8                             | 166                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold44_P4_3472    | scaffold44                              | 3472                          | CATATATATATATATATATGTATA<br>TATATATATATATATATATATAT/C<br>ATATATATATATATATGTATATAT<br>ATATATATATATATATATATAT | CATTGGGAAAGCAAGT<br>GGAT | ATGTTTGGATTTTGGC<br>TCG  | 59.9                             | 548                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold440_P4_30262  | scaffold440                             | 30262                         | CAAAA/CAAA                                                                                                  | ACCAAAATAAGCCAG<br>GGAG  | TTGCCATTGCATGAAC<br>ATTT | 60.3                             | 354                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                            | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                          |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold440_P4_30494  | scaffold440                             | 30494                         | TAAAA/TAAAA                                                                                              | ACACAAACACCCGAT<br>TGGA   | TTGCCATTGCATGAAC<br>ATTT     | 59.9                             | 103                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold440_P4_43804  | scaffold440                             | 43804                         | A/AT                                                                                                     | ATTGGCAAATCGATT<br>ATGC   | ATTTTGGTCCTCCCTAC<br>GCT     | 60.8                             | 756                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold440_P4_8696   | scaffold440                             | 8696                          | CAAAAA/CAAAAA                                                                                            | ATCAGCATCAAGTGCA<br>CAGC  | TCCAGATTTGTGACGA<br>GCAA     | 60.0                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold442_P4_20594  | scaffold442                             | 20594                         | TGGGGGGG/TGGGGGGG                                                                                        | TGGACGCACAAGATT<br>GTTA   | AGGTCATTTTCGTCCTC<br>CCT     | 60.1                             | 370                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold442_P4_37151  | scaffold442                             | 37151                         | TAAAA/TAAAA                                                                                              | AGGGAGGACGAAATG<br>ACCT   | TGTGCGTCCAATAGGT<br>GTGT     | 59.9                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4452_P4_13113 | scaffold4452                            | 13113                         | ATTTTT/ATTTTT                                                                                            | CAGGGATGTAAACCA<br>ACAAAA | TGGTCTGACCCATTTT<br>GACA     | 58.9                             | 633                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4452_P4_57646 | scaffold4452                            | 57646                         | ATATTATTATTATTATTATTATTA<br>TTATT/ATATTATTATTATTATTATTA<br>TTATTATTATTATT                                | CACCCTCCCTCCCTTA<br>AGTC  | GCTGGATGGTCTGCAA<br>TTTT     | 59.9                             | 255                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold446_P4_163582 | scaffold446                             | 163582                        | CAAATGAAATTTAA/CAAATGAA<br>ATTTAAATGAAATTTAA                                                             | TTGCATCATGCTATTT<br>CCA   | ACATAACTTTGTGGGC<br>CAGC     | 60.0                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold446_P4_224556 | scaffold446                             | 224556                        | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATA/AA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATA | TTCATCTGGTCTTTTG<br>GGC   | CATTGAGTACAACATA<br>AAACGACG | 60.1                             | 771                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold446_P4_234701 | scaffold446                             | 234701                        | CAAA/CAAAA                                                                                               | TTGGGCGATTTTCTA<br>CCAC   | TCTTCGTTATGCAGTCA<br>AACTTTA | 59.9                             | 689                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)    | Forward primers (5'-3')         | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------|---------------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                  |                                 |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold446_P4_235656 | scaffold446                             | 235656                        | TAA/TA                                                           | TCTGACAACTCAATTT<br>GCTCTATG    | GTTGTACTTCATAACGA<br>ACACAATACT | 59.8                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold446_P4_261035 | scaffold446                             | 261035                        | TAACA/TAACAACA                                                   | TTCGTTTTGATGTTGTA<br>CTTACTTACG | GGGTTTCGGTTTTAAG<br>GCTC        | 59.9                             | 434                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold446_P4_54637  | scaffold446                             | 54637                         | TTATATATAT/TTATATAT                                              | GAACAAATCGAGGACC<br>CAGA        | GATGAAATCGAGGACC<br>AGGA        | 60.1                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold446_P4_67842  | scaffold446                             | 67842                         | A/ATAT                                                           | GGACGGCCTAGTCTAT<br>TCCC        | ACGACGTAGAACTATA<br>AAACGGTAA   | 59.9                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold450_P4_108759 | scaffold450                             | 108759                        | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATAT<br>TATAT | TTTTTCGAGTAGGTCG<br>GGTG        | AGCAAAAGGAAGCAAC<br>GAAA        | 60.1                             | 620                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold450_P4_207073 | scaffold450                             | 207073                        | AATATATATATATATATATA/AATATA<br>TATATATATATATATA                  | TTCAAAATAGGTGAGGT<br>TCCGA      | TTGCCGGTATGCTATA<br>AGGA        | 59.6                             | 701                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4508_P4_26689 | scaffold4508                            | 26689                         | ATTTTTTTT/ATTTTTTTTTT                                            | CAGGACACGTCAAGGC<br>TTTT        | CAATTTTCATCCATGATT<br>TTTGAAC   | 60.3                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4508_P4_33683 | scaffold4508                            | 33683                         | CTTTTTTT/CTTTTTT                                                 | TGAATGTCGTCAATGG<br>GAGA        | AAGAATCGAATGGGAA<br>ATCG        | 60.0                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4508_P4_36727 | scaffold4508                            | 36727                         | TAA/TA                                                           | TTGTGTTTGTACAGG<br>CCAT         | TCAGGAACAACAACCT<br>AACCC       | 60.0                             | 371                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4508_P4_4751  | scaffold4508                            | 4751                          | TAAAAAAAAA/TAAAAAAAAA                                            | CCGGAAACTTCATTC<br>CAAA         | AGAAAACCGAATTGTC<br>CCTT        | 59.9                             | 810                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')  | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|--------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                 |                          |                         |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold451_P4_288952 | scaffold451                             | 288952                        | ACCCCCCCCC/ACCCCCCCCC                                                           | TTGGAAGGTCAGGTGCTTTT     | CCAACAGAGCGATGTGTAACCA  | 59.7                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold451_P4_30168  | scaffold451                             | 30168                         | TA/TAA                                                                          | GCAGCCACAAATAAGGTGGT     | AACCAAGCCTGAGCTTGAA     | 60.0                             | 810                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold451_P4_34559  | scaffold451                             | 34559                         | TTATATATATATATATATATATATATAT<br>T/TTATATATATATATATATATATAT                      | TCCATTGCACTCACTCCAAA     | CCTATCATGGCCTGACCTGT    | 60.2                             | 746                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold451_P4_379558 | scaffold451                             | 379558                        | TA/TAGTCTAGGGAAAGAAGA                                                           | TCGGTGATGATAATGGGTT      | ACATCGAAGAACCCAACTGC    | 60.0                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold451_P4_388927 | scaffold451                             | 388927                        | TA/T                                                                            | CAACATCCATGAAGACACCG     | AATTGGTTTCATGACCTGCAC   | 60.0                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold451_P4_390571 | scaffold451                             | 390571                        | AAATAATAATAATAATAATAATA<br>ATAATAA/AAATAATAATAATAATA<br>AATAATAATAATAATAATAATAA | TGCATGATTCCAGAATTCCA     | AGGCAAACAAGAACCGAAAA    | 60.0                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold451_P4_482750 | scaffold451                             | 482750                        | TAAAAAAAAAAAA/TAAAAAAAAAAAA                                                     | AAATTCAACCCAAAACATCG     | CGGGAATCAATTAGAAACAA    | 58.8                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold451_P4_514062 | scaffold451                             | 514062                        | GTATATATATATATATATATATATAT<br>A/GTATATATATATATATATATATAT<br>TATATATA            | CCTTCAAATATTGGAGAGAACAAA | AAGACCAATCGGGAGAAAA     | 60.0                             | 852                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold451_P4_65486  | scaffold451                             | 65486                         | AT/ATT                                                                          | TGTCGATTATGAGTATTAGGTGG  | ACAACCTCTCATGCTCGCAA    | 60.3                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold453_P4_147436 | scaffold453                             | 147436                        | AAAATTCCCAAATTCCCAAATT/AAA<br>ATTCCCAAATT                                       | AAGAGAGGTCACCTTGGCGA     | AACCTCGAGACCACCATCAC    | 60.0                             | 771                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold453_P4_271003 | scaffold453                             | 271003                        | TTATATATATATATATA/TTATATATA<br>TATATATATA                     | GTCGCGTCGAAAAC<br>TCTC       | CTGAGTTGCGACGAG<br>ATTG     | 60.2                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold453_P4_296142 | scaffold453                             | 296142                        | CATATATATATATATATATATA/CA<br>TATATATATATATATATA               | AACAACTAGGAATGA<br>TGTTGTTCA | ATTAGGGGAGCATGCA<br>TTTG    | 59.0                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold453_P4_464893 | scaffold453                             | 464893                        | TTATATATATATATATAT/TTATAT<br>ATATATATATATATATATAT             | TGCATTCTCTTCTCTA<br>GGC      | AGAGGACGAATGTGGC<br>AAAA    | 60.2                             | 211                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold453_P4_503657 | scaffold453                             | 503657                        | TAAA/TAA                                                      | GAACATTGCAGAAACG<br>CAGA     | CTATTGACGCCTTGCG<br>TGTA    | 60.0                             | 728                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold453_P4_504101 | scaffold453                             | 504101                        | GA/G                                                          | TACACGCAAGGCGTCA<br>ATAG     | GCAAGACAAGAATACC<br>ACTCACA | 59.9                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold453_P4_504160 | scaffold453                             | 504160                        | TC/T                                                          | TACACGCAAGGCGTCA<br>ATAG     | GCAAGACAAGAATACC<br>ACTCACA | 59.9                             | 334                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4531_P4_1897  | scaffold4531                            | 1897                          | ATTT/ATTTT                                                    | AGGTCATTTTCGTCCT<br>CCCT     | TGGATGCACAAGAATG<br>GGTA    | 59.9                             | 367                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4551_P4_19293 | scaffold4551                            | 19293                         | GAATAAGATTTAATAAGATTT/GAAT<br>AAGATTT                         | GCGGGACTTCTTCTAA<br>ACATGA   | TGTGCACACGTTACAA<br>ATAATCA | 60.6                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4551_P4_6498  | scaffold4551                            | 6498                          | TAAAAAAA/TAAAAA                                               | CTGGTGAGGTTGCTTG<br>GAAT     | CATGCCTTGAGACCT<br>TCAT     | 60.1                             | 883                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4580_P4_704   | scaffold4580                            | 704                           | CATATA/CATATATATA                                             | TTGGTTTATTTGGGTT<br>GGGA     | CCATGAAAAGAAGAAG<br>GGCA    | 60.0                             | 717                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                 |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold4582_P4_7612  | scaffold4582                            | 7612                          | A/AG                                                                                            | TCCAGATGAAATCGAG<br>GACC | CGAAATTTGACACGGA<br>ACCT | 60.0                             | 258                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold46_P4_6079    | scaffold46                              | 6079                          | CTTTT/CTTTT                                                                                     | GGGCCGAGAGTCCCTT<br>ATAG | GGTCCTCGATTCATCT<br>GGA  | 60.1                             | 304                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold46_P4_9094    | scaffold46                              | 9094                          | ATTTT/ATTT                                                                                      | TTGAAATCGGACATGG<br>AACA | GATGAAATCGAGGACC<br>AGGA | 59.9                             | 852                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold466_P4_12138  | scaffold466                             | 12138                         | AATATATA/AATATATATA                                                                             | ATTGAGTCCCTTGCA<br>GCAT  | TCTCCGCATAAGCTTTC<br>GAT | 59.7                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold466_P4_254290 | scaffold466                             | 254290                        | TCTTCTCCACTT/TCTT                                                                               | GGATTCCGCGTAAGAT<br>TTCA | ACTAGGTTTTGGGTTC<br>CGCT | 60.0                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold466_P4_286406 | scaffold466                             | 286406                        | CATATATATATATATATATATATA<br>TATATATATATATAT/CATATATATAT<br>ATATATATATATATATATATATATA<br>TATATAT | GGAAGAAGGAAGGAGT<br>TGCG | TGCTGAAATTTGTGCC<br>AGAC | 60.0                             | 445                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold469_P4_49590  | scaffold469                             | 49590                         | AATATATATATATATATATATATAT<br>AT/AATATATATATATATATATATA<br>TATATATAT                             | CGGTGAATCCTTTACG<br>GAGA | GAGGAGGGAGGGATT<br>TGAG  | 60.1                             | 293                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold469_P4_58499  | scaffold469                             | 58499                         | AATATATATATATAT/AATATATATAT<br>ATATAT                                                           | CTTGGAACCTGGAGAG<br>CAAG | GAGGAGGGAGGGATT<br>TGAG  | 60.0                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4696_P4_3564  | scaffold4696                            | 3564                          | T/TA                                                                                            | CAAACACCTGTTGG<br>ATGC   | AGGTCATTTTCGCCTC<br>CCT  | 60.0                             | 180                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold470_P4_169493 | scaffold470                             | 169493                        | TAAAAAAAAAAAAA/TAAAAAAAAAAA<br>A                                                                | TCAAGAGGAAGCGAAA<br>GGAA | GCCCCCATTTTTGCAA<br>TTT  | 60.1                             | 277                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                 |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold470_P4_186075 | scaffold470                             | 186075                        | ATGAACTGAACTGAACTGAA/ATGAA<br>CTGAACTGAA                                                        | ACCAGGAAAAGAAGAA<br>GGGC | TTGGTTTATTTGGGTTG<br>GGA | 59.7                             | 456                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold470_P4_241092 | scaffold470                             | 241092                        | AATATATATATATATATATATATAT/A<br>ATATATATATATATATATATATATAT                                       | AATCGGAAGGGTAAAC<br>TCGT | TTTCGTTTGCAAGGTTT<br>TGA | 57.7                             | 660                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold470_P4_336358 | scaffold470                             | 336358                        | TTATGTAT/TTAT                                                                                   | GTCATCCTAGCCATCG<br>TCGT | GTGTCCCAAACTCAA<br>GGGA  | 60.1                             | 876                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold470_P4_365605 | scaffold470                             | 365605                        | CTTTTTTTTTTT/CTTTTTTTTTTT                                                                       | AGAAGCAAGCTAGCTC<br>GTGG | ATTGGAGCACATTGAG<br>GCTT | 59.9                             | 815                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold470_P4_370786 | scaffold470                             | 370786                        | TAAAAAA/TAAAAA                                                                                  | CATGCCAGTTGCTACA<br>TGCT | GCTTGGACTCAGTGGC<br>TAGG | 59.9                             | 949                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold470_P4_372719 | scaffold470                             | 372719                        | GAAA/GAAAA                                                                                      | ATTTTATGCTGCGACAT<br>CCC | GCAAATCCCACTTG<br>GAGT   | 59.9                             | 265                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold470_P4_375954 | scaffold470                             | 375954                        | AATATATATATATATATATATATAT<br>ATATATATATATAT/AATATATATATA<br>TATATATATATATATATATATATAT<br>ATATAT | AGGGAATCGAGGGAAA<br>AATG | AGGTGGCAACCTTCTC<br>ATTG | 60.3                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4708_P4_22066 | scaffold4708                            | 22066                         | TAA/TA                                                                                          | GTATTTGCGGACCAGA<br>CGAT | ATCGTCGATGGGTACG<br>AAAG | 60.0                             | 762                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4711_P4_5708  | scaffold4711                            | 5708                          | GTTTTTTTT/GTTTTTTTT                                                                             | AGGTCATTTTCGTCCT<br>CCCT | TTGGATGCACAAGATT<br>GGTT | 59.9                             | 271                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4711_P4_6211  | scaffold4711                            | 6211                          | GTTTTTTTT/GTTTTTTTT                                                                             | TTTCGTCCTCCCTAG<br>GCTT  | AGGAACTTATTGGATG<br>CCCA | 60.2                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold4713_P4_1946  | scaffold4713                            | 1946                          | TG/TGG                                                        | TCATCCAATGACACAA<br>CGC    | AGGTCATTTTCGTCCTC<br>CCT     | 60.5                             | 193                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4733_P4_507   | scaffold4733                            | 507                           | AT/ATT                                                        | ACAGTGAACGTGCACC<br>CATA   | CTGGTTATGCCGTTTG<br>GAGT     | 60.0                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold475_P4_141188 | scaffold475                             | 141188                        | A/AAAAATGGGG                                                  | GAGGAGCGACCAGTTG<br>TTTC   | GAAACTAATGCGACCG<br>GTGT     | 59.9                             | 884                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold475_P4_163488 | scaffold475                             | 163488                        | ACATGCATGC/ACATGC                                             | ACCGAACTCTCCCATC<br>CTTT   | ACCTCTTGGTGTGGT<br>GGAG      | 59.9                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold475_P4_174713 | scaffold475                             | 174713                        | GTTTTTTT/GTTTTTTT                                             | AAGGTTGACTGCATAA<br>CGAAGA | CAACACCATTGACAAC<br>ACCA     | 58.9                             | 730                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4759_P4_538   | scaffold4759                            | 538                           | AAAA/AGGACTAAA                                                | TTTCCCGACTTGGTCC<br>TTTA   | GGCAGCCGTGAACCT<br>ACTC      | 59.5                             | 371                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4769_P4_4939  | scaffold4769                            | 4939                          | TAAAA/TAAAAA                                                  | ACAACCTCTCATGCTC<br>GCAA   | GGGAAAATCATGTTTAT<br>CACAATC | 59.6                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold477_P4_11283  | scaffold477                             | 11283                         | C/CA                                                          | TGTCATCTTGTTCCT<br>TGG     | TGATGAAACTCTGAACT<br>CGTGG   | 59.7                             | 114                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold477_P4_19778  | scaffold477                             | 19778                         | GTTT/GTT                                                      | AGTTGCTTTGTTGGAG<br>GCAG   | ACCAAAATTAGGATGC<br>ACCG     | 60.4                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold477_P4_20714  | scaffold477                             | 20714                         | T/TG                                                          | CCCCCTAATGCTCAAT<br>TTCA   | TGCAACAAGAGGCAAA<br>ACAC     | 59.9                             | 288                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold477_P4_28410  | scaffold477                             | 28410                         | TAAAAA/TAAA                                                   | GTAGGAGGATCTCAAG<br>GGGC    | CCAAAATTAGGAAGCA<br>CCCA  | 60.0                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold477_P4_44806  | scaffold477                             | 44806                         | CTTTTTTTTT/CTTTTTTTTT                                         | TTGTTGCCACTATCGA<br>ACTGA   | GCTGTGGCTGACTCTG<br>ATGA  | 59.3                             | 673                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold477_P4_46653  | scaffold477                             | 46653                         | GAAAAA/GAAAAAA                                                | ATGCAACTGTCGTTTTA<br>GCA    | TTAGAGCGCCTTCTGA<br>TGGT  | 57.0                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold477_P4_49382  | scaffold477                             | 49382                         | GCTCTCACTCTCACTCTC/GCTCTC<br>ACTCTCACTCTCACTCTC               | CCC CGAATAACTCCA<br>ATAA    | TACCCACCACTGAC<br>CAGA    | 59.9                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4773_P4_14453 | scaffold4773                            | 14453                         | CT/CTCTTCCGATTTTTT                                            | TCCCTTCGGTTTTTAGA<br>GCA    | CTCTTTAAGACGTTTCG<br>CGG  | 59.8                             | 421                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4773_P4_16885 | scaffold4773                            | 16885                         | TNNNNNNNNNN/TNNNNNNNNN                                        | TGCGGCTATTCATAAC<br>ATGG    | GCATATCTGAGGCTGC<br>CAAT  | 59.5                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4773_P4_21493 | scaffold4773                            | 21493                         | TA/TATCA                                                      | TTTTGAGCTTTGGATT<br>GACTG   | TGCGATTAAAGAAAGC<br>AGTTC | 59.4                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4773_P4_22167 | scaffold4773                            | 22167                         | ATTTT/ATT                                                     | CCAACAAAATTATGGT<br>CTCCAA  | ATCTCCACCCAAATTT<br>TCC   | 60.1                             | 157                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4773_P4_22452 | scaffold4773                            | 22452                         | GTTTTTTT/GTTTTTT                                              | GGAAATTTGGGTGGG<br>AGAT     | TCTTTAAACGAAGTCG<br>GGC   | 60.0                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4773_P4_33470 | scaffold4773                            | 33470                         | GAAAA/GAAAAA                                                  | TGAATAGTGGTGGTGA<br>GTTTTCA | TGTGGAGAAGAGGGAG<br>CAAT  | 59.5                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold4773_P4_33716 | scaffold4773                            | 33716                         | CTTTTTTTT/CTTTTTTTTTT                                         | TGTATGAAAACGGTTG<br>AAAGGA | ACGTGCATGAGCCATA<br>TGAA | 59.5                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4773_P4_58139 | scaffold4773                            | 58139                         | TAAAA/TAAA                                                    | AACGCAAAACCTAAA<br>CCCT    | AGAACTTCCCGAACAC<br>GATG | 59.9                             | 174                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4773_P4_58332 | scaffold4773                            | 58332                         | CTTTT/CTTTT                                                   | CATCGTGTTCGGGAAG<br>TTCT   | AGATCTGGGTGGAATC<br>GTTG | 60.1                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4777_P4_52787 | scaffold4777                            | 52787                         | CATTTTGATTTTGATT/CATTTTGATT                                   | CGAGGCACTAAGCACC<br>TCTC   | GTTCCCTTTTCTACGA<br>GGG  | 60.2                             | 189                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4784_P4_684   | scaffold4784                            | 684                           | TG/TGATGGCTAG                                                 | TCCTGGTCCTCGATT<br>CATC    | GGGCCGAGAGACCCTT<br>ATAG | 60.0                             | 339                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold479_P4_125059 | scaffold479                             | 125059                        | T/TG                                                          | TTGATCCTTGCAGTCA<br>CTCG   | CGGAGGACGAAAATGA<br>CCTA | 60.0                             | 720                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold479_P4_125417 | scaffold479                             | 125417                        | CTTTT/CTTTT                                                   | ACAACCAATCGATTTC<br>CCA    | CGGAGGACGAAAATGA<br>CCTA | 60.2                             | 180                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold479_P4_16760  | scaffold479                             | 16760                         | ATTTTTTTTTTTTT/ATTTTTTTTTT                                    | TGTTCAATGTAACACCC<br>CGA   | TTAAGCCAATGCCACA<br>AACA | 59.8                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold479_P4_7594   | scaffold479                             | 7594                          | TTA/TTAGGCATA                                                 | TGTGTTTGTGGCATTG<br>GATT   | AGGGAGGACGAAAATG<br>ACCT | 59.8                             | 329                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold48_P4_11860   | scaffold48                              | 11860                         | TATATATATATATAGA/TA                                           | TTTGCACTTTGCGATG<br>AACT   | TTTTTAACGCGTGCATT<br>TTT | 59.5                             | 977                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                     | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                                                                                                                                   |                            |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold48_P4_15048  | scaffold48                              | 15048                         | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAA/AAATAATAATA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>ATAATAATAATAATAATAATAAT | TCGGTTCATCATGTTG<br>GAAAT  | TCTTTTGATGTGGGTTA<br>GTGAGAA | 60.2                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold48_P4_15983  | scaffold48                              | 15983                         | CATATAT/CATATATAT                                                                                                                                                 | GACTTGGTTCATCTTG<br>TTGGAA | ATCGAGGGACAGATGG<br>TGAG     | 59.1                             | 987                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold48_P4_16742  | scaffold48                              | 16742                         | GAAAAAAAAA/GAAAAAAAAA                                                                                                                                             | CCATCTGTCCCTCGAT<br>CACT   | CCGGAACCAACCCTT<br>ATT       | 60.1                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold48_P4_186752 | scaffold48                              | 186752                        | AATATATATATATATATATATAT<br>ATATATATATATATA/AATATATAT<br>ATATATATATATATATATATATA<br>TATATATATATATA                                                                 | CTCCCTCTCTCATCT<br>CCCT    | TCACCATCCAGAGTCC<br>AATG     | 59.8                             | 673                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold48_P4_245387 | scaffold48                              | 245387                        | AGT/AGTAAGGATGT                                                                                                                                                   | CGAACAAGAAGGAAGA<br>ACCG   | GATGGATAATCGAAAC<br>CCGA     | 59.8                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold48_P4_304640 | scaffold48                              | 304640                        | AAATAATAATAATAATAATAATA<br>A/AAATAATAATAATAATAATAAA                                                                                                               | CCATGATGCGACCTCC<br>TACT   | TGTGATTGTAATGTG<br>GCAAA     | 60.1                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold480_P4_43150 | scaffold480                             | 43150                         | TCCC/TCCCC                                                                                                                                                        | AACGTACTGCCTATCA<br>CGGG   | TGTTTCATCGTATTTGGC<br>GTG    | 60.0                             | 836                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4804_P4_1921 | scaffold4804                            | 1921                          | TAAG/TAAGCCAAG                                                                                                                                                    | TTGGATGCACAACATT<br>GGTT   | AGGTCATTTTCGTCCTC<br>CCT     | 59.8                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4804_P4_8867 | scaffold4804                            | 8867                          | CTT/CT                                                                                                                                                            | TGGATGCACCAGATTG<br>GTTA   | AGGTCATTTTCGTCCTC<br>CCT     | 59.9                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4804_P4_893  | scaffold4804                            | 893                           | TAAAAAAAA/TAAAAAAAA                                                                                                                                               | AGCCTAGGGGTGACGA<br>AAAT   | GTCCTCCCAGGCTTA<br>ATTG      | 60.0                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold4804_P4_9853  | scaffold4804                            | 9853                          | CAAAA/CAAAA                                                   | AAGCCTGAGGATGACG<br>AAAA  | TGCATCCAACAGGTG<br>GTTT   | 59.8                             | 571                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4822_P4_847   | scaffold4822                            | 847                           | A/AGAATACT                                                    | CAGCGGATCCCCAGAT<br>ATAC  | AGGTCATTTTCGTCTC<br>CCT   | 59.4                             | 545                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4829_P4_6279  | scaffold4829                            | 6279                          | TCCC/TCCCC                                                    | GACCCGCATTTTCCTC<br>ATTA  | GGAGAACGTTAAGGCA<br>GCAG  | 59.9                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4829_P4_8205  | scaffold4829                            | 8205                          | TAAAA/TAAA                                                    | CAATAGCATGCAGTTG<br>GAGG  | GGAGACTCCCATACAT<br>TGGC  | 59.3                             | 500                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4833_P4_3774  | scaffold4833                            | 3774                          | T/TA                                                          | CCAAGCCAGTCAAACA<br>CAAA  | GGGCTCGCTATGTACA<br>GCA   | 59.7                             | 839                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4833_P4_3926  | scaffold4833                            | 3926                          | CATATATATAT/CATATATATAT                                       | CAATTCAAATTGGCCC<br>TGTC  | GGGCTCGCTATGTACA<br>GCA   | 60.3                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4833_P4_740   | scaffold4833                            | 740                           | TTTTTGT/TTTT/TTTTT                                            | TGGGAATGTAGTGGAT<br>GAACC | TCCCGAACACCTATGC<br>TTTT  | 59.7                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold484_P4_136302 | scaffold484                             | 136302                        | TCCCC/TCCC                                                    | ACCGAGGTGCCACTTA<br>TCAC  | ATAGTGGTGACTGGAT<br>GGGC  | 60.0                             | 229                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold484_P4_319973 | scaffold484                             | 319973                        | ATTTTTTTTT/ATTTTTTTTTT                                        | TTGCACTCACGGAACG<br>AATA  | TCGCCATTTAAAATTGA<br>GGTG | 60.3                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold484_P4_323657 | scaffold484                             | 323657                        | GTTTT/GTTTT                                                   | TGCTCCATGTCTTGAA<br>AAGGT | CGCAAGAAGAAATAGA<br>CGCA  | 59.7                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)             | Forward primers (5'-3') | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                          |                                  | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------|-------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------|----------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                            |                         |                           |                                  |                                               | Sequence components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | Tfs |
| scaffold484_P4_57166  | scaffold484                             | 57166                         | AATATATATATATATATATATATATATATATATAT/AATATATATATATATATATATATA TATATATATATAT | TATGGCTACACCAATG CACC   | AATGTTGTTTGCTATCG CCC     | 59.4                             | 889                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold484_P4_656687 | scaffold484                             | 656687                        | AC/A                                                                       | TATCACCTATCAGAGC GGGG   | TGATTCCGGGAAGTA CAAC      | 60.1                             | 472                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold484_P4_660209 | scaffold484                             | 660209                        | GAAAAAAAA/GAAAAAAAAA                                                       | TGCCAACGATGTTATC CTTTT  | CTAGGCCTGCCTCCTC TCIT     | 59.5                             | 819                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold484_P4_740550 | scaffold484                             | 740550                        | CT/CTT                                                                     | TCACTCATCACTGTGA GCAAGA | TGTAGTCAAATCCAAG GGGA     | 59.6                             | 540                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold485_P4_149909 | scaffold485                             | 149909                        | CG/CATCATCCCATG                                                            | TTGAAACCAATGGCAG GATT   | TGGATCCAACAATTCTC ATCC    | 60.3                             | 180                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold485_P4_46559  | scaffold485                             | 46559                         | GAAAAAAAAAAAA/GAAAAAAAAAAAAA A                                             | TTTTGAGCGTGTGAGT CCTG   | GGCTAAATTACATCTGT GGTTCCT | 60.0                             | 411                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold4851_P4_3486  | scaffold4851                            | 3486                          | GTT/GT                                                                     | CTATAAGGGTCTCTCG GCCC   | CCGATGCTAAAATGG CAGT      | 60.1                             | 733                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold4851_P4_3617  | scaffold4851                            | 3617                          | TAAAAAA/TAAAAAA                                                            | CGCGGAACCTGAAACA CTAT   | CCGATGCTAAAATGG CAGT      | 60.1                             | 616                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold486_P4_38993  | scaffold486                             | 38993                         | CAAAAAA/CAAAAAAA                                                           | CTCCCCCTTTTGTCATT GAA   | TGACCAGCTGAAGCAC AATC     | 59.9                             | 415                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold4869_P4_702   | scaffold4869                            | 702                           | TATAATAATAATAAAT/TATAATAA TAATAAT                                          | AGCCAGTAAGCACCC TTGA    | GACGCTACCACCTGAC ATGA     | 59.9                             | 276                                           | INTERGENIC                                     | --                               | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome:<br>CDC Frontier/PII)               | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                             |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold487_P4_3721   | scaffold487                             | 3721                          | T/TG                                                                        | AAGTGCATAAGTCCCA<br>ACGG | TGCCTAAGAACCAAG<br>TGGG  | 60.0                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold487_P4_87751  | scaffold487                             | 87751                         | T/TC                                                                        | ACATTGAGGTCATTTTC<br>GCC | AGCCTAGGGAGGATGC<br>AAAT | 59.9                             | 229                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4872_P4_661   | scaffold4872                            | 661                           | G/GTCTATCA                                                                  | TGGGCACATGCTTCTC<br>AGTA | TACTGGAACGGACCAC<br>ACAA | 60.4                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4874_P4_7885  | scaffold4874                            | 7885                          | AATATATATATA/AATATATATA                                                     | GCGCGCTTGTTATATT<br>CGTT | GTTGGTTCCTAGCAC<br>CGTA  | 60.3                             | 773                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4902_P4_19478 | scaffold4902                            | 19478                         | ATTTTTTTTT/ATTTTTTTTT                                                       | GCCACAGGCAACCACT<br>AAAT | AATAGGTGATGCCTCT<br>CGGA | 60.0                             | 123                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4902_P4_23548 | scaffold4902                            | 23548                         | AATA/AA                                                                     | CCATCCAAGTGCCTAC<br>CATT | TTCTGTTCAATCGTGCA<br>AGC | 59.8                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4902_P4_23572 | scaffold4902                            | 23572                         | TAATAAATAA/TAATAA                                                           | CCATCCAAGTGCCTAC<br>CATT | TTCTGTTCAATCGTGCA<br>AGC | 59.8                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4902_P4_34435 | scaffold4902                            | 34435                         | TTATATATATATATATATATATATA<br>TATATATAT/TTATATATATATATATA<br>TATATATATATATAT | TTTGGTCCCCACATTT<br>GAT  | TTACCTGAAAATTGTC<br>GCA  | 60.0                             | 684                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4902_P4_7183  | scaffold4902                            | 7183                          | TTCTATCTCTATCTCTAT/TTCTATCT<br>CTATCTCTATCTCTAT                             | AAACTGCATTTAGGA<br>TGCC  | CTTGGCAGTGATGAAG<br>ATCG | 60.1                             | 545                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4902_P4_73019 | scaffold4902                            | 73019                         | AA/AACTGAAATTTA                                                             | GGGGTTACATTAACGG<br>GGTT | CACCTCATAACGTGTT<br>GGGC | 59.8                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                 |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold4902_P4_8464  | scaffold4902                            | 8464                          | CG/C                                                                            | CGTCTAGTCGAATGGA<br>TCTGC | AAAAATGGGTTTAACGT<br>TATGCTT | 59.9                             | 321                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold491_P4_29285  | scaffold491                             | 29285                         | TAAAAAAA/TAAAAAA                                                                | AAGGGACCACGAGTGG<br>TATT  | ACCCGGAACCCCTAAC<br>ATTC     | 58.4                             | 279                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold492_P4_35889  | scaffold492                             | 35889                         | ATTT/ATTTTGTTCATTTT                                                             | CCCGAAAAGTCCAGAT<br>GAAA  | GCGATTTTAGTACCAC<br>CCGA     | 60.0                             | 698                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold492_P4_36765  | scaffold492                             | 36765                         | CC/CCATTTTC                                                                     | TCCAAGGGTACAAAA<br>TCGC   | TCCAGTCCTCGATTT<br>CATC      | 59.9                             | 505                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4923_P4_11425 | scaffold4923                            | 11425                         | AATATATATATATATATATATA/AA<br>TATATATATATATATATA                                 | TTGGATTTTGGCTCATA<br>GGC  | CGCGTTAACAGAGGAA<br>GAGG     | 60.0                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold493_P4_106607 | scaffold493                             | 106607                        | T/TAA                                                                           | GAGATGAATGGGAGAG<br>AGCG  | GCATGGTAGCTCCCAA<br>CATT     | 59.9                             | 883                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold493_P4_124059 | scaffold493                             | 124059                        | ACTCTC/ACTC                                                                     | TCTTTGGTTTTACGGC<br>TGCT  | TGAAATCGGGTCACTT<br>GTCA     | 59.9                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold493_P4_239068 | scaffold493                             | 239068                        | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATAT                           | AATATCTTTTGGTGCC<br>CCG   | AGCGTGGAGATGAGCA<br>ACTT     | 61.0                             | 647                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold493_P4_981    | scaffold493                             | 981                           | CATATATATATATATATATATATA<br>TATATATATA/CATATATATATATATA<br>TATATATATATATATATATA | CGGTGGGATATGATTA<br>TGCC  | TCAAACAAATAAAACCG<br>TTGG    | 60.0                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4945_P4_4235  | scaffold4945                            | 4235                          | CTTTT/CTTT                                                                      | TGCTCGTCCTTCTTTT<br>GGA   | TCCGAAAAAGTAATG<br>TCGG      | 60.9                             | 545                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold495_P4_111241 | scaffold495                             | 111241                        | TTTTGAAATAACCCCTT/TTT                                         | GGTTTGCCTTTGGTGT<br>CTGT  | GTGCTTTGCATGGAAC<br>AAGA     | 60.0                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold495_P4_112606 | scaffold495                             | 112606                        | ATGTGTGTGTGTGTGTGTGT/AT<br>GTGTGTGTGTGTGTGTGTGT               | CCACAAATGTCACATA<br>GCCG  | AGCATGCATCTGCACA<br>CAAT     | 60.0                             | 814                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold495_P4_122958 | scaffold495                             | 122958                        | GAAAAAAAA/GAAAAAAAAA                                          | TTTCAACCCTAAATCGC<br>AGG  | TCAACACAAATCAAACC<br>CCA     | 60.1                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold495_P4_133654 | scaffold495                             | 133654                        | GAAAAA/GAAAAA                                                 | TTTTATTCTTTTGTGGC<br>GGC  | ACCCCAAAATCAAAACC<br>CTC     | 60.1                             | 787                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold495_P4_135684 | scaffold495                             | 135684                        | GTTTTTTTTT/GTTTTTTTTTTT                                       | TCGTACGAAGTGCAGAA<br>TTGA | AACACAAATCTCCGGA<br>AAAA     | 60.4                             | 414                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold495_P4_137461 | scaffold495                             | 137461                        | CTTTTTTTTTT/CTTTTTTTTTTT                                      | GAAATGGATGGAGGAG<br>TGGA  | CTTTGGTGCCTGGTAA<br>GGAT     | 59.9                             | 346                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold495_P4_15332  | scaffold495                             | 15332                         | G/GTTGTT                                                      | GGGGGACATGATTAGA<br>CCCT  | CAACAATTCCCATTGA<br>CCC      | 60.0                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold495_P4_23387  | scaffold495                             | 23387                         | TAAAAAAAA/TAAAAAAAAA                                          | CCCTCTATGTGGTGGT<br>GCTT  | TCAGTTTCTTGCCTTTT<br>TATGTTG | 60.0                             | 761                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold496_P4_121429 | scaffold496                             | 121429                        | CT/C                                                          | TCCTGGTCCTCGATT<br>CATC   | AATCGCCTGAAAAGAC<br>GAGA     | 60.0                             | 379                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold496_P4_219686 | scaffold496                             | 219686                        | TTT/TTTGCTGCTT                                                | GACAGTGGATGTTCCA<br>AGCA  | ATTGAGGGAAAGGATG<br>GCTT     | 59.7                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                           |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold496_P4_31400 | scaffold496                             | 31400                         | GAAAA/GAAA                                                    | TTGTGCGAGGGGTACG<br>AAAC  | CCGGTCCTCGATTCTA<br>TCTA      | 60.0                             | 605                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold496_P4_42316 | scaffold496                             | 42316                         | TTTA/TCCGAGCTTA                                               | GGACAGAAATGGGAGTA<br>GGCA | CCCATATGCGCTCGAT<br>AACT      | 60.1                             | 337                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold496_P4_42549 | scaffold496                             | 42549                         | GC/G                                                          | AGCGATGCATGTCTCA<br>AGTG  | TTCTGGTGGGATTCA<br>CATT       | 60.0                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold497_P4_55035 | scaffold497                             | 55035                         | TA/T                                                          | CGTTCCTGAGGGAATT<br>GTGT  | AGTACTGAGCCCCCTG<br>GTTT      | 60.0                             | 578                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold497_P4_69293 | scaffold497                             | 69293                         | ATTTATTTT/ATTTATTTTATTTT                                      | GGTAGTCAAGCCTGAG<br>GCAG  | TCTTGATGTTTGATT<br>ATGTTAGGTG | 60.0                             | 585                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold497_P4_69480 | scaffold497                             | 69480                         | ACAATAAAT/AAAAT                                               | GGTAGTCAAGCCTGAG<br>GCAG  | GCACTTTTCCAAAAGC<br>ACC       | 60.0                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold497_P4_69995 | scaffold497                             | 69995                         | GTTTTTTTTTTTT/GTTTTTTTTT                                      | TGGTGCTTTTGAAAA<br>AGTG   | ATTTGGTTTGGTTGCAT<br>TCG      | 58.8                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold497_P4_70043 | scaffold497                             | 70043                         | CAATAAATAAATAAATAAT/CAATAA<br>ATAAAT                          | TGGTGCTTTTGAAAA<br>AGTG   | ATTTGGTTTGGTTGCAT<br>TCG      | 58.8                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold497_P4_73410 | scaffold497                             | 73410                         | T/TC                                                          | CGCATTTATGCATTGG<br>TGAA  | CTGCTGCCTTTGCAAC<br>AAAT      | 60.5                             | 442                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold497_P4_73440 | scaffold497                             | 73440                         | CTTTTT/CTTTTT                                                 | CGCATTTATGCATTGG<br>TGAA  | CTGCTGCCTTTGCAAC<br>AAAT      | 60.5                             | 442                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)            | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                          |                           |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold497_P4_73674  | scaffold497                             | 73674                         | AT/ATCTCTT                                                               | CGCATTTATGCATTGG<br>TGAA  | ACCGTGTGTCGAAGTC<br>AAGG      | 60.5                             | 793                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold497_P4_88034  | scaffold497                             | 88034                         | GAATTCGGTAATAATTC/GAATTC                                                 | CGGCCGTTTCTAACAT<br>CATT  | ACCGAGTGTGGAAGTC<br>AAGG      | 60.0                             | 673                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold498_P4_206145 | scaffold498                             | 206145                        | GTTTTTTTT/GTTTTTTTT                                                      | CACCGCTCTGTTCAT<br>TATT   | GAGATTTAGAACCATCA<br>AATTGTCA | 60.0                             | 829                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold498_P4_214216 | scaffold498                             | 214216                        | AA/AAAAGTCA                                                              | TTTCATGGTCATGTTTT<br>GGC  | GAAAGGCCAATGTCCA<br>GAAA      | 59.4                             | 781                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold498_P4_214228 | scaffold498                             | 214228                        | CATAATAAACTAATAAACTAA<br>TAAT/CATAATAAACTAATAAAAA<br>CTAATAATAAACTAATAAT | TTTCATGGTCATGTTTT<br>GGC  | GAAAGGCCAATGTCCA<br>GAAA      | 59.4                             | 781                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold498_P4_214273 | scaffold498                             | 214273                        | TACACACACACAC/TACACACAC<br>CAC                                           | TTTCATGGTCATGTTTT<br>GGC  | GAAAGGCCAATGTCCA<br>GAAA      | 59.4                             | 781                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold498_P4_214558 | scaffold498                             | 214558                        | CTTTTT/CTTTTTT                                                           | CACACACACGTAAGAA<br>GGCTG | TTGGACAGAATCAAGG<br>CTCC      | 59.4                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold498_P4_45313  | scaffold498                             | 45313                         | CTTTTTTTTT/CTTTTTTTTTT                                                   | CAGGAAAAGGCGTTGT<br>GTTT  | CCTCAATTTTATCCGAC<br>CAA      | 60.1                             | 348                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold498_P4_97243  | scaffold498                             | 97243                         | CTTTTTTTTTTT/CTTTTTTTTTTT                                                | GGCGAGTTCGAAAAAG<br>AGAA  | AAGAGGGGGATGAAGT<br>GAGAA     | 59.6                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4983_P4_27196 | scaffold4983                            | 27196                         | AAT/AATAT                                                                | AAGGTGGTACGAAAAAT<br>CCCC | GCACGTGGGAAAATGA<br>GATT      | 60.1                             | 893                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold4983_P4_27256 | scaffold4983                            | 27256                         | C/CT                                                                          | AAGGTGGTACGAAAT<br>CCCC    | GCACGTGGGAAATGA<br>GATT   | 60.1                             | 893                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold4983_P4_27276 | scaffold4983                            | 27276                         | ATTT/ATT                                                                      | AAGGTGGTACGAAAT<br>CCCC    | GCACGTGGGAAATGA<br>GATT   | 60.1                             | 893                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5_P4_1535     | scaffold5                               | 1535                          | CTT/CTTT                                                                      | CGATTGTGTTGTCAC<br>AGGG    | GAAGCAAATCGATTGG<br>GAAA  | 60.0                             | 316                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5_P4_17558    | scaffold5                               | 17558                         | AAATTCAAAAGA/AAATTCAAAAGAA<br>TTCAAAAGA                                       | TCGTGTTGCGCCTAAC<br>AAT    | CCTTTGCTGTATAAGTG<br>GGCA | 60.3                             | 619                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold50_P4_102188  | scaffold50                              | 102188                        | AATATATATATATATATATATATAT<br>ATAT/AAATATATATATATATATATAT<br>TATATATATATATATAT | TTTTCGGTCTGACCTG<br>ATTTTT | GCCTTTTCACGCTTCA<br>CATT  | 60.0                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold50_P4_165794  | scaffold50                              | 165794                        | GATATATATATATATATATATATAT/G<br>ATATATATATATATATAT                             | GCGACTTGGAACCTGG<br>AGAG   | GCACCGTGAGTAAATT<br>CGGT  | 60.0                             | 846                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold50_P4_191851  | scaffold50                              | 191851                        | GAAAAAAAAA/GAAAAAAAAA                                                         | GTTCTTCCGCAGAAGT<br>CAGG   | GAGATCTCGGTGCTAC<br>TGCC  | 60.0                             | 325                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold50_P4_191880  | scaffold50                              | 191880                        | GAAAAAAAAA/GAAAAAAAAA                                                         | GTTCTTCCGCAGAAGT<br>CAGG   | GAGATCTCGGTGCTAC<br>TGCC  | 60.0                             | 325                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold50_P4_192238  | scaffold50                              | 192238                        | A/AGTGATAGAAATT                                                               | CTGCCCATTAGCCCTT<br>CATA   | CTGAATGCAAGAGAGA<br>GGGG  | 60.1                             | 291                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold50_P4_195701  | scaffold50                              | 195701                        | C/CTCTAC                                                                      | TTTGGCAGATACCATG<br>ACGA   | TATGAAGGGCTAATGG<br>GCAG  | 60.1                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                           |                             |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold50_P4_196038  | scaffold50                              | 196038                        | A/ACTG                                                                    | CTGCCATTAGCCCTT<br>CATA     | AGGAAGGAGTGATGCG<br>AAGA      | 60.1                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold50_P4_202474  | scaffold50                              | 202474                        | A/AGACTAACGGGAAGCAC                                                       | CCTTTCCTAGCTCTTG<br>CCCT    | AAGCCATGGTTTTTGG<br>ACAG      | 60.0                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold50_P4_2969    | scaffold50                              | 2969                          | G/GGGT                                                                    | ATCGATTGAACCAAAT<br>CCCA    | TTGGTGAGGGAGAATC<br>GAAC      | 60.1                             | 684                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold50_P4_299723  | scaffold50                              | 299723                        | G/GTAACGTACAACAT                                                          | GCGAAGCAAAGTCCAT<br>CATT    | AAATTCGCTCGCTAGG<br>TTGA      | 60.2                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold50_P4_333436  | scaffold50                              | 333436                        | AATATATATATATATATAT/AATATAT<br>ATATATATATATAT                             | TGGCGTGACAATAACC<br>TCAA    | AAATTGGTCCACTAGC<br>ACCG      | 60.1                             | 878                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold50_P4_337379  | scaffold50                              | 337379                        | CATATATATATATATATATA/CATA<br>TATATATATATATATATATA                         | AACTTTTCCGCTGCTT<br>GAA     | CGACTCTGTTGGGGAT<br>GTCT      | 60.0                             | 383                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold50_P4_400843  | scaffold50                              | 400843                        | AAATAATAATAATAATAATAATA<br>ATAATAA/AAATAATAATAATAAAT<br>AATAATAATAATAATAA | ACAATTTGTTGACCCG<br>CATT    | TTGTGCTCTCCAATTCT<br>CCC      | 60.2                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold501_P4_87430  | scaffold501                             | 87430                         | CATATATATATATATAT/CATATATAT<br>ATATATATAT                                 | TGGGTGTGCCTATATA<br>CACGTAA | TTCTTTGCCACACACCA<br>TGT      | 59.3                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5016_P4_4506  | scaffold5016                            | 4506                          | GTATATATATATATATA/GTATATA<br>TATATATATA                                   | TCCTGGGCTAGCGACT<br>TCTA    | TTGTCGAAATTACATT<br>TCTAAGTCA | 60.1                             | 848                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5030_P4_11801 | scaffold5030                            | 11801                         | GCTT/GCTTGTACTT                                                           | AATGACATTTAACAGC<br>GCC     | TGGCCGCACAGTATGT<br>AGAG      | 60.0                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold5030_P4_906   | scaffold5030                            | 906                           | AAATAATAAT/AAATAAT                                            | TGGGGATACGTAGGAG<br>CAAG | TGTTGGTCCATTTTGA<br>CGA  | 60.1                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold506_P4_18074  | scaffold506                             | 18074                         | TAAA/TAAAA                                                    | CTATGGTAGAGCGGTT<br>TCGC | TTCTCCCGAGTTTGG<br>TCTC  | 59.9                             | 487                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold506_P4_1872   | scaffold506                             | 1872                          | CAT/CATAT                                                     | TGCTCCACTTTTAGAT<br>GCCC | GGTGCATTGCAAGCTA<br>GTGA | 60.2                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold506_P4_18975  | scaffold506                             | 18975                         | TA/TAA                                                        | TCTCGATACCATCGTG<br>GACA | TCCCATTTGATTGCTGA<br>ACA | 60.1                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold506_P4_39357  | scaffold506                             | 39357                         | TTAA/T                                                        | TTTGAAAAGTTGGCATT<br>TCG | TTGCGACTTCACACTT<br>GGTT | 58.8                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold509_P4_172908 | scaffold509                             | 172908                        | AT/A                                                          | TTGAGCCCATGTAAC<br>TCCC  | TTGTCCGTGAGAGATT<br>GCAG | 59.9                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold509_P4_219223 | scaffold509                             | 219223                        | A/AG                                                          | AGGTCACGTTCTTCCT<br>CCCT | TTTGCTCCAAATCAGA<br>GGCT | 60.1                             | 383                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold509_P4_266782 | scaffold509                             | 266782                        | AG/A                                                          | GGTGGTAGCTGGTAG<br>GGTGA | TGCACCTTGACCTTCTT<br>CCC | 60.0                             | 935                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold509_P4_295368 | scaffold509                             | 295368                        | TAAA/TAAAAAA                                                  | AACGTACTGCCTATCA<br>CGGG | GGTAAGGGCTCCTTCC<br>AAAC | 60.0                             | 899                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold509_P4_323919 | scaffold509                             | 323919                        | A/AGT                                                         | TGTGCATCCAACAAGT<br>TCGT | AGGGAGGACGAAAATG<br>ACCT | 60.2                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)      | Forward primers (5'-3')        | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------|--------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                    |                                |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold5094_P4_2305  | scaffold5094                            | 2305                          | TAA/TA                                                             | TGGCACATGAATAGTT<br>CCACA      | GCCACCTCATTCAAATA<br>TTGC | 60.0                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold510_P4_85609  | scaffold510                             | 85609                         | TAACA/TA                                                           | TTGTCAAATAAAGTAAC<br>AACAAAACG | TTGCAACAATTGTACCC<br>GAA  | 58.7                             | 995                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold511_P4_101350 | scaffold511                             | 101350                        | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATAT<br>TATATAT | CGGTGAATCCTTTACG<br>GAGA       | GGAGGAGAAGGAGGG<br>ATTTG  | 60.1                             | 306                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold511_P4_193038 | scaffold511                             | 193038                        | AATATATATATATATATATATA/AATA<br>TATATATATATATATATATA                | TTTCAGGTTATCGACT<br>GGGG       | AACAAGAAAGCGCAAG<br>CAAT  | 59.9                             | 729                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold511_P4_194484 | scaffold511                             | 194484                        | CTTTTT/CTTTTT                                                      | AATCTGCTTCCGTTAG<br>CTGC       | TGCACAATAAACCTGCT<br>TGC  | 59.6                             | 667                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold511_P4_194529 | scaffold511                             | 194529                        | AAA/AAACAA                                                         | AATCTGCTTCCGTTAG<br>CTGC       | TGCACAATAAACCTGCT<br>TGC  | 59.6                             | 667                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold511_P4_194615 | scaffold511                             | 194615                        | AT/ATATT                                                           | AGGCCTGGGAAGTAG<br>GAACA       | TGCACAATAAACCTGCT<br>TGC  | 61.0                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5115_P4_16853 | scaffold5115                            | 16853                         | GAA/GAAA                                                           | AATGGCCACGAATCTG<br>AAAG       | GAAGTACGCCTAAGAG<br>GGGG  | 60.1                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5120_P4_13346 | scaffold5120                            | 13346                         | TTAATAATAATAATAATAATAA/T<br>TAATAATAATAATAATAATAATA<br>A           | TTTGAAGCAAATTGCG<br>AGTG       | GGTGTGGTGTGGTGCA<br>AGTA  | 60.0                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5120_P4_14840 | scaffold5120                            | 14840                         | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATA<br>TATAT    | TATCGTGCTGTTGAG<br>AACG        | CTAATTAGCGTCGGAG<br>TCGG  | 59.9                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold5120_P4_15547 | scaffold5120                            | 15547                         | TAGAGTACGAGA/TAGA                                             | CCGAAGTAATAGTGGG<br>GCAAT  | GGACCAGGTTCTGCAT<br>CAAT   | 60.0                             | 214                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold515_P4_15833  | scaffold515                             | 15833                         | AA/AAATCACTTGTCAT                                             | CCCGAAAAGTCCAGAT<br>GAAA   | TTGAAATCTAGCGCGG<br>AACT   | 60.0                             | 258                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold515_P4_28282  | scaffold515                             | 28282                         | TA/T                                                          | CGCAGCAAAAGTCTTG<br>ATGA   | CGGTCGATTTTCGTAC<br>CACT   | 60.0                             | 169                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold515_P4_31767  | scaffold515                             | 31767                         | ATTT/ATT                                                      | TTGGGTTTTAGGTTTC<br>GTGC   | TTTCATCTGGACTTTTC<br>GGG   | 60.0                             | 765                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold515_P4_43016  | scaffold515                             | 43016                         | GAAAA/GAAAA                                                   | CAAGAGTCTCTGGTC<br>CTCG    | CTCCGAAAAGTCCAA<br>ATGA    | 60.0                             | 912                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold515_P4_61810  | scaffold515                             | 61810                         | TCTC/T                                                        | CTCGAAACCCGAAACA<br>CAAT   | GCGTCGTTTGAACCA<br>AAAT    | 60.0                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold515_P4_98159  | scaffold515                             | 98159                         | GCC/GC                                                        | CCATCGTCTGAACCGA<br>AAAT   | CGGAACCCGAAACACT<br>TTTA   | 59.9                             | 143                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5152_P4_20235 | scaffold5152                            | 20235                         | CTTTTTTTTT/CTTTTTTTTTT                                        | CCAAGGGGAGCAATTA<br>TGAA   | TGATGCAATTGTGTGA<br>GTCATT | 59.9                             | 366                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5155_P4_5482  | scaffold5155                            | 5482                          | ATTTTT/ATTT                                                   | GCAGCTCTTCTCATT<br>GCTT    | AAAATTGCATCTTCCT<br>TTTGA  | 59.7                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5155_P4_5708  | scaffold5155                            | 5708                          | AAAAA/AAAAAAGAAAAA                                            | CAGAGATGACATACGA<br>TGCTCC | TTTGGGGAAAACTAAC<br>ACACAA | 59.7                             | 124                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold5155_P4_5909  | scaffold5155                            | 5909                          | AATATATAT/AATATAT                                             | CAGAGATGACATACGA<br>TGCTCC | GCGTTGACTTAACAAC<br>TTGTACTTG | 59.7                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5157_P4_21879 | scaffold5157                            | 21879                         | TAAAAAAAA/TAAAAAAAA                                           | TTGGATGCACAAAATT<br>GGTT   | AGGTCATTTTCGTCTC<br>CCT       | 58.9                             | 371                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5158_P4_13889 | scaffold5158                            | 13889                         | C/CA                                                          | CACATAGGGCATAAAT<br>GGGG   | GCATGTGACAAGCCAT<br>GTGT      | 60.0                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5158_P4_17065 | scaffold5158                            | 17065                         | TAAAAAAAA/TAAAAAAAA                                           | GGCCATCACGTTTCATC<br>TTCT  | GATACTATGTCACCGC<br>GCAA      | 60.1                             | 832                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5158_P4_17947 | scaffold5158                            | 17947                         | ATTTGATTTTGATTTTGATTTGA/AT<br>TTGATTTTGATTTGA                 | CAATTGTGGGCGAATT<br>TCTT   | TACCCCCAAAATGGAA<br>ATGA      | 59.9                             | 203                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5158_P4_5514  | scaffold5158                            | 5514                          | AAAT/AAATAAT                                                  | ACGCGGAAGTAGGAG<br>GAAAT   | TGAGCCCCAGATGAAT<br>CTTT      | 60.1                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5158_P4_6317  | scaffold5158                            | 6317                          | TAAAAAAAA/TAAAAAAAA                                           | CCAAACAAATCTATTCC<br>CCATC | TGATTGTTCTGGACGC<br>ATCT      | 59.6                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5158_P4_6559  | scaffold5158                            | 6559                          | TAT/TATCATTATCAT                                              | CCAAACAAATCTATTCC<br>CCATC | CGGCTTATGTTGTTG<br>ACCA       | 59.6                             | 618                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5165_P4_1609  | scaffold5165                            | 1609                          | CTTTTTTTTT/CTTTTTTTTTTTT                                      | TTTCAGTTAATTCGTG<br>GTTCC  | CAAAATTTTCAACAAA<br>ACGCA     | 58.2                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5186_P4_13636 | scaffold5186                            | 13636                         | AT/A                                                          | GCATCCAATAGGTGGG<br>TTTG   | ATCGGATTCAACAAGATT<br>GGC     | 60.2                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold5186_P4_8653 | scaffold5186                            | 8653                          | GA/G                                                          | GAGTGTGGGGTCGTT<br>GAAT  | CCTAGGGAGGCTAAAA<br>TGCC | 59.8                             | 270                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5195_P4_4588 | scaffold5195                            | 4588                          | TA/TGCTATGTGCA                                                | AATAACATGTGCAGGG<br>AGCC | GGTTTGGAACGGAACC<br>CTAT | 60.0                             | 766                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold520_P4_96290 | scaffold520                             | 96290                         | TTATATATATAT/TTATATATATATAT                                   | TTCTCCAAAATGGGCA<br>ATTG | CATGCGTTCCTTGTTG<br>TAGA | 59.9                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5211_P4_2563 | scaffold5211                            | 2563                          | AGG/AG                                                        | TCTTCATCTGGTTGCA<br>GTGG | AGAACCTTGAAGTGCG<br>AGGA | 59.8                             | 148                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5211_P4_3755 | scaffold5211                            | 3755                          | TAAAAAAAA/TAAAAAAAA                                           | GTTCTCGAAGCAGAAA<br>ACGG | CTTTGGTCAAGTCTGG<br>CACA | 60.0                             | 702                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold523_P4_73607 | scaffold523                             | 73607                         | CAAAAAA/CAAAAAA                                               | GCACAAGCCAAGAACA<br>TCAA | CTCGCAGTTCCTCCAG<br>GTAG | 59.8                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5234_P4_584  | scaffold5234                            | 584                           | ATTTTTTTTT/ATTTTTT                                            | ATGACGAAGCTGCTGG<br>AGTT | AATCTCCCCCTGAGTTT<br>TGG | 60.0                             | 664                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5234_P4_996  | scaffold5234                            | 996                           | G/GTT                                                         | ATTCCAAACTCAGGG<br>GGAG  | TTGGTTGATTCTTGA<br>GTTGC | 60.3                             | 246                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5235_P4_1115 | scaffold5235                            | 1115                          | CTAT/CTATTATTAGTTATAT                                         | CGGAAAATTTACAGC<br>AGGT  | AGCCTTTTGGTTCCAT<br>GTG  | 60.0                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5251_P4_1190 | scaffold5251                            | 1190                          | CTCTTCTT/CTCTT                                                | TGGCCACCATTAGCAT<br>TACA | AGCGCAGTGGTGAAAA<br>GAAT | 60.0                             | 383                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold5251_P4_2057  | scaffold5251                            | 2057                          | CT/CTAT                                                       | CCTTGTGTGCAGTTCT<br>TTGC    | CTGCAAGTGCAACATC<br>TGGT   | 59.5                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold527_P4_104697 | scaffold527                             | 104697                        | CA/CAA                                                        | CAAATACACCGGGGA<br>AATG     | GTGGAGATCACCCGAG<br>TTGT   | 60.0                             | 284                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold527_P4_2067   | scaffold527                             | 2067                          | CG/C                                                          | CCAGTCCATGTTTGTG<br>CAAG    | TTTGCTCATTGTGCTT<br>CAG    | 60.2                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold527_P4_4805   | scaffold527                             | 4805                          | AT/ATTACTT                                                    | TCGTTGGTGCAATTATT<br>CCA    | TTGCAAGAAGGGGTTT<br>TGAC   | 59.9                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold527_P4_807    | scaffold527                             | 807                           | CAA/CAAA                                                      | TGCAGCCACATATTC<br>GCTT     | GCGTTGAGTTTGAAAC<br>CAGG   | 59.4                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold527_P4_81215  | scaffold527                             | 81215                         | AC/ACACC                                                      | CAATGGGAGAGGAGTT<br>CCAA    | TTGGTGCATAGAAGAAA<br>TTGGG | 60.0                             | 687                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5275_P4_1550  | scaffold5275                            | 1550                          | TAAAAA/TAAAAA                                                 | TCGGTTTTGAAACACA<br>ACACA   | AGTTTTGAGGAACCC<br>CACT    | 60.0                             | 691                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5279_P4_3482  | scaffold5279                            | 3482                          | TGA/T                                                         | AGCGAGTTGGTTGAGA<br>TGCT    | CTGCACGTGTATCGCA<br>GTCT   | 60.0                             | 557                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold528_P4_183983 | scaffold528                             | 183983                        | CAAAAA/CAAAAA                                                 | TGAACTCAAAATTCGAT<br>TTGTCT | TGAAAAACATTTGCCTG<br>AACA  | 57.9                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold528_P4_71886  | scaffold528                             | 71886                         | TTATATATATATATATATATA/TTA<br>TATATATATATATATATATATATA         | TCTCTGTCCGTTTCCTT<br>GCT    | CTGAGTTGCGACGAGA<br>GTTG   | 60.0                             | 218                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                 | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold5291_P4_5244  | scaffold5291                            | 5244                          | TAA/TAAA                                                                                                                      | CATGTGCGTCCATTAA<br>GTGC   | CCAAGGGAGAACGAAA<br>ATGA   | 60.1                             | 165                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold53_P4_137170  | scaffold53                              | 137170                        | CTT/CTTTT                                                                                                                     | GGACTGGTGGCTCAAA<br>GGTA   | TCGACCGGGAGTTTTG<br>ATTA   | 60.1                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold53_P4_2091    | scaffold53                              | 2091                          | A/AT                                                                                                                          | TCCTGGGCTTAATTCA<br>ATCG   | CGTGGTAATCGCGTAG<br>GAAT   | 60.0                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold53_P4_62729   | scaffold53                              | 62729                         | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT/TT<br>TATTATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTATTAT<br>TATT | GCTGGGCTTAAACAAA<br>TGGA   | TTGGAAGGCCACCT<br>ACAC     | 60.1                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold530_P4_1095   | scaffold530                             | 1095                          | A/ACACCTAT                                                                                                                    | AGGGAGGACGAAAATG<br>ACCT   | TCCAATCGGTGTGTTT<br>GTGT   | 59.9                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold530_P4_28571  | scaffold530                             | 28571                         | TAAAA/TAAAAA                                                                                                                  | AGGGAGGACGAAAATG<br>ACCT   | GGTGTGTTGGTGTGTCAT<br>TGGA | 59.9                             | 646                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold531_P4_206400 | scaffold531                             | 206400                        | TAAAAAAAAA/TAAAAAAAAA                                                                                                         | GATCATAACCAACGAT<br>TGCAGA | TGCGTGAAGAGAACGA<br>AAAA   | 60.0                             | 900                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold535_P4_125817 | scaffold535                             | 125817                        | AATATATATATATATATATATA/AAATA<br>TATATATATATATATATATATATAT<br>A                                                                | TTTGGAAGCATTGGAG<br>ATCA   | GAAGGTTGTCTCCACA<br>GGGA   | 59.2                             | 681                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold535_P4_94648  | scaffold535                             | 94648                         | GATATATATAT/GATATATATATAT                                                                                                     | AATGGAGGAGAAGGGA<br>GGAA   | TGAAAAGGGGTAGGCA<br>ACAC   | 60.0                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold537_P4_123048 | scaffold537                             | 123048                        | TAATAATA/TAATAATAATAATAATA<br>AAATAATA                                                                                        | ATGTTTTCCGGAAGAG<br>GCTT   | CAAAGTCGGCCCTGTT<br>TTTA   | 60.1                             | 730                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                              |                             |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold537_P4_212689 | scaffold537                             | 212689                        | GTAATAATAATAATAATAATAAT<br>AA/GTAATAATAATAATAATAATA<br>A                                                     | AGTCTGCCTCACGTTT<br>GTCC    | TGTTCAGGCTTGCAC<br>AACT      | 60.3                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold537_P4_82843  | scaffold537                             | 82843                         | TAAA/TAAAA                                                                                                   | GTTTTGGCGTTGGTTT<br>CACT    | AATTCGACTATTCTCT<br>AATGATGG | 60.0                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5420_P4_685   | scaffold5420                            | 685                           | ACC/ACCC                                                                                                     | AAGGGAGGATGGAAAT<br>GACC    | ATTTTGTCTCCTTGG<br>GCT       | 60.1                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold543_P4_39888  | scaffold543                             | 39888                         | TTTTATTTATTTATTTATTTATTT<br>ATTTATT                                                                          | TGCGAAAAATCATGAG<br>AGCA    | CATTGTGTTGTCAGCC<br>CCT      | 60.5                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold543_P4_55990  | scaffold543                             | 55990                         | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTAT/ATATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT | AGCAACAACAATGAC<br>GTGG     | AAATAAATTTTACTCAG<br>CGGGAAA | 59.6                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold544_P4_192787 | scaffold544                             | 192787                        | AG/A                                                                                                         | TGGTTCAAAGCCCTTA<br>TTGG    | AGGTCATTTTCGTCCTC<br>CCT     | 59.9                             | 554                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold544_P4_221561 | scaffold544                             | 221561                        | GA/G                                                                                                         | ACACACCTATGGGATG<br>CACA    | AGGTCATTTTCGTCCTC<br>CCT     | 59.8                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold544_P4_266680 | scaffold544                             | 266680                        | TAAAAAAAAA/TAAAAAAAAA                                                                                        | CGCGAGAGGTTTGCTT<br>GTAT    | TCGTCGACAACAACAT<br>CAAAA    | 60.4                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold544_P4_267099 | scaffold544                             | 267099                        | ATTTTTTTTT/ATTTTTTTT                                                                                         | TTTTCATCTCCAACAAC<br>ATCAAA | ACATGTATAGCCTCAG<br>GGCG     | 59.5                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold544_P4_269437 | scaffold544                             | 269437                        | CTTTTTTTTT/CTTTTTTTTT                                                                                        | ACGAGCGAGGACGAA<br>GTAAA    | GCTACGTGGGAAGACT<br>CTGG     | 60.0                             | 916                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold544_P4_316944 | scaffold544                             | 316944                        | TGGG/TGGGG                                                                    | AGTTTGGAGTGGTGTG<br>AGGG   | CCAACACTCCATTTTAC<br>CCC  | 60.0                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold544_P4_343264 | scaffold544                             | 343264                        | CAAAAAAAAA/CAAAAAAAAA<br>AAA                                                  | ATTGTGGAGTTGATGC<br>CTCC   | CACACCGATGGCTAAA<br>CAAA  | 59.9                             | 842                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold544_P4_343923 | scaffold544                             | 343923                        | CAAAAAAAAA/CAAAAAAAAA                                                         | GTGAAAAAAGGGGGA<br>AGGG    | TTTTCTTCTCTTTCCT<br>GCG   | 59.6                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold544_P4_41662  | scaffold544                             | 41662                         | CT/CTT                                                                        | GTACCCTGTGGATGGG<br>AATG   | TGGATGCACTCGATTG<br>GTAA  | 60.1                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold544_P4_57260  | scaffold544                             | 57260                         | TAAAA/TAAAA                                                                   | AATTCCTTGGGACCGT<br>GATT   | TCCTCCCAGGCTTAT<br>TCTT   | 60.6                             | 822                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold544_P4_85733  | scaffold544                             | 85733                         | GAAAAAAAA/GAAAAAAAA                                                           | TTTATCTGGCTTCCTC<br>CCA    | TTTAAGTTGGAACATG<br>GTGGA | 59.6                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold545_P4_158136 | scaffold545                             | 158136                        | CATATATATATATATATATATATA<br>TATATATATAT/CATATATATATATAT<br>ATATATATATATATATAT | CCCACTTGGTTCTGTT<br>TCGT   | TCGCAGATTCATCCTTT<br>TCA  | 60.0                             | 822                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold545_P4_193109 | scaffold545                             | 193109                        | CAAAAA/CAAAAA                                                                 | AATCTCCCCTGAGTT<br>TTGG    | ATCTTTGGACACCGTC<br>GTTC  | 60.3                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold547_P4_155914 | scaffold547                             | 155914                        | ATCAAA/ATCAAGTTCAAA                                                           | TCGATCTGTACGAACA<br>TTGACC | CGGAACCCGAAACACT<br>TTTA  | 60.0                             | 295                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold547_P4_156143 | scaffold547                             | 156143                        | CAAA/CAAAA                                                                    | TTCGGTCTATTTTTGTC<br>GGG   | CGGAACCCGAAACACT<br>TTTA  | 59.9                             | 219                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                   |                           |                            |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold547_P4_96984  | scaffold547                             | 96984                         | CAAAA/CAAAA                                                                       | CACGATGGCTAGTGCT<br>TGAA  | CGATCGGTATGAACAT<br>TGACC  | 60.0                             | 276                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold548_P4_146650 | scaffold548                             | 146650                        | ATATTATTATTATTATTATTATTA<br>TTATTATTA/ATATTATTATTATTATT<br>ATTATTATTATTATTATTATTA | TTGGCTGCTTTTCTTC<br>CAGT  | TGGTTTTATACGGATT<br>ATTGGG | 60.0                             | 559                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold548_P4_255463 | scaffold548                             | 255463                        | TAAA/TAAA                                                                         | GTGTGCTGGAGATGG<br>GTCTT  | CACCAGCTCATCCAGT<br>GTTG   | 60.1                             | 253                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold548_P4_354551 | scaffold548                             | 354551                        | AATATATATATATATATATATA/AA<br>TATATATATATATATATATA                                 | AACGTGGCAAAGAGCA<br>ACTT  | TCGCGGAATTACTACC<br>CTTG   | 59.9                             | 963                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold548_P4_367547 | scaffold548                             | 367547                        | GATATATATATATATA/GATATATA<br>TATATATATATA                                         | CGAGCAAAGTGAGAC<br>TGCT   | CAACAAAGTTTTGGGT<br>TTCTG  | 60.7                             | 654                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold548_P4_438414 | scaffold548                             | 438414                        | C/CCCAAATG                                                                        | ATTCTGGGATAAGTGGA<br>ACCC | CCATCGGATCCAAA<br>GAGA     | 60.0                             | 713                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold548_P4_474518 | scaffold548                             | 474518                        | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATA<br>TATAT                   | GGATTTTGGGAAAAT<br>TGAAA  | GCCTGTTAGGTACATG<br>GTTGC  | 60.0                             | 315                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold548_P4_588992 | scaffold548                             | 588992                        | GA/G                                                                              | GCCCTCAGATGAGAGT<br>CAGG  | CCAAGTGTAAACACCC<br>GTTT   | 59.9                             | 451                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold548_P4_593356 | scaffold548                             | 593356                        | CATATATATATATATATATATATA<br>TATATA/CATATATATATATATATA<br>TATATATATATATATATATA     | CTAGCACCTTAGCGTG<br>GAGG  | AAAACGTGGTTTGGA<br>AGTG    | 60.0                             | 481                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold548_P4_612534 | scaffold548                             | 612534                        | A/AT                                                                              | TATTTTGATTTTGGCT<br>CGG   | AGGAAGAGTGGAGTTG<br>CGAA   | 59.9                             | 416                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                 |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold548_P4_9476   | scaffold548                             | 9476                          | ATTTTTTTTT/ATTTTTTTTT                                           | TTTTTGTCGCTTGAC<br>TAATG  | TCAAACCCATTGGTCT<br>CCTT  | 59.0                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold549_P4_44442  | scaffold549                             | 44442                         | ATTTTTTTTTTT/ATTTTTTTTTTTT                                      | TCAATGCAGAAAACCT<br>AACCT | AGGTGGTGTGGTGAA<br>GGAG   | 57.5                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold549_P4_61007  | scaffold549                             | 61007                         | GTATATATATATATATA/GTATATATA<br>TATATA                           | TGCCAATTCGAAGATC<br>AAAA  | CACCCCTTACCTCGAC<br>TGAA  | 59.2                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold55_P4_606     | scaffold55                              | 606                           | CA/CAA                                                          | GATGTGGCACACAAGG<br>ATGT  | TGGTGGAATCAAATTG<br>ACGA  | 59.4                             | 321                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5504_P4_1323  | scaffold5504                            | 1323                          | T/TTA                                                           | ACCAATCAAGTGCATC<br>CCAT  | TAAGCCTAAGGAGGAC<br>GCAA  | 60.2                             | 175                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5511_P4_12638 | scaffold5511                            | 12638                         | AT/ATT                                                          | TGGTCCCGTGGTTGTT<br>TACT  | CAACAGCCCCTTAAC<br>CAAA   | 60.3                             | 238                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold553_P4_118780 | scaffold553                             | 118780                        | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATA<br>TATAT | TCGATGTAACACCCCA<br>CATTT | TCGATGATGAAGCTCC<br>CTTT  | 60.1                             | 858                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold553_P4_128858 | scaffold553                             | 128858                        | ATATTATTATTATTATTATTATTA<br>TT/ATATTATTATTATTATTATTATTA<br>TT   | CGTGCGCATTTGGTTT<br>ACTA  | TGTGTGTTTGATGTGG<br>TGTGA | 59.8                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold553_P4_2570   | scaffold553                             | 2570                          | ATGATT/AT                                                       | TTGGTTCACTCCCTGG<br>ATTG  | AACATCAGTCAAGCGC<br>ACAA  | 59.9                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold553_P4_2669   | scaffold553                             | 2669                          | CTT/CT                                                          | TTGGTTCACTCCCTGG<br>ATTG  | AACATCAGTCAAGCGC<br>ACAA  | 59.9                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold553_P4_476018 | scaffold553                             | 476018                        | A/AC                                                          | TCAACAGCAGCTTTGC<br>ATTC | TGCGAATGAGCAGAAT<br>TTCA | 60.1                             | 377                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold553_P4_527326 | scaffold553                             | 527326                        | AGG/AG                                                        | CATTTCAAGTTGGGGC<br>AGTT | TCGTCTTCGGGTTGGT<br>TATC | 60.0                             | 837                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold553_P4_583352 | scaffold553                             | 583352                        | C/CT                                                          | TGACAGGATAACAGAG<br>CCCC | GGAGGGTTTTGGTTTG<br>GAAT | 60.1                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold553_P4_76075  | scaffold553                             | 76075                         | TTATATATATATATATATAT/TTAT<br>ATATATATATATATATATATATATA<br>T   | GGGAGAATTGTAACAC<br>CCCA | AGCAGCTGCCGTATAC<br>CTTG | 59.6                             | 890                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold553_P4_800299 | scaffold553                             | 800299                        | ATTTTTTT/ATTTTTTTT                                            | CAAAATCGGGGATAGG<br>GTTT | CGGGGTCATTCTCTTC<br>ACAT | 60.0                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold553_P4_927370 | scaffold553                             | 927370                        | GAA/GAAA                                                      | TTGGCCAAGTCCCTGT<br>TTAC | CGTGGTAATCGCGTAG<br>GAAT | 60.0                             | 140                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold553_P4_927395 | scaffold553                             | 927395                        | CAAAA/CAAAAA                                                  | TTGGCCAAGTCCCTGT<br>TTAC | CGTGGTAATCGCGTAG<br>GAAT | 60.0                             | 140                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5548_P4_32964 | scaffold5548                            | 32964                         | CTTTTTTT/CTTTTTTT                                             | TTTCTCATTGCTCTTGG<br>GGT | GCCACAGTCACATGAC<br>AACA | 59.7                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5551_P4_550   | scaffold5551                            | 550                           | CTTTTTTT/CTTTTTTTT                                            | GATACGTTGGAGCATC<br>GACA | CACGAAACACCCTCTT<br>CCAT | 59.7                             | 230                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold556_P4_1384   | scaffold556                             | 1384                          | ATTT/ATT                                                      | TTTCGTCTCCCTAG<br>GCTT   | TGGATGCACAAGATGG<br>GTTA | 60.2                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                           | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                         |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold556_P4_2877   | scaffold556                             | 2877                          | CAAA/CAA                                                                                                | TTTCGTCCTCGAGAGC<br>CTTA  | GGAGGACGCAATGAC<br>CTAA     | 60.1                             | 311                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold559_P4_75157  | scaffold559                             | 75157                         | CAATCGATTGGGAAATCGATT/CAAT<br>CGATT                                                                     | TTAACCAATCGTGTGC<br>ATCC  | TTCATTCAATCGATTTC<br>CCA    | 59.4                             | 422                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold559_P4_93166  | scaffold559                             | 93166                         | AAAATAAATAAATAAATAAATAAATA<br>AATAAATAAATAAATAAATAA/AAAA<br>TAAATAAATAAATAAATAAATAAATA<br>AATAAATAAATAA | TTAGGTGCGCTTGACT<br>GATG  | TTTGGCATTGGTTTCAC<br>TCA    | 60.0                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5598_P4_13569 | scaffold5598                            | 13569                         | ATTTTTTTTTTTTT/ATTTTTTTTTTT                                                                             | CGGCATTGGATCATGG<br>TTAG  | TTTCGACTGCCTAGCG<br>ATTT    | 61.2                             | 549                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold560_P4_134002 | scaffold560                             | 134002                        | TTAAAGAAT/TT                                                                                            | TGGCACGATATCATCA<br>TCATT | ATGAAGTTGACGTATG<br>GGGG    | 58.8                             | 918                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold560_P4_156538 | scaffold560                             | 156538                        | ATTTTTTTTT/ATTTTTTTTTTT                                                                                 | AGGTGGTGTGGTGAA<br>GGAG   | TCAATGCAGAAAACCTCA<br>ACCT  | 60.0                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold560_P4_160364 | scaffold560                             | 160364                        | TTATATATATATATATA/TTATATATA<br>TATATATATA                                                               | TCACCATGCACAATCA<br>GTTTC | TCATGAAACGCACAAC<br>AACTT   | 59.6                             | 744                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold560_P4_30079  | scaffold560                             | 30079                         | TATAATAAATAAATAAATAA/TATAATA<br>AATAATAAATAAATAAATAA                                                    | GCATTCTCGTTCATCT<br>CACG  | CGAATCTTGATTTTCGGT<br>AACCT | 59.4                             | 906                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5600_P4_533   | scaffold5600                            | 533                           | TAAAAAAAAAAAAA/TAAAAAAAAAAA                                                                             | TATAGGCCGGTCTGTG<br>AAGC  | TAACCTTCCGAGGATA<br>TGCG    | 60.2                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5600_P4_640   | scaffold5600                            | 640                           | AC/ACAAGGTTTC                                                                                           | TATAGGCCGGTCTGTG<br>AAGC  | TAACCTTCCGAGGATA<br>TGCG    | 60.2                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold561_P4_124753 | scaffold561                             | 124753                        | GCTCTCTCTCTCTCTCTCT/GCTC<br>TCTCTCTCTCTCTCT                   | GATCGTTTTGGCGTTG<br>ATT  | TTCATGGGTAAAGCCC<br>AAGT    | 59.9                             | 355                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold561_P4_66066  | scaffold561                             | 66066                         | TTATATATATATATAT/TTATATAT<br>ATATATATATAT                     | TGGCAACACCCCTAA<br>AATA  | TTGACATCCCAAGTCAA<br>ACATC  | 60.2                             | 713                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold561_P4_84146  | scaffold561                             | 84146                         | AT/ATT                                                        | ATTCGACTAGTGGTGG<br>TGCC | AGGCCGCCACAAAATA<br>TTAC    | 60.0                             | 669                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold562_P4_186797 | scaffold562                             | 186797                        | GTATATATATATATATATATATAT<br>AT/GTATATATATATATATATATAT<br>AT   | GCAGCAAGGACAAATG<br>ACAA | CTATTCGTTCAATCGCC<br>GTT    | 59.8                             | 940                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold562_P4_238893 | scaffold562                             | 238893                        | CAAACAGTAAACAGTAAAA/CAAA<br>AGTAAAA                           | TCCTTGCAATTCCTCA<br>TTC  | CTGAAGGATCATCCCA<br>AAGC    | 60.0                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold562_P4_299510 | scaffold562                             | 299510                        | CTTTT/CTTT                                                    | GGCAACCTGTTTTAG<br>GCTA  | TGTTAATGGTGTGCCA<br>ATCG    | 60.2                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold564_P4_12224  | scaffold564                             | 12224                         | A/AC                                                          | GGTATTGGGCTCCCTT<br>CCTA | CTCGTGAGGAGCAACA<br>ACAA    | 60.3                             | 552                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold564_P4_14245  | scaffold564                             | 14245                         | T/TTTAA                                                       | TGCCAATTGTTTTATC<br>TCCG | CCACCAAATTACCATTT<br>AAGACA | 60.0                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold564_P4_15097  | scaffold564                             | 15097                         | TTAT/TTATAT                                                   | TGGAGAAATGCTAAAT<br>CCCG | GATGGCAGGTAAAAGC<br>GAAA    | 60.0                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold564_P4_25971  | scaffold564                             | 25971                         | TAA/TAGTTTATTAATAGTTAAA                                       | GTATCTGAGCCTCTGC<br>CAGC | AATTGGTGTGTCTGCG<br>TCAA    | 60.1                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                               |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold564_P4_26112 | scaffold564                             | 26112                         | A/AG                                                          | GTATCTGAGCCTCTGC<br>CAGC      | AATTGGTGTGTCTGCG<br>TCAA | 60.1                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold564_P4_2634  | scaffold564                             | 2634                          | ATTTTT/ATTTT                                                  | TCGAATGCTCGACTTT<br>ACCC      | GCGGAATAACATGGTT<br>GCTT | 60.2                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold564_P4_5029  | scaffold564                             | 5029                          | GAAAAA/GAAAAAA                                                | TGGGATGCAAACAATT<br>CTCA      | ATTGAAACCAATGGGA<br>GGAA | 60.0                             | 178                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold564_P4_5212  | scaffold564                             | 5212                          | G/GAAC                                                        | TGGGATGCAAACAATT<br>CTCA      | TTGTCAATTTGGGAGT<br>GCAA | 60.0                             | 560                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold564_P4_8317  | scaffold564                             | 8317                          | TAAAAAA/TAAAAAA                                               | CAACATCCAAATTTTGT<br>TATAGAGC | CGACATGCATGCCTTA<br>TTTG | 58.3                             | 143                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5679_P4_741  | scaffold5679                            | 741                           | GTTT/GTT                                                      | ATCATCAAGGCCATTC<br>AAGC      | ACAATTACTATGCGGG<br>TGGG | 60.0                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold568_P4_19505 | scaffold568                             | 19505                         | AGGG/AGG                                                      | TCTTGGGCTTCCAATA<br>GGTG      | AAGCCTCAAGAGGACG<br>AACA | 60.1                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold568_P4_21283 | scaffold568                             | 21283                         | AGG/AGGG                                                      | CACTTTCTTCCTCACAG<br>GGC      | GGAGGACGAAATGACC<br>AAAA | 59.8                             | 510                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5700_P4_8121 | scaffold5700                            | 8121                          | ATTTTTTTTTTT/ATTTTTTTTTTT<br>T                                | CGTCTCTGGATGATG<br>TGATG      | TGGGATGTTGCACATC<br>TTGT | 59.1                             | 890                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold571_P4_11860 | scaffold571                             | 11860                         | A/AACTGGACGC                                                  | CCAATTTGTTGTGTGC<br>CAAG      | TTTGCGGAGTTTGTGT<br>GAAG | 60.0                             | 383                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold571_P4_79289  | scaffold571                             | 79289                         | GTT/GT                                                        | AATAAGCCTAGGGAAG<br>CCGA | CCTAGGAATATTCGCG<br>TCCA | 60.2                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5730_P4_653   | scaffold5730                            | 653                           | ATTT/ATTTT                                                    | ACAAAGGCAACCTTTT<br>GTGG | CTGCCACCGTTGTTA<br>TTCT  | 60.0                             | 866                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_100417 | scaffold575                             | 100417                        | TCAACC/TC                                                     | ATAAGCTAAGGACGCC<br>AGCA | CCCTGAGACAAGCCAG<br>CTAC | 60.0                             | 214                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_103253 | scaffold575                             | 103253                        | AGGGG/AGGGGG                                                  | AAACAACGAGTATGGG<br>CGAC | AGCTTGCTTTGAAAGG<br>GACA | 60.0                             | 113                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_103640 | scaffold575                             | 103640                        | ACCCCC/ACCCC                                                  | AAACAACGAGTATGGG<br>CGAC | CGCAATTAGCCTCTTTC<br>GTC | 60.0                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_103819 | scaffold575                             | 103819                        | ATT/ATGCCTTATTT                                               | TCTTCTCGCTGACTTG<br>GGAT | CGCAATTAGCCTCTTTC<br>GTC | 60.0                             | 205                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_110510 | scaffold575                             | 110510                        | GT/GTGTA                                                      | CTTTCTGGTCAAGGCC<br>TCAG | CTAGACCTGCGGAAGA<br>CAGG | 60.0                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_111632 | scaffold575                             | 111632                        | TA/TAAACAAATAA                                                | GTTCTCGCTGCTTAT<br>CGAC  | TTTAACAACCGTGGGC<br>TAGG | 60.0                             | 229                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_112821 | scaffold575                             | 112821                        | TT/TTAGAGTACT                                                 | CCTTACACTTTGCTCCT<br>CGC | GGCTTGAGCCTAGCCT<br>TTTT | 60.0                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_112885 | scaffold575                             | 112885                        | GCCTGACCT/GCCT                                                | CCTTACACTTTGCTCCT<br>CGC | GGCTTGAGCCTAGCCT<br>TTTT | 60.0                             | 419                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold575_P4_113273 | scaffold575                             | 113273                        | ATT/AT                                                        | TTCGGCAACATTCCGT<br>ATT  | GCCTGACCTATGGCT<br>ATCA  | 60.3                             | 283                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_113322 | scaffold575                             | 113322                        | ATTTTAAATAGGCTT/ATTTTAAATA<br>GGCTTTTAAATAGGCTT               | TTCGGCAACATTCCGT<br>ATT  | TCCCAGTCTCTGGTCA<br>ATCC | 60.3                             | 652                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_113457 | scaffold575                             | 113457                        | CTGGC/CTGGCATGGC                                              | TGATAGGCCATAGGTC<br>AGGC | GCTAAGTGGTCTTTCC<br>GCTG | 60.1                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_113513 | scaffold575                             | 113513                        | ATCTC/ATCTCTC                                                 | TGATAGGCCATAGGTC<br>AGGC | GCTAAGTGGTCTTTCC<br>GCTG | 60.1                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_113710 | scaffold575                             | 113710                        | GAAAAA/GAAAAAA                                                | TGATAGGCCATAGGTC<br>AGGC | GCTAAGTGGTCTTTCC<br>GCTG | 60.1                             | 440                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_114104 | scaffold575                             | 114104                        | CA/CAGA                                                       | AAAGACCACTTAGCGC<br>AGGA | TCAACTTGCTTGCTTTC<br>CCT | 60.0                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_114732 | scaffold575                             | 114732                        | AGTG/AGTGCTGTG                                                | GGGAAAGCAAGCAAGT<br>TGAG | AACACAAGTCCTCCCA<br>CCAG | 60.0                             | 808                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_118237 | scaffold575                             | 118237                        | C/CGGGGCACAG                                                  | AGCAGGTAGTTGGCTC<br>CTGA | TTGAAGTGGAGCATAG<br>TGCG | 60.0                             | 739                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_120383 | scaffold575                             | 120383                        | AGG/AG                                                        | GTGCTCCATCCCAATG<br>AACT | AGAGCCGTGTTATGGG<br>TGAC | 59.9                             | 899                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_126333 | scaffold575                             | 126333                        | CT/CTTTT                                                      | CCGACATGTTGTTGAC<br>TTGG | GAGCAAATCCCTGCAC<br>TCTC | 60.0                             | 762                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold575_P4_66804 | scaffold575                             | 66804                         | CTTTTTTT/CTTTTTTT                                             | AACCGGATGTTGGGAT<br>GTAA | CCCATTCACTCCCACT<br>CTGT  | 60.1                             | 348                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_67025 | scaffold575                             | 67025                         | ATTTAGGGTA/ATTTAGGGTATGGTT<br>TAGGGTA                         | ACAGAGTGGGAGTGAA<br>TGGG | CCTAAGCCTGACCCTA<br>CCCT  | 60.0                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_67830 | scaffold575                             | 67830                         | TGGTTTAGGGTTTAGGGTT/TGGTT<br>TAGGGTT                          | GGGTTAGGGTAGGGT<br>CAGGA | AGGCTGGAATCGGTAA<br>GTGA  | 60.2                             | 357                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_7660  | scaffold575                             | 7660                          | AAGAAG/A                                                      | TCAATTTCCAATGGGT<br>GCTT | GCCAGACCATAAGTAG<br>GCCA  | 60.3                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_82549 | scaffold575                             | 82549                         | TAAAAAA/TAAAAAA                                               | GCAATAACGAAATGGC<br>TGTG | CCCTAACTCCCTAAAC<br>CCCA  | 59.2                             | 101                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_82903 | scaffold575                             | 82903                         | TTTAAGGTTA/TTTA                                               | GCAATAACGAAATGGC<br>TGTG | TAACCCCAAACCTAAA<br>CCC   | 59.2                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_89948 | scaffold575                             | 89948                         | TAAAAAA/TAAAAAA                                               | GGATTGGCCCCAAATA<br>GAAT | CCCTTGTCATTGCTGC<br>TGTA  | 60.0                             | 722                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_90216 | scaffold575                             | 90216                         | G/GA                                                          | CCCAAATTGCAATAAC<br>CAGG | TACCGTTTCCCACT<br>CACA    | 60.2                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_90829 | scaffold575                             | 90829                         | ATTTTTTT/ATTTTTTT                                             | TGTGAGTGTGGGAAAC<br>GGTA | GGCAATGTGCATAAAC<br>AAAAA | 60.0                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_91034 | scaffold575                             | 91034                         | AATATATATATATATATATATAT/A<br>ATATATATATATATATATAT             | TGTGAGTGTGGGAAAC<br>GGTA | GGCAATGTGCATAAAC<br>AAAAA | 60.0                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold575_P4_91358 | scaffold575                             | 91358                         | TC/T                                                          | TTTTTGTTCATGCACAT<br>TGCC | TTCAAGACACCGTAA<br>CACCA | 58.6                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_92874 | scaffold575                             | 92874                         | A/A/T                                                         | GCCCTTGAAATTGACA<br>AAGC  | TTCGTGACCGTGCAAT<br>ACAT | 59.7                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_98341 | scaffold575                             | 98341                         | GCC/GCCC                                                      | AGTGCCCAACGACGGT<br>ATAG  | TACGGGGTTTTAGCGA<br>GTTG | 60.0                             | 869                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_98810 | scaffold575                             | 98810                         | TC/T                                                          | TAAGCCAGGGCTTTCT<br>TTCA  | CCTCCACTCCAAACCT<br>ACCA | 60.0                             | 404                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_98925 | scaffold575                             | 98925                         | TC/TCC                                                        | TAAGCCAGGGCTTTCT<br>TTCA  | GGCTAAGTCTGAAAGT<br>GGCG | 60.0                             | 647                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_99188 | scaffold575                             | 99188                         | CT/CTGT                                                       | TGGTAGGTTTGAGTG<br>GAGG   | GGCTAAGTCTGAAAGT<br>GGCG | 60.0                             | 263                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_99345 | scaffold575                             | 99345                         | A/ACGGCCC                                                     | CGCCACTTTCAGACTT<br>AGCC  | CGTGTGCTTTACCCGT<br>AGGT | 60.0                             | 240                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold575_P4_99548 | scaffold575                             | 99548                         | CGG/CGGG                                                      | CGCCACTTTCAGACTT<br>AGCC  | AGGAAGCAAGGGGGAT<br>TCTA | 60.0                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5761_P4_1101 | scaffold5761                            | 1101                          | C/CG                                                          | TCCTGGTCCTCGATT<br>CATC   | AACGCCTTAAAGCCC<br>AAAT  | 60.0                             | 362                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5761_P4_842  | scaffold5761                            | 842                           | CTTTT/CTTTTT                                                  | GGTCCTCGATTTCATC<br>TGGA  | AACGCCTTAAAGCCC<br>AAAT  | 60.0                             | 684                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold5777_P4_16517 | scaffold5777                            | 16517                         | CTT/CTTT                                                      | TTGCAATTGGCACACA<br>AAAT  | TGAGTTGCTTCAAAGT<br>GATGTG | 60.0                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5777_P4_16606 | scaffold5777                            | 16606                         | ACTT/ACTTTCTT                                                 | TTGCAATTGGCACACA<br>AAAT  | TGAGTTGCTTCAAAGT<br>GATGTG | 60.0                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold578_P4_11617  | scaffold578                             | 11617                         | CTTTTTTTT/CTTTTTT                                             | TTCAATTGATCTTTTCG<br>GGG  | CCTCGAGAAAAATGGA<br>CCAA   | 59.9                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold578_P4_38009  | scaffold578                             | 38009                         | C/CGGTCTT                                                     | GACTTTTCGAGCGATT<br>TTCTG | ATCGAGGATGAGGAGA<br>CCCT   | 60.0                             | 312                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5780_P4_2877  | scaffold5780                            | 2877                          | AC/A                                                          | GGAATCCGGTTTCTTT<br>CCAT  | GACCATTATTCACACG<br>GTGG   | 60.1                             | 765                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5780_P4_5394  | scaffold5780                            | 5394                          | CAAAAAA/CAAAAAA                                               | CGTGTTCTCCCCGTGT<br>ATTT  | ATGTGACACCCTAAAC<br>CCCA   | 59.9                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5780_P4_5464  | scaffold5780                            | 5464                          | ATT/AT                                                        | CGTGTTCTCCCCGTGT<br>ATTT  | ATGTGACACCCTAAAC<br>CCCA   | 59.9                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5780_P4_8742  | scaffold5780                            | 8742                          | CTTTTT/CTTTT                                                  | AAGTTCGCGATTAGGC<br>CTTT  | GTTTGGGTCAAGGCTA<br>TGGA   | 60.1                             | 444                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5780_P4_9297  | scaffold5780                            | 9297                          | GAAAC/GAAACGTCAATAAAAC                                        | TCCATAGCCTTGACCC<br>AAAC  | CCCCTGCTTGCAATA<br>ATGA    | 59.9                             | 404                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5792_P4_89682 | scaffold5792                            | 89682                         | TAAAAA/TAAAAA                                                 | TGACTCATTCGATTGT<br>GCATT | CTTCCACCCAAGTATC<br>CCCT   | 59.1                             | 687                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)      | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                    |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold584_P4_25000  | scaffold584                             | 25000                         | TTT/TCATTGTTTCATT                                                  | GTGACTTACCAGCCAA<br>CCGT | GGTGCAGGTAGTCCCA<br>AAAA   | 60.0                             | 180                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold584_P4_29046  | scaffold584                             | 29046                         | ATT/AT                                                             | CAATCCGAGACAGTCC<br>CCTA | TTTGCAGCGCTTGATC<br>ATTA   | 60.1                             | 524                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold584_P4_76492  | scaffold584                             | 76492                         | ATATATAT/ATATATATATATCTATAT<br>AT                                  | AGTGAAACCAACGCCA<br>AAAC | CCGGAATCACTAGGCT<br>TGTC   | 60.0                             | 766                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold584_P4_82259  | scaffold584                             | 82259                         | TC/TCC                                                             | TTCAAACGACAGCTTG<br>ATGC | CCTTGTCAGGATTGCC<br>ATTT   | 60.0                             | 742                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold586_P4_3901   | scaffold586                             | 3901                          | AATATATATATATATA/AATATATATA<br>TATA                                | CGCAGCGATCCAAAA<br>TAGT  | GGTGCTTGTTAAGTTG<br>TGCCT  | 60.2                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5869_P4_1633  | scaffold5869                            | 1633                          | TTTATTATTATTATTATTATTATT<br>ATTATT/TTTATTATTATTATTAT<br>TATTATTATT | GGGTAGGAAAAGCATC<br>ACGA | TGATTGATTGTGGAC<br>CGA     | 60.1                             | 387                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5869_P4_18300 | scaffold5869                            | 18300                         | GAAAAAAAAA/GAAAAAAAAA                                              | TTCCAAATGCTTGG<br>GACAC  | TGAACCTTTTACACGG<br>TTCTCA | 59.8                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5869_P4_5404  | scaffold5869                            | 5404                          | GTAT/GT                                                            | TTGAAGCGCAAATCTT<br>CCT  | ACCGAATCAAACCAA<br>CGAC    | 60.0                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold587_P4_15236  | scaffold587                             | 15236                         | C/CA                                                               | TACCATTTACCGTAAC<br>GCA  | CTCAGCTGTTGAAAGT<br>GCCA   | 60.0                             | 399                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold587_P4_29094  | scaffold587                             | 29094                         | GAA/GAAATTTAGGAAATAA                                               | TCCAGTCCTCGATT<br>CATC   | TACGAACATCCCCGA<br>AAAG    | 60.0                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold587_P4_35297 | scaffold587                             | 35297                         | C/CA                                                          | TTCAAACGTTCTCTCAC<br>CCC  | AAAAATGGGAATTGGA<br>AGGG | 60.1                             | 530                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold587_P4_5009  | scaffold587                             | 5009                          | AATA/AATATA                                                   | ATGTGAATCCCACCAG<br>GAAA  | AGCGCTCTAAAATGCC<br>TCCT | 60.2                             | 320                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold587_P4_50853 | scaffold587                             | 50853                         | TAAAAA/TAAAAA                                                 | AGGGGAATTTTCGTAC<br>CACC  | ATCGAAGACCAGGAGA<br>CCCT | 60.1                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold587_P4_51041 | scaffold587                             | 51041                         | CAAAAAAAAA/CAAAAAAAAA                                         | AGGGGAATTTTCGTAC<br>CACC  | ATCGAAGACCAGGAGA<br>CCCT | 60.1                             | 638                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold587_P4_53018 | scaffold587                             | 53018                         | CAAAAA/CAAAA                                                  | TACACGAAACCCGAAA<br>CACA  | CGAGGACCAGGAGACC<br>ATTA | 60.0                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold587_P4_54888 | scaffold587                             | 54888                         | AATATATATATATATA/AATATATA<br>TATATATA                         | CAAGACATGCGAAAGT<br>CGAA  | TCCAGCTTCCTCAAAG<br>CCTA | 60.0                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold587_P4_5518  | scaffold587                             | 5518                          | TC/TCC                                                        | AAAAAGCGCTGTAAAA<br>GAGCC | AGGGTTCCCAAAGGAA<br>GAGA | 60.0                             | 244                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold587_P4_56115 | scaffold587                             | 56115                         | GAA/GAAA                                                      | AACTGCCAAAGAGATG<br>TGGG  | TGCAGTTCCATCTCAT<br>GCTC | 60.1                             | 338                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold588_P4_16402 | scaffold588                             | 16402                         | GAAAAA/GAAAA                                                  | TTGCATGCACAAGATT<br>GGTT  | AGGTGTGTTCTGTTCC<br>TTGG | 60.1                             | 793                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold588_P4_16586 | scaffold588                             | 16586                         | A/AT                                                          | GGACGACGAAAATTGC<br>CTAA  | AGGTGTGTTCTGTTCC<br>TTGG | 60.1                             | 247                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)              | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                          |                                  | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------|----------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                             |                         |                         |                                  |                                               | Sequence components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| scaffold589_P4_101331 | scaffold589                             | 101331                        | GAAAAAAAA/GAAAAAAAAAAAAA                                                    | GCCCTCAGATGAGAGT CAGG   | GTGCTCTTTCTGTAAC GCCC   | 59.9                             | 729                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold589_P4_103178 | scaffold589                             | 103178                        | C/CA                                                                        | TGATATGACAATCCCC GACA   | CGCAATTCTTGAGTTC GACA   | 59.7                             | 115                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold589_P4_202092 | scaffold589                             | 202092                        | TTATATATATATATATATATATATA TATATATAT/TTATATATATATATATA TATATATATAT           | TGAATGTTCTTCCCACA CGA   | CATGTGTTTCGCATTCT GAGG  | 60.1                             | 412                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold589_P4_228193 | scaffold589                             | 228193                        | AATT/AATTTTTATTTATT                                                         | GCGTTTGAGTAGATGT GCGA   | CGCGTGTTTGAGTAGA TGTGA  | 60.0                             | 686                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold589_P4_309093 | scaffold589                             | 309093                        | TTAAAAAA/T                                                                  | TTTGAAAACGGGGTG CTAC    | GTTTTGGCGTTGGTTT CACT   | 60.0                             | 886                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold589_P4_78175  | scaffold589                             | 78175                         | GTATATATATATATATATATATAT ATATATATATATAT/GTATATATATAT ATATATATATATATATATATAT | TGACC CGCAAGAGCAAT TATG | AAGTGAAGGAATCGCG AAAA   | 59.8                             | 572                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold589_P4_78733  | scaffold589                             | 78733                         | A/AGC                                                                       | GCCATAGGCCCAT AAC TCAA  | TGAGAACTTTTCCGCT GCT    | 59.9                             | 641                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold589_P4_88433  | scaffold589                             | 88433                         | C/CAAGACATTAA                                                               | ACCTATCACGGGT AAG CACG  | TACGGTGCTAGG GAAC CAAC  | 60.0                             | 771                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold590_P4_18892  | scaffold590                             | 18892                         | TAA/TA                                                                      | AAATTTGGCCAAGCAA ACAC   | GAATTGGTGGGGTAGC TTTC   | 60.0                             | 573                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold590_P4_19258  | scaffold590                             | 19258                         | TT/TTACCATAGT                                                               | TCCTAAGAAAGCT ACC CCACC | TGGCAAAGCACAAGAC ACTC   | 59.6                             | 398                                           | INTERGENIC                                     | --                               | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold590_P4_19292  | scaffold590                             | 19292                         | CAAAAAAAAA/CAAAAAAAAAA<br>A                                   | TCCTAAGAAAGCTACC<br>CCACC  | TGGCAAAGCACAAAGAC<br>ACTC   | 59.6                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold590_P4_19474  | scaffold590                             | 19474                         | AG/AGG                                                        | CTATCCATGCATGTGC<br>AACAC  | TGGCAAAGCACAAAGAC<br>ACTC   | 60.0                             | 175                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold590_P4_3079   | scaffold590                             | 3079                          | AT/ATT                                                        | AATAAAAGACCAAATC<br>GGAAAA | TGACAACCATTTATATT<br>TGCCAC | 58.2                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold590_P4_46710  | scaffold590                             | 46710                         | AATATATATATATATAT/AATATAT<br>ATATATATAT                       | GAGAAGGCTGGGTGAA<br>ACAA   | CGTAGCGTGGTAGTGA<br>GCAA    | 60.2                             | 874                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5901_P4_5039  | scaffold5901                            | 5039                          | CAT/CATATAT                                                   | AATCGTGGCACTTTTG<br>CTCT   | TTCAGGATTGTTGGGG<br>AATC    | 59.9                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5904_P4_17347 | scaffold5904                            | 17347                         | TG/T                                                          | TCCGTGGAATAACTTG<br>TGGA   | ACACCTTCTTTTGCCCT<br>TGA    | 59.1                             | 958                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5904_P4_22420 | scaffold5904                            | 22420                         | ATTTT/ATTTT                                                   | TCAGTGTCAACGGTGT<br>CGAT   | CCCCCTTTTCTAAAT<br>TCG      | 60.2                             | 636                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5916_P4_1178  | scaffold5916                            | 1178                          | CAAAA/CAAAA                                                   | TGACACCATTCTCTAG<br>GCCC   | AGGGAGGACGAAAATG<br>ACCT    | 60.1                             | 310                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5916_P4_851   | scaffold5916                            | 851                           | GAAA/GAA                                                      | TCATTTTCGTCTTCCT<br>TGG    | TGGGCCTAGAGAATGG<br>TGTC    | 60.0                             | 749                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold592_P4_38363  | scaffold592                             | 38363                         | GTTTTTTT/GTTTTTT                                              | TTTGGTCATTTTCGTCC<br>TCC   | ACACACCTATTGGACG<br>CACA    | 59.9                             | 281                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold5928_P4_1917  | scaffold5928                            | 1917                          | C/CT                                                          | GCATTGCCCCAAGAAT<br>TTTA   | GCGTGAAGATCATCTG<br>GGAT   | 59.9                             | 210                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold593_P4_61557  | scaffold593                             | 61557                         | ATT/ATTTT                                                     | TTGGTCACAATTTTGAA<br>TGCTT | CATGTTTTGCATGGGG<br>TTTA   | 59.5                             | 525                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold593_P4_6803   | scaffold593                             | 6803                          | TAAAAAAAAA/TAAAAAAAAA                                         | CGTGTTTGGTGGGACT<br>TTCT   | AATGAGCCACTTTGGC<br>AATC   | 60.0                             | 925                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold593_P4_95845  | scaffold593                             | 95845                         | AATATATATATATATATA/AATATA<br>TATATATATATA                     | GATGATCCAATCGGTC<br>TTGC   | TTGTTGAAGAAAAACA<br>AAGTCA | 60.4                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5954_P4_1414  | scaffold5954                            | 1414                          | A/AG                                                          | TGGATGCACAAGGTTG<br>GTTA   | AGGTCATTTTCGTCCTC<br>CCT   | 60.0                             | 367                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5954_P4_716   | scaffold5954                            | 716                           | GTT/GT                                                        | TGGATGCACAAGGTTG<br>GTTA   | TTCATTTTCGTCCTCCC<br>TTG   | 60.0                             | 767                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5977_P4_4626  | scaffold5977                            | 4626                          | A/ATTTTTG                                                     | CGTGGAATCGCGTAG<br>GAAT    | GGACTTCTGCTGAGCC<br>AATC   | 60.0                             | 166                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold598_P4_184836 | scaffold598                             | 184836                        | ATTTTTTTTT/ATTTTTTTTT                                         | TGTGGGAATAGTCCTC<br>CTTGA  | AACATCGGCTCCATTT<br>CTTG   | 59.5                             | 306                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold598_P4_244177 | scaffold598                             | 244177                        | GAAAAAAAAA/GAAAAAAAAA                                         | ACTACTTGGAGCGCAC<br>GTTT   | CCCATCCAGACGCTAT<br>CACT   | 59.9                             | 995                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold598_P4_278799 | scaffold598                             | 278799                        | ATTTTTTT/ATTTTTTTT                                            | TCTTTCGTTTTGCATC<br>GTG    | CCACTTGTGTCCTAAC<br>AACTCA | 59.8                             | 384                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                   |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold598_P4_304104 | scaffold598                             | 304104                        | TT/TTTAT                                                                          | ATATACGGATGGTGCA<br>AGCC   | TTGATGTGATGACCTC<br>CACTC | 59.8                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold598_P4_392260 | scaffold598                             | 392260                        | CATATATATATATATATAT/CATATAT<br>ATATATATAT                                         | ATTCCCCCTTCATCTTG<br>GAC   | TTGTTTGCAAATGCATG<br>CTC  | 60.1                             | 345                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold598_P4_420243 | scaffold598                             | 420243                        | GATATATATATATAT/GATATATATAT<br>ATATAT                                             | GCCGAATAAAACCCTC<br>ACAA   | GACATCTCATTCCCC<br>TTCA   | 59.9                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold598_P4_455301 | scaffold598                             | 455301                        | C/CGTCT                                                                           | CTTGGTATGAGAAGCT<br>CGGC   | ACAGCTCCCAGCTGCT<br>ATGT  | 60.0                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold598_P4_467163 | scaffold598                             | 467163                        | GAAAAAAAAAAAAA/GAAAAAAAAAAAA<br>A                                                 | TGGGTATGGATTGGTT<br>GGTT   | CGCATGGGTCAATCTT<br>TCTT  | 59.9                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold598_P4_503397 | scaffold598                             | 503397                        | TAAAAAAAAAAAAA/TAAAAAAAAAAAA                                                      | TGGGATTATTGGGGTG<br>ACAT   | ATCGTGTGAAAGGCCA<br>GTCT  | 59.9                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold598_P4_568507 | scaffold598                             | 568507                        | CTCAAAATCAAAATCAAAATCAAAAT<br>CAAAATC/CTCAAAATCAAAATCAAA<br>ATCAAAATCAAAATCAAAATC | CAGCCACTACATTGGC<br>CTTT   | AGGATTCTCCAAGTTG<br>GCCT  | 60.1                             | 499                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold598_P4_84328  | scaffold598                             | 84328                         | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>ATATA                   | CGCAAATTCAAAAGAAT<br>TCAAA | TTCAAATGAGCATGAT<br>GGGA  | 59.3                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold598_P4_90421  | scaffold598                             | 90421                         | AGGGGGGG/AGGGGGGGG                                                                | AGCATTCTCATCAGA<br>GCGT    | ACGGCCTAGCCTATTT<br>CCAT  | 60.0                             | 333                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold598_P4_94510  | scaffold598                             | 94510                         | CTT/CTTT                                                                          | CCCCAATGCTACACCA<br>AAAG   | TCTTCGCAATCGACA<br>CAAG   | 60.4                             | 193                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold599_P4_169675 | scaffold599                             | 169675                        | TAA/TTTTTCTGAAA                                               | CCCTGAGACTCACGAA<br>GAGG   | AAAATCCAACAATCTCC<br>CCC  | 60.0                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_187793 | scaffold599                             | 187793                        | CCT/C                                                         | TTGGTATTGAACTCGG<br>AGGC   | TTCTTTCCACACAACC<br>ACA   | 60.1                             | 690                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_236863 | scaffold599                             | 236863                        | T/TTGAA                                                       | AACTAGCGTTGAAGTC<br>GGGA   | AAAGCAAACCAATTTGT<br>TCCA | 59.9                             | 394                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_249441 | scaffold599                             | 249441                        | TAAAAAAAA/TAAAAAAAAA                                          | GTTTTCGGGTCGTGAC<br>AAGT   | ATTTCAAGGCCCTG<br>TACG    | 60.0                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_249479 | scaffold599                             | 249479                        | CAAAAAAAAA/CAAAAAAAAAA                                        | GTTTTCGGGTCGTGAC<br>AAGT   | ATTTCAAGGCCCTG<br>TACG    | 60.0                             | 735                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_254652 | scaffold599                             | 254652                        | GAAAAAAAAA/GAAAAAAAAA                                         | CGTCCTCATAAATTGG<br>CACC   | CACTGCACCCTGCTTC<br>ATTA  | 60.3                             | 270                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_266127 | scaffold599                             | 266127                        | ATTGTGTGTTGTGTG/ATTGTGTG                                      | AACCAGAAGCATAAAA<br>ACCAGG | TGCAAGTGAATCATTTT<br>GGC  | 59.5                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_270007 | scaffold599                             | 270007                        | TTCTCTCTCTCTCTCTCT/TTCTC<br>TCTCTCTCTCTCTCTCTCTCTCT           | TCAAACACATCAAACG<br>AGCA   | AATGTATGTCGCCGA<br>AGAG   | 58.8                             | 845                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_284681 | scaffold599                             | 284681                        | GAAAAAAAA/GAAAAAAAA                                           | AACGAACCTACCGGG<br>CTTT    | GGCCTGAAAGCATACC<br>AAAA  | 60.1                             | 634                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_286707 | scaffold599                             | 286707                        | AT/A                                                          | TTGAAATTACCGCTGG<br>AGATG  | CACTGCGTATCACTG<br>CGTT   | 60.1                             | 485                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                              |                            |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold599_P4_291369 | scaffold599                             | 291369                        | GACTT/GACTTACTT                                                              | TTGTTTGTTCGCAATC<br>CTCC   | TTTCCAACCGGTGAGT<br>TTTC   | 60.0                             | 597                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_307088 | scaffold599                             | 307088                        | CTTATTATTATTATTATTATTATT<br>ATT/CTTATTATTATTATTATTATT<br>TATTATTATTATTATTATT | TCTTCCCATTCCTTGTC<br>TGG   | GGCGTAGCCCAAATAT<br>TCAA   | 60.0                             | 120                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_307530 | scaffold599                             | 307530                        | AATATATATATATATATATATATAT<br>ATATAT/AATATATATATATATATAT<br>TAT               | TCTTCCCATTCCTTGTC<br>TGG   | TGTGTGCTTCCTATGAT<br>GTTCT | 60.0                             | 855                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_307709 | scaffold599                             | 307709                        | TAAAAAAAA/TAAAAAAAAA                                                         | TCCTCCAAACCATC<br>TAATTTT  | CAACATTAAGAAGC<br>GCGA     | 58.9                             | 949                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_307947 | scaffold599                             | 307947                        | AT/A                                                                         | AGAACATCATAGGAAG<br>CACACA | CAACATTAAGAAGC<br>GCGA     | 57.4                             | 317                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_312391 | scaffold599                             | 312391                        | AATATATATATATATATATATATAT<br>ATATATATATAT/AATATATATATA<br>TATATATATATATATAT  | TTTTGCATGCAGTTT<br>GCT     | AAATCCTACCGACGAC<br>AACG   | 59.5                             | 817                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_312899 | scaffold599                             | 312899                        | CTTTTTTTTT/CTTTTTTTTTTTT                                                     | CGTTGTCGTCGGTAGG<br>ATT    | TTCAAAAGTTATTCGGT<br>GGAAA | 60.0                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_319689 | scaffold599                             | 319689                        | CT/C                                                                         | CACGCAAAATTGACG<br>ATTG    | TTTTCTTCTCGATTG<br>GTATTTT | 60.1                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_320346 | scaffold599                             | 320346                        | TAAAAAAAA/TAAAAAAAAA                                                         | CGCAGTAGCAATTGTG<br>CCTT   | CAAATTGCAAGCCAAA<br>ACA    | 61.3                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_322634 | scaffold599                             | 322634                        | GTTTTTTTTT/GTTTTTTTTTTT                                                      | TTGATAAACCGCCATG<br>ACAA   | TTTGTCTTGCCGTATT<br>TTT    | 59.9                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                         | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                       |                             |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold599_P4_323301 | scaffold599                             | 323301                        | TTATATATATATATATATATATATA<br>/TTATATATATATATATATATATATA                               | AAAAATACGGCAAAGC<br>AAAA    | TTGAGGTTGAGAGTCT<br>TTTCCA    | 57.5                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_323562 | scaffold599                             | 323562                        | GAAAAAAAAA/GAAAAAAAAA                                                                 | TTACAAATTCAGATTAC<br>ATGGCA | TACATTCATTCCAGGCT<br>TGC      | 57.3                             | 766                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_328747 | scaffold599                             | 328747                        | AATATATATATATATATATATATAT<br>ATATATATATATATA/AATATATATAT<br>ATATATATATATATATATATATATA | TTCCCATTCCTTGTCTA<br>GCG    | AAGATTTTAGGCGATT<br>TACGTG    | 60.2                             | 703                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_329422 | scaffold599                             | 329422                        | CAAAAAAAAA/CAAAAAAAAA                                                                 | CACGTAAATCGCCTA<br>AAATCT   | CCGATAGTAAACGAC<br>ATCCTG     | 57.6                             | 562                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_335351 | scaffold599                             | 335351                        | CTTTTTTTTT/CTTTTTTTTTTT                                                               | GCCAACCATGTAAATC<br>GCAT    | TCAATCATCAATTTTTG<br>TGTGTTTC | 60.7                             | 327                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_347393 | scaffold599                             | 347393                        | CTTTTTTT/CTTTTTTT                                                                     | CCTCTTTTCTTCGCATT<br>TCG    | AACAACAGCCCCAATG<br>TAGC      | 60.0                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_358249 | scaffold599                             | 358249                        | AATATATATATATATA/AATATATATA<br>TATA                                                   | GCTACGCCTATTGGTC<br>TCCA    | CGTGAATTGGTAATTAA<br>AGCGA    | 60.2                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_364148 | scaffold599                             | 364148                        | CTATATATATATATATATATATAT/CT<br>ATATATATATATATATATATAT                                 | GCAAGCACCGTTGTGA<br>GTAA    | TCTTTAGTAGCCCGCC<br>AAGA      | 59.9                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_366068 | scaffold599                             | 366068                        | ATTTTTTTTT/ATTTTTTTTTTT                                                               | AGAGCGCAATCATTTCC<br>AGGT   | CTTTTGGAAGAAGCC<br>CTCC       | 59.8                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_371527 | scaffold599                             | 371527                        | TAAAAAAA/TAAAAAAA                                                                     | CAGCGTTGTTGTTGTT<br>GTTTTT  | TTTCGAATGAACATGG<br>ATGA      | 60.1                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                                                       | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                                                                                     |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold599_P4_389087 | scaffold599                             | 389087                        | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATT/ATATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA | TGATTTCCCCACACAAT<br>CAA   | TCCGCTACGAATTTTC<br>TCAA   | 59.8                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_391466 | scaffold599                             | 391466                        | ATTTTTTTTT/ATTTTTTTTTTT                                                                                                                                                                             | TGCGGTGAAGAAGAAC<br>AGTG   | CACATCAAAGAGGAAA<br>TGCC   | 60.0                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_392616 | scaffold599                             | 392616                        | GAAAAA/GAAAAA                                                                                                                                                                                       | AAAAAGATATGGCAAG<br>GCAAAA | TGAGGTTGAGAGTCCT<br>TTCCAT | 60.0                             | 689                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_392830 | scaffold599                             | 392830                        | CAAAAAAAAA/CAAAAAAAAAAA<br>AA                                                                                                                                                                       | CAAGATTTTGATGGCG<br>TAACA  | CAACACATTCATTGAG<br>GCTT   | 58.7                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_39375  | scaffold599                             | 39375                         | CAAAAA/CAAA                                                                                                                                                                                         | TGAACTCTGAGCGTGT<br>GACC   | TCCTTGGTCAAAATGG<br>CTTC   | 60.0                             | 576                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_410067 | scaffold599                             | 410067                        | GTTTT/GTTT                                                                                                                                                                                          | ATCGATTCCCAATCG<br>GTTA    | TATACCTATAGCCAC<br>GGCG    | 59.2                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_50922  | scaffold599                             | 50922                         | TCC/TC                                                                                                                                                                                              | CCTGGGCTTATTCTTG<br>TCCA   | AGGGAGAACGGAAATG<br>ACCT   | 60.1                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_56997  | scaffold599                             | 56997                         | TTT/TTTAACATT                                                                                                                                                                                       | AGGTCGTTTTCGTCCT<br>CCTT   | GGAACTTTTTGAGGCG<br>ACAA   | 60.1                             | 373                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_83001  | scaffold599                             | 83001                         | TC/T                                                                                                                                                                                                | TAATGCCAGACCTTT<br>CGTC    | TGAGAACAAAAAGAGG<br>CAGC   | 60.1                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold599_P4_83911  | scaffold599                             | 83911                         | CAAAAAAAAA/CAAAAAAAAAAAAA                                                                                                                                                                           | ACACAAAAGAAAACGG<br>TGCC   | ACTGAGTTCGGGACCA<br>GATG   | 60.0                             | 593                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)        | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                      |                               |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold599_P4_96808  | scaffold599                             | 96808                         | ATTTT/ATTTT                                                          | CCCCAATTTTCAAACAT<br>CCTT     | GGTCATTTTCGTCTTCC<br>CAA  | 60.0                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5992_P4_1041  | scaffold5992                            | 1041                          | TACACAC/TACACACAC                                                    | CTCTCCCAAATCTCG<br>TCCA       | TCATCTCACCCCTTACC<br>TCG  | 60.2                             | 423                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5992_P4_1551  | scaffold5992                            | 1551                          | G/GA                                                                 | CGAGGTAAGGGGTGA<br>GATGA      | TCCCGAATCACTAGG<br>TTTG   | 60.1                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5993_P4_18562 | scaffold5993                            | 18562                         | GTTTTTTT/GTTTTTT                                                     | TTGATGTACGAAAAGTT<br>TTAGCAAG | GGGGGCACTTATTTAT<br>CACTT | 59.0                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold5993_P4_18598 | scaffold5993                            | 18598                         | CTTATATTTTATATTTTATATTTT/<br>CTTATATTTTATATTTT                       | TTGATGTACGAAAAGTT<br>TTAGCAAG | GGGGGCACTTATTTAT<br>CACTT | 59.0                             | 267                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold601_P4_142564 | scaffold601                             | 142564                        | GATATATATATATATATATATATAT<br>TAT/GATATATATATATATATATAT<br>ATATATATAT | TGAGACGGAAGATTGA<br>AAGTAGG   | CCCCGATGAATCTCTA<br>CGAA  | 59.8                             | 739                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold601_P4_49572  | scaffold601                             | 49572                         | CTTTTTTT/CTTTTTT                                                     | GGGGACATTTTCGAGAG<br>TCAA     | TCACAAGGGAGGCTCT<br>ATGG  | 60.1                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6036_P4_545   | scaffold6036                            | 545                           | GT/GTT                                                               | TCATTTTCGTCCTTCCT<br>TGG      | CACACCTATTGGATGC<br>GAGA  | 60.0                             | 373                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold604_P4_37903  | scaffold604                             | 37903                         | TAA/TAAA                                                             | TGGGCTTCAACTTTT<br>GGAC       | ACCACCTTATTTGTGG<br>CTGC  | 60.1                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold605_P4_1279   | scaffold605                             | 1279                          | CAA/CAAA                                                             | TTACCTTGCTTACGGC<br>TGCT      | TCATGTTAATCGGAGT<br>GCCA  | 60.0                             | 868                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold605_P4_25215  | scaffold605                             | 25215                         | TC/TCGGAGGGGGAC                                               | CAGGCCAGGTAATCT<br>TTGA    | CATGCCAGGAGCACAC<br>ATAC     | 60.1                             | 784                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold605_P4_52612  | scaffold605                             | 52612                         | AAATAATAATAATAAT/AAATAATAAT<br>AATAATAAT                      | GGTTGCATGAATGACG<br>TTTG   | TTTCCTAGCAGAAGGA<br>CCCC     | 60.0                             | 176                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold605_P4_83655  | scaffold605                             | 83655                         | CT/CCCCCAGT                                                   | GCCTTGGTAGTCGTGG<br>ACAT   | AACGTGAGGGACAAAA<br>CCTG     | 60.0                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6055_P4_14409 | scaffold6055                            | 14409                         | GT/GTT                                                        | GGTAAGGGCTCCTTCC<br>AAAC   | AACGATTTCCACCCAAA<br>ACA     | 59.9                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6066_P4_2831  | scaffold6066                            | 2831                          | CCT/C                                                         | CTGCAAAGCAACCATC<br>TCAA   | CCTCAGATGAGAGCCA<br>GGAC     | 60.0                             | 797                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6113_P4_1438  | scaffold6113                            | 1438                          | GAAAA/GAAAAA                                                  | ACAAGCCTATCGTTTG<br>GCAC   | GATGCAACATTGGAGC<br>ATGA     | 60.1                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold612_P4_17406  | scaffold612                             | 17406                         | CATAATAATAATAATAAA/CATAAT<br>AATAATAATAATAATAATAA             | CCCAAATCACCTAACTT<br>GTGAA | TGTAAAAGCTGCATCG<br>GACA     | 59.0                             | 221                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold612_P4_28576  | scaffold612                             | 28576                         | GAAAAA/GAAAAAA                                                | AAAAAGGAGGGTCAC<br>ATGAT   | TCACCAATATCTTAACC<br>ACCAAAA | 59.7                             | 701                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold612_P4_3402   | scaffold612                             | 3402                          | GTTTT/GTTT                                                    | AAGTCACAGTGAAC<br>CCAG     | CCCAAGAAAGTAGCCA<br>CCAG     | 60.0                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6120_P4_1380  | scaffold6120                            | 1380                          | ACTCTCTCT/ACTCTCT                                             | CCAAAATGCTTCATTCT<br>GCAA  | CCACCAGACCGACTTT<br>GATT     | 61.1                             | 493                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold6120_P4_2075 | scaffold6120                            | 2075                          | CTTTTT/CTTTTT                                                 | AATCAAAGTCGGTCTG<br>GTGG  | AGCAAGCTCTGCTTGA<br>CACA   | 60.0                             | 797                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6125_P4_1553 | scaffold6125                            | 1553                          | TAAAGA/TA                                                     | ATGCGATCCTCTCGGT<br>TCTA  | GAGACCGAAGAGTATT<br>GGGAGA | 59.8                             | 838                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold613_P4_2067  | scaffold613                             | 2067                          | ATTT/ATT                                                      | TCCAATTGGGGTGTTT<br>TTGT  | AGGAATAAGCCAAGGG<br>AGGA   | 60.1                             | 359                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6154_P4_548  | scaffold6154                            | 548                           | CCGCCTCA/CCGCCTCAGGCGCCT<br>CA                                | AACCGCTCCAATGGTG<br>TTAG  | GAAGATGATGTGCGCT<br>TGAA   | 60.0                             | 221                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6169_P4_821  | scaffold6169                            | 821                           | GAAAAAAAA/GAAAAAAAAA                                          | CCAAACTTTCCGGATC<br>AAAA  | TCGTTTTGTTACACCC<br>AAA    | 59.9                             | 492                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold617_P4_8886  | scaffold617                             | 8886                          | A/AAC                                                         | CCAAATGGACGAGAA<br>TAGACC | TGGTTTAGGGTTTAGG<br>CCAAT  | 59.8                             | 408                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6177_P4_3708 | scaffold6177                            | 3708                          | AG/A                                                          | TTTTTGTCATCATCGGA<br>CCA  | AAATCCGTTTGGATTG<br>CAG    | 59.9                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6179_P4_967  | scaffold6179                            | 967                           | TAAAAAAAA/TAAAAAAAA                                           | TGGGTGCACAAGATTG<br>GTTA  | AGGTCATTTTCGTCCTC<br>CCT   | 60.0                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold618_P4_87840 | scaffold618                             | 87840                         | AT/ATTATTTT                                                   | TGAGGGTGTTGGGGTA<br>TTTG  | TATTGTACGTAGCGAG<br>CCCC   | 60.6                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6185_P4_569  | scaffold6185                            | 569                           | TTATCCCACTCAAAA/TTATCCCACT<br>CAAAATATCCCACTCAAAA             | TGAGTTGGACTCGTTG<br>GAAA  | TTGGGTGAAATGGCTA<br>AAGG   | 59.3                             | 864                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')         | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                                 |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold6199_P4_832  | scaffold6199                            | 832                           | G/GTATTG                                                      | TCATCCAATGACCCAA<br>ACAA        | TTACGTAATTTTCGTCG<br>CCC  | 59.8                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold62_P4_150220 | scaffold62                              | 150220                        | TAAAAAA/TAAAAAA                                               | AACATTTAAGAAAATTG<br>AGTTGTCAAA | GTGTGTTGGGCTGTTT<br>AGGG  | 58.7                             | 405                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold62_P4_150949 | scaffold62                              | 150949                        | CA/CAACTCTA                                                   | CAGCCCAACACACTAA<br>ACCC        | CAACACAATTGAGCTG<br>TCAAA | 60.4                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold62_P4_338714 | scaffold62                              | 338714                        | ATT/ATTT                                                      | CCATCGTCAAGTCCGA<br>AAAT        | CCAAAACTCGAAACCC<br>AAAA  | 59.9                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold62_P4_81760  | scaffold62                              | 81760                         | ATTT/ATTTT                                                    | TGAGCAACAAATCAGC<br>AAGG        | GGTTGCATGAATGACG<br>TTTG  | 60.0                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold62_P4_81843  | scaffold62                              | 81843                         | CAAAA/CAAAAA                                                  | TGAGCAACAAATCAGC<br>AAGG        | GGTTGCATGAATGACG<br>TTTG  | 60.0                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold622_P4_10235 | scaffold622                             | 10235                         | TAAAAAA/TAAAAAA                                               | ATAGGCCTAGGGAGGA<br>CGAA        | TTTAGCCAACTTGTGCA<br>TCG  | 60.1                             | 381                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold622_P4_30718 | scaffold622                             | 30718                         | ACC/ACCC                                                      | TGGGTGCACAAGATTG<br>GTTA        | AGCTCATTTTCGTCCTC<br>CCT  | 60.0                             | 402                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold622_P4_30884 | scaffold622                             | 30884                         | A/AC                                                          | TGGGTGCACAAGATTG<br>GTTA        | AGGGGTGTTTGAGTCA<br>TTGG  | 60.0                             | 832                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold622_P4_48194 | scaffold622                             | 48194                         | AC/A                                                          | TCCGATGACACAAACA<br>CACC        | TTTGTCATTTTCGTCC<br>TCC   | 60.4                             | 194                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                 |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold622_P4_61725  | scaffold622                             | 61725                         | GACACACACACAC/GACACACAC<br>ACAC                                                                 | CAAAACCCACCTATTGG<br>ATGC | GGTCATTTTCGTCCTC<br>GCTA | 60.2                             | 310                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold622_P4_79107  | scaffold622                             | 79107                         | GC/GCC                                                                                          | AGGGAGGACGAAAATG<br>ACCT  | TAACCAATCTTGTGCAC<br>CCA | 59.9                             | 271                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold624_P4_148382 | scaffold624                             | 148382                        | CCTCTCTCTCTCTCTCTCTCTCTCT<br>CTCTCTCTCTCT/CCTCTCTCTCTCT<br>CTCTCTCTCTCTCTCTCTCTCTCTC<br>TCTCTCT | CCTCTCGGTCTCTCTCC<br>TTCT | TGTGAATGCGTCGATT<br>GTTT | 59.9                             | 351                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_172733 | scaffold626                             | 172733                        | C/CAATTA                                                                                        | GTGAGCAAAATGCTGG<br>GAAT  | GTTGTTGAGTTGTTGG<br>GGCT | 60.1                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_219233 | scaffold626                             | 219233                        | CAAA/CAAAA                                                                                      | GGATTTAGGGTTTTGG<br>CCTT  | GATGAAATCGAGGACT<br>GGGA | 59.3                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_224966 | scaffold626                             | 224966                        | CTTTTTTT/CTTTTTT                                                                                | CGCAAGAACTCCACAA<br>CAAA  | GGAGGGCTGGAACATC<br>TGTA | 59.9                             | 433                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_236880 | scaffold626                             | 236880                        | AGGG/AGG                                                                                        | CCCATCCACAAAATAT<br>GCC   | GATGAAATCGAGGACC<br>AGGA | 60.0                             | 302                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_242103 | scaffold626                             | 242103                        | A/AG                                                                                            | GGCAGTCATCATCAAC<br>ATGG  | ACCAATCCGAAGACGA<br>TCAC | 59.9                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_242253 | scaffold626                             | 242253                        | A/AAAAATGATCGTTTTT                                                                              | CCGATGCGTAGATTGA<br>CAGA  | GGTAACCAATCCGAAG<br>ACGA | 59.8                             | 177                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_268228 | scaffold626                             | 268228                        | CAA/CAAA                                                                                        | TAACCCAAACCTCAAA<br>CCCA  | TTCATCTGGACTTTTTG<br>GGC | 60.2                             | 760                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)      | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                    |                           |                          |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold626_P4_270284 | scaffold626                             | 270284                        | AAGGA/AA                                                           | CCCCAGAAAAGACCAG<br>ATGA  | AGGGTCTCTTGGTCCT<br>CGAT | 60.0                             | 669                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold626_P4_274715 | scaffold626                             | 274715                        | ACC/ACCC                                                           | GACCGGGAGACCCCTTA<br>TAGC | CCCAGTCGTCGATTTC<br>ATCT | 59.9                             | 541                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold626_P4_275345 | scaffold626                             | 275345                        | TCGAG/TCGAGGACCGAG                                                 | TCCGCATCAAATTTCAA<br>ACA  | ATGCTATGTGGGACTC<br>TCGG | 60.1                             | 390                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold626_P4_33804  | scaffold626                             | 33804                         | TAAAAA/TAAA                                                        | TTTTGGCGATTTTCTTA<br>CCG  | GGTTCGCGTTAGATT<br>TCAA  | 60.1                             | 581                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold626_P4_355966 | scaffold626                             | 355966                        | AATATATATATATATATATATATATATATATATATATAAATATATATATATATATATATATATATA | TTACAGTGTCTCAACTT<br>CGC  | CCGTGCTAATCTCTGC<br>TTCC | 60.0                             | 662                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold626_P4_452023 | scaffold626                             | 452023                        | A/AC                                                               | TAACTCGGAACCCGAA<br>ACAC  | TCCAGATGAAATCGAG<br>GACC | 60.0                             | 842                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold626_P4_452443 | scaffold626                             | 452443                        | CAAA/CAAAA                                                         | GGTCCTCGATTTCATC<br>TGGA  | CGAAAATCGCTCGAAA<br>AGTC | 60.0                             | 336                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold626_P4_454559 | scaffold626                             | 454559                        | ACC/ACCCC                                                          | TAACTGTTTTTCGGGTT<br>CCG  | GGTCCTCGATTTCATCT<br>GGA | 60.0                             | 292                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold626_P4_510274 | scaffold626                             | 510274                        | TG/T                                                               | GGTCCTCGATTTCAATT<br>GGA  | ACTGAATTCGGTTTCC<br>ACG  | 59.9                             | 455                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold626_P4_512589 | scaffold626                             | 512589                        | ATTTA/ATTTAGGGTTTA                                                 | CCCGACAAAAACGGAC<br>TAAA  | ATAACCCGAACCTCAAA<br>CCC | 60.0                             | 359                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                                |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold626_P4_515112 | scaffold626                             | 515112                        | TTAT/TTATAT                                                   | CGTTATAAAGTAAACT<br>ACATTGCGAA | AAATTTAGGAGACGAAT<br>GCTTTTT | 59.2                             | 848                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_520360 | scaffold626                             | 520360                        | CTTT/CTTTT                                                    | AAGGTCTCCTGGTCCT<br>TGGT       | CACGAAACCCGAAACA<br>AAGT     | 60.0                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_522371 | scaffold626                             | 522371                        | CTTT/CTT                                                      | TTTGTCGAGGGGTACG<br>AAAC       | GGTCCTCGATTTCATCT<br>GGA     | 60.0                             | 691                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_524724 | scaffold626                             | 524724                        | ATTTTTTTTTTT/ATTTTTTTT                                        | AAATCCCCCGAAAATA<br>CCAG       | TCCAGATCAAATCGAG<br>GACC     | 60.0                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_527539 | scaffold626                             | 527539                        | A/AC                                                          | CTCGGACGAAATCTAA<br>AGCG       | GATGAAATCGAGGACT<br>GGGA     | 60.0                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_542516 | scaffold626                             | 542516                        | T/TACC                                                        | TTCCGGTTCTCGATT<br>CATC        | GTTTAAGGTTCCGCAC<br>CAAA     | 60.0                             | 414                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_553162 | scaffold626                             | 553162                        | AT/A                                                          | TCCAGATGAAATCGAG<br>GACC       | TTTCATTTGGGCTTTTC<br>AGG     | 60.0                             | 325                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_553900 | scaffold626                             | 553900                        | CA/C                                                          | TTAAACTGATGCGGA<br>ACCC        | TCCTGATGAAATCGAG<br>GGTC     | 59.9                             | 250                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_554690 | scaffold626                             | 554690                        | TAAGAAGAAGAA/TAAGAAGAA                                        | GGTCCTCGATTTCATC<br>TGGA       | CCATCGTCTGGTTCGA<br>AAAT     | 60.0                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_561543 | scaffold626                             | 561543                        | GA/G                                                          | CGTCGATGGGTACGAA<br>AGTT       | TTTCATCTGGTCTTTTC<br>GGG     | 60.0                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')        | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|--------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                             |                                |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold626_P4_631432 | scaffold626                             | 631432                        | ATAT/A                                                                      | TTGATTTGACCACTT<br>TTTT        | CAGCCCAACACACTAA<br>ACCC  | 59.2                             | 242                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold626_P4_94461  | scaffold626                             | 94461                         | CATATATATATAT/CATATATATAT                                                   | AGTGTGTCAATGTTA<br>CTTTATTTCAA | GGGTTTGAGGTTCTGGG<br>TTAT | 57.6                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold627_P4_22209  | scaffold627                             | 22209                         | TGGGGCT/TGGGGCTCTGGGGCT                                                     | AGTTTGAGTCGGTGCG<br>AGTT       | GCCCATAGGCCCACTT<br>ATT   | 59.9                             | 842                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold629_P4_30227  | scaffold629                             | 30227                         | AATATATATATATATAT/AATATAT<br>ATATATATATATAT                                 | TGAACAACCCGAACCT<br>TCAT       | TTAGGGTGATCAGTT<br>CGGT   | 58.1                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold629_P4_77734  | scaffold629                             | 77734                         | TTATATATATATATATATATATATAT<br>TATATAT/TTATATATATATATATATAT<br>TATATATATATAT | AGTTGGGAAATTTGT<br>GCTG        | CAGCGTGACAATGAGC<br>AACT  | 60.0                             | 568                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold63_P4_59319   | scaffold63                              | 59319                         | TAA/TAATAAA                                                                 | CGAGGTAAGGGGTGA<br>GATGA       | AGGTTTGTGACACCTT<br>CCCT  | 60.1                             | 481                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold63_P4_65090   | scaffold63                              | 65090                         | TA/TAA                                                                      | TTGGACCAATTTTGTG<br>GCTT       | CACCGATTCCCAACAA<br>TTAGA | 60.3                             | 826                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold631_P4_53707  | scaffold631                             | 53707                         | GC/GCC                                                                      | AAGCACACCTATTGGA<br>TGCC       | TCATTTTCGTCTCCCT<br>TTG   | 60.0                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold637_P4_107635 | scaffold637                             | 107635                        | ATT/ATTT                                                                    | GCCTTGAGGAATCGGT<br>ATCA       | GTGTGAATGCAACCTT<br>CCCT  | 60.0                             | 313                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold637_P4_107771 | scaffold637                             | 107771                        | TAA/TA                                                                      | GCCTTGAGGAATCGGT<br>ATCA       | GAGCGAGACATGGGAG<br>AAAG  | 60.0                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                      | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                    |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold6382_P4_1419  | scaffold6382                            | 1419                          | CTCCCTATGCTT/CT                                                                    | AGGTCATTTTCGTCCT<br>CCCT  | CAAACACACGTTTGG<br>ATGC   | 59.9                             | 181                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold639_P4_103317 | scaffold639                             | 103317                        | AATATATATATATATAT/AATATATAT<br>ATATATATATAT                                        | TTCGACTCCCTTCCCT<br>TTTT  | CATTCTTTTATGCGTTT<br>GGC  | 60.0                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold639_P4_11325  | scaffold639                             | 11325                         | T/TC                                                                               | TGGTGCAATTACTTTC<br>TCGG  | TCGGTTCCTTGTTGCC<br>TTT   | 60.1                             | 783                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold639_P4_160230 | scaffold639                             | 160230                        | GACCCTTAACCCCTTAACCCCTTAACC/<br>GACCCTTAACCCCTTAACCCCTTAACC<br>CTTAACC             | TGGGTTTAGGGTGTGT<br>TTTGA | TTTTGGGTTTCAGGTTT<br>AAGG | 60.2                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6391_P4_2187  | scaffold6391                            | 2187                          | CAAAA/CAAAA                                                                        | CGCATAGTAAATTGA<br>CCTCCC | CTCGAATGAGGAAGTG<br>GCAT  | 59.9                             | 205                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold642_P4_27247  | scaffold642                             | 27247                         | TGATTGGTTTGTGTTGAGATTGGTTT<br>GTTTG/TGATTGGTTTGTGAGATT<br>GGTTTGTGAGATTGGTTTGTGTTG | GAGAAGCGAAAGCGAA<br>GAGA  | GGAAGGGTAGAACGTA<br>GGGC  | 60.0                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold642_P4_27309  | scaffold642                             | 27309                         | CT/CTGAAGATTGT                                                                     | GAGAAGCGAAAGCGAA<br>GAGA  | GGAAGGGTAGAACGTA<br>GGGC  | 60.0                             | 451                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold642_P4_285620 | scaffold642                             | 285620                        | CTTTTTTT/CTTTTTTTT                                                                 | TCATGCATACATGGGC<br>CTTA  | GGCGTTTAGTTTTTGG<br>GTCA  | 59.9                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold642_P4_302870 | scaffold642                             | 302870                        | GAAAAAAAAA/GAAAAAAAAA                                                              | AAATGGTGCAACACAC<br>TCCA  | ATGGATTCGGGTTGTT<br>CTTG  | 60.0                             | 280                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold642_P4_314115 | scaffold642                             | 314115                        | GTTTTTTTT/GTTTTTTTTT                                                               | CTCCAGGTGAGATGGT<br>GGAT  | TCGAGCATGATTGGAA<br>CAAA  | 59.9                             | 693                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                      | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                                                    |                             |                           |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| scaffold642_P4_416715 | scaffold642                             | 416715                        | TAAAA/TAAAAA                                                                                                                                                       | TCACGACCAAGTTGAT<br>TCCA    | TTCCACCTTTGGTTTGC<br>TTC  | 60.1                             | 301                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold642_P4_427901 | scaffold642                             | 427901                        | TAGAGAGAGAGAGAGAGAGAGAGA<br>GAGA/TAGAGAGAGAGAGAGAGAGAG<br>AGAGAGAGAGAGAGA                                                                                          | CCTCGATACAATGACA<br>CGGA    | ATCATGGCAATTCCACA<br>AAA  | 59.5                             | 455                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold642_P4_432508 | scaffold642                             | 432508                        | G/GCAGACCTTACA                                                                                                                                                     | ATGCAATGCGTATATG<br>CCAA    | AATGGCAGTCCATATG<br>CCTC  | 59.9                             | 637                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold642_P4_445514 | scaffold642                             | 445514                        | TTATATATATATATATA/TTATATA<br>TATATATATA                                                                                                                            | TTTTATTTTAAATTGCA<br>CCATCC | TTTCTCGACAAATTGT<br>TTCA  | 59.2                             | 861                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold642_P4_446621 | scaffold642                             | 446621                        | GAA/GAAA                                                                                                                                                           | TCGAGTGTCGAACTCA<br>AGGA    | GATGCAGGTCATGAAA<br>CCAA  | 59.5                             | 393                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold642_P4_507941 | scaffold642                             | 507941                        | ATTTTTT/ATTTTT                                                                                                                                                     | TTCATGGTGTTCCTTG<br>GCA     | CGGTGTACACACCAA<br>TTTT   | 60.1                             | 309                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold642_P4_542397 | scaffold642                             | 542397                        | GTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAAT/GTAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT                               | TTTGCCAGACCACCT<br>TTAC     | CGTCACATGTTTCTCTT<br>GCTG | 60.0                             | 403                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold642_P4_598254 | scaffold642                             | 598254                        | GATAATAATAATAATAATAATAA<br>TAATAATAATAGGAATAAAAAATA<br>ATAATAATAATAATAATAATAAT<br>AA/GATAATAATAATAATAATAAT<br>AATAATAATAGGAATAAAAAATAA<br>TAATAATAATAATAATAATAATAA | AAGCGATTTCACGAA<br>CTGAA    | CGGTATGAGGTGTCAT<br>GGCT  | 59.9                             | 443                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold642_P4_59861  | scaffold642                             | 59861                         | TG/T                                                                                                                                                               | TTCTTCCCTCATTTGAT<br>CCG    | CGAGCCAAGATCCCCA<br>AATA  | 60.0                             | 486                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold642_P4_60062  | scaffold642                             | 60062                         | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATA                                                                                                                | TATTTTGGGATCTTGG<br>CTCG    | CGTAGCGTGGTAGTGA<br>GCAA  | 60.0                             | 619                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                           |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold642_P4_697756 | scaffold642                             | 697756                        | CATATATATATATATATATATATATA<br>T/CATATATATATATATATATATATAT<br>ATATATATATAT | CAATTGAGTTGCGACG<br>AGAG | GTTGGTCCCTAGCAC<br>CGTA  | 59.6                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6429_P4_4894  | scaffold6429                            | 4894                          | CCTA/C                                                                    | GGGTGGACGAAATGA<br>GCTA  | TGTGTCATTGGATTG<br>CATT  | 60.1                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold643_P4_71253  | scaffold643                             | 71253                         | G/GC                                                                      | CCACATTCTTAACGCC<br>CAGT | CATTGCGAACGGAGAT<br>TTTT | 60.0                             | 446                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold645_P4_224616 | scaffold645                             | 224616                        | AAATAATAATAATAATAATAATA<br>ATAATAA/AAATAATAATAATAAT<br>AATAATAA           | AGGGTTTGGAGGAGC<br>GTAAT | CATCCTCCCTCCCTCT<br>TTC  | 60.0                             | 143                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold645_P4_287301 | scaffold645                             | 287301                        | GT/G                                                                      | CACAGCTATTGGAGGC<br>ACAA | AGGTCATTTTCGTCCTC<br>CCT | 59.9                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold645_P4_287773 | scaffold645                             | 287773                        | TAAAAA/TAAAA                                                              | AGGGAGGACGAAAATG<br>ACCT | GCGTGTTTGTGTCATT<br>GGAC | 59.9                             | 348                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold645_P4_62567  | scaffold645                             | 62567                         | CTTT/CTTTT                                                                | TACTCAGACGGCCAAA<br>AAGC | CTTGCTTCGGTCTACA<br>AGGG | 60.4                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold645_P4_73896  | scaffold645                             | 73896                         | AGGGG/AGGGGG                                                              | ACATCTTGCTTGGGT<br>TTGG  | CCCCCTCAGAATATGC<br>TTCA | 60.0                             | 229                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold645_P4_87205  | scaffold645                             | 87205                         | AAATGCAATGCAATGCAATGCA/AAA<br>TGCAATGCAATGCAATGCAATGCAA<br>TGCA           | ACTGCAATTTACAAAC<br>GCA  | GAGGACAAGGCCAATT<br>TGAA | 60.3                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6480_P4_530   | scaffold6480                            | 530                           | ATTTT/ATTT                                                                | TAATCGATCATCCCAG<br>ACCC | TACAATTGGGCTCCTT<br>CACC | 59.7                             | 900                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold662_P4_50819  | scaffold662                             | 50819                         | GAAAAA/GAAAAA                                                 | TGGGAAATCGATTGGG<br>TAAG  | TCATGTTAATCGGAGT<br>GCCA  | 59.8                             | 252                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold665_P4_16345  | scaffold665                             | 16345                         | TA/T                                                          | GGTCCTCGATTTCATC<br>TGGA  | CCAGGTTCCGTGTCAG<br>ATTT  | 60.0                             | 607                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6694_P4_1671  | scaffold6694                            | 1671                          | TAAAAAAA/TAAAAAAA                                             | CCCACACTACGACCAC<br>GTTA  | CGTAACTCGAATGAAC<br>GGAAA | 59.5                             | 671                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6695_P4_690   | scaffold6695                            | 690                           | T/TG                                                          | ATATTGTGATGCGACG<br>TTGG  | GGGCGACATGAGAGAA<br>GAAG  | 59.4                             | 767                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6695_P4_721   | scaffold6695                            | 721                           | TG/TGG                                                        | ATATTGTGATGCGACG<br>TTGG  | AAAACCTGAAAGGGCA<br>ACCT  | 59.4                             | 837                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold670_P4_131335 | scaffold670                             | 131335                        | GAAAA/GAAA                                                    | TCGTTATGCAGTCAAA<br>CCTCA | GCTATTTTCGTACCACC<br>CGA  | 59.3                             | 403                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold670_P4_197970 | scaffold670                             | 197970                        | AAAT/AAATAAT                                                  | TGGCCAATGATCCAAG<br>AGAT  | CCGACAAAAATGGACC<br>AAAA  | 60.4                             | 823                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6719_P4_505   | scaffold6719                            | 505                           | GTTTGTTTT/GTTT                                                | TGTTGGTCCATTTTGT<br>GGTT  | GCTTTGCTGTTTCTTT<br>GCAT  | 60.1                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold672_P4_206989 | scaffold672                             | 206989                        | GCC/GCCCC                                                     | AGGGAGGACGAAAAATG<br>ACCT | TCAACCAATCTTGTGCA<br>TCC  | 59.9                             | 373                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6720_P4_5246  | scaffold6720                            | 5246                          | CA/CAA                                                        | TTTTCGTCTCCCTAG<br>GCTT   | CAACTATTGGATGCGC<br>AAGA  | 60.2                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold6720_P4_536   | scaffold6720                            | 536                           | TAAAAAAAAA/TAAATAAAAAAAAAA<br>A                               | CGATACTCACCCCTCG<br>TTGT   | ATGTGACACCCTAAAC<br>CCCA  | 60.0                             | 338                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold673_P4_13021  | scaffold673                             | 13021                         | TAACCAATA/TAACCAATATTGTGCA<br>ACCAATA                         | TAGGTCATTTTCGTGC<br>TCCC   | CAAACACACCTATTGCA<br>CGC  | 60.1                             | 366                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold674_P4_138669 | scaffold674                             | 138669                        | GTATTTTAT/GTATTTTATTTTAT                                      | TTGTGTTTCGTGTTGG<br>CAAT   | TGTTAAATGGTGCGAA<br>ATCGT | 60.0                             | 554                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold674_P4_150228 | scaffold674                             | 150228                        | TAAAAAAAAA/TAAAAAAAAA                                         | CATGACCCCTTCATATT<br>GGG   | CTCGTTGTGGTTGTTG<br>GTTG  | 60.0                             | 294                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold674_P4_163043 | scaffold674                             | 163043                        | CCGTTTCGCGTTCGCGTTC/CCGTTTC<br>GCGTTCGCGTTCGCGTTC             | TGCGTTTTCAATCGTT<br>GTGT   | GACCTCCACTCGCCAT<br>TTTA  | 60.2                             | 165                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold674_P4_181866 | scaffold674                             | 181866                        | CACTTG/CACTTGACTGACTTG                                        | GCCTGAAGCACTTTTT<br>CCAG   | GGAAGGCTTGTGCACT<br>TGAG  | 60.0                             | 355                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold674_P4_223997 | scaffold674                             | 223997                        | TAAAAAAAAA/TAAAAAAAAA<br>A                                    | TACCACTTTTGTATGC<br>GACG   | CTACGTGTGGGCTTGG<br>TTTT  | 59.7                             | 381                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold674_P4_226407 | scaffold674                             | 226407                        | CAAAAAAAAA/CAAAAAAAAA                                         | GCTCGGGGTATAGGTT<br>CCTC   | CACTTCAAATTTTAGGC<br>CGC  | 59.9                             | 296                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold674_P4_230865 | scaffold674                             | 230865                        | CTTGTG/CTTGTGTTGTG                                            | TGACGCTTTGTGATCC<br>CTATC  | CCGGAAGAGCACAATC<br>AAAT  | 60.1                             | 552                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold674_P4_248531 | scaffold674                             | 248531                        | GAT/GATAT                                                     | ACTTTTATGTGCGTTTG<br>ACTGA | TCCAACCTCCCTTCCCTT<br>TTT | 57.5                             | 534                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                           |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold674_P4_253414 | scaffold674                             | 253414                        | CTTTTT/CTTTTT                                                             | TGGCAAAATCAATACA<br>CCTCA   | TTGGTTTCGGCTAGAA<br>ATGG  | 59.0                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_343997 | scaffold674                             | 343997                        | AAATTTTAAATTTTAAATTT/AAATT<br>TTTAAATTTTAAATTTTAAATTT                     | TGGACCAACTTGTGTA<br>AGATTTT | GCTTTATTGCTTTTGGC<br>AGC  | 59.0                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_401251 | scaffold674                             | 401251                        | AAGA/AA                                                                   | GAGATGGAGTACGGG<br>CTTGA    | ATATCCTGAGCGTCGA<br>TTGG  | 60.2                             | 310                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_401295 | scaffold674                             | 401295                        | GA/GATTTCGAA                                                              | GAGATGGAGTACGGG<br>CTTGA    | ATATCCTGAGCGTCGA<br>TTGG  | 60.2                             | 310                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_401473 | scaffold674                             | 401473                        | TAAAA/TAAA                                                                | TGCATTAGTCGATGTC<br>CCAA    | AATCGATTTCGCGTTTG<br>TTC  | 60.1                             | 134                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_414956 | scaffold674                             | 414956                        | ATTTTTT/ATTTTT                                                            | AGCCGCTGAAAACTG<br>AAGA     | GTTCAACAATTTGAGC<br>CCGT  | 60.1                             | 127                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_457376 | scaffold674                             | 457376                        | AATATATATATATAT/AATATATATAT<br>ATATATAT                                   | TTGATGGAGCAAGCAC<br>TCAC    | TGTGCTTTTGGACTIONG<br>TGG | 60.0                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_457568 | scaffold674                             | 457568                        | TAAAAAAAA/TAAAAAAAA                                                       | TTGATGGAGCAAGCAC<br>TCAC    | CATATTTGGCATGAATT<br>GCG  | 60.0                             | 699                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_468848 | scaffold674                             | 468848                        | TAAAAAAAA/TAAAAAAAA                                                       | GCTAAGAGCATCTCCA<br>ACGG    | TTTAGAGCATCTCCAAC<br>GGG  | 60.0                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_476011 | scaffold674                             | 476011                        | GTATATATATATATATATATATATAT<br>AT/GTATATATATATATATATATATAT<br>ATATATATATAT | TGAATTTGTGCTCTTG<br>GTGG    | AGTTTGGGAGGAAAGG<br>GAAA  | 59.7                             | 806                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold674_P4_507406 | scaffold674                             | 507406                        | GGAGAGAGAGAGAGAGAGA/GGAG<br>AGAGAGAGAGAGA                     | CCAGCAAGCTGCATAA<br>TCAA   | CAAAAGCCAAACTCTG<br>CTCC   | 60.0                             | 620                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_512302 | scaffold674                             | 512302                        | TCACTACGCCA/TCA                                               | TCGCCAAGTTAGCACC<br>TTCT   | GGAGAGGAAGGTTTCGT<br>AGGG  | 60.0                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_512606 | scaffold674                             | 512606                        | TAAAAA/TAAAAA                                                 | CTCGCCAAGTTAGCAC<br>CTTC   | TCAGCATGTCAATTTCC<br>CAA   | 60.0                             | 880                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_529799 | scaffold674                             | 529799                        | A/AC                                                          | CACCTAAGTTGGCGGG<br>TTAC   | CGCCTCGTGTGACCTA<br>AGTT   | 59.5                             | 290                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_554875 | scaffold674                             | 554875                        | GAAAAAA/GAAAAAA                                               | CAAGAGTTTAGTGGGG<br>GCAA   | TTATTGCAACCGCAAC<br>CATA   | 60.1                             | 161                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_558081 | scaffold674                             | 558081                        | A/AT                                                          | AAGAACCAATGGTTT<br>GGAA    | TCAATGGAATACAATT<br>TGGTCA | 57.0                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_593635 | scaffold674                             | 593635                        | ATTTTTTTTT/ATTTTTTTTT                                         | CGGTTTCCAAATCAAT<br>ATGGT  | CCGTATTGCACTGAATT<br>GTCA  | 60.0                             | 647                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_594801 | scaffold674                             | 594801                        | GAAAAAAAA/GAAAAAAAA                                           | GGATTGATGAAATTT<br>GCATTAT | TTTTGCTCTCCTTTTG<br>TCCA   | 59.2                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_624095 | scaffold674                             | 624095                        | TAA/TA                                                        | CCTCGGATCTGGATT<br>TTCA    | GGTCAAGCTTAAAGCC<br>ACTCA  | 60.2                             | 271                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_626448 | scaffold674                             | 626448                        | AATATATATATATA/AATATATATA<br>TATATATA                         | CATGATGATAATTAGC<br>CGCAGA | TAATACAAAGCGGGGA<br>ACCA   | 60.1                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold674_P4_648750 | scaffold674                             | 648750                        | CAAAAAAAAA/CAAAAAAAAA                                         | AGCCACATGAAACGT<br>GACA     | CATGGGCGTTTACATC<br>ACAC   | 60.2                             | 230                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_675885 | scaffold674                             | 675885                        | TAA/TA                                                        | AAAGGGTGACCTCCAC<br>ACAC    | AGCTCAGGAGGATGAG<br>CTTG   | 59.9                             | 324                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_682263 | scaffold674                             | 682263                        | GAAAAAAAAA/GAAAAAAAAA                                         | AGACTCCATGCCCAA<br>ACAC     | TTCAACCCAAGCCATT<br>AAG    | 60.0                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_744234 | scaffold674                             | 744234                        | ATTTTTTTT/ATTTTTTT                                            | CAATTCCTTTCATGCC<br>ATT     | TCGACAGTTTTGGTCC<br>CTTT   | 59.8                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_75733  | scaffold674                             | 75733                         | GAAAAAAAAA/GAAAAAAAAA                                         | AGTCGCGTGGAGAAAG<br>GTTA    | CCGCCTCTTTGTCTCTT<br>CAC   | 59.9                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_762735 | scaffold674                             | 762735                        | TNNNNNNNNN/TNNNNNNNN                                          | TGCTTCATTGCTTCCA<br>CTTG    | CCAGCAAATGATAGGG<br>GAGA   | 60.0                             | 180                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_829987 | scaffold674                             | 829987                        | CAA/CAAAA                                                     | AATGTGGATCCTGCAC<br>ACAA    | TTGTTGCTTTTGCTCCT<br>CCT   | 60.0                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_839502 | scaffold674                             | 839502                        | A/AG                                                          | CAATGGGAATAAAACG<br>TGCC    | CGGTGATTTTTCAGCA<br>ACCT   | 60.2                             | 254                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_84428  | scaffold674                             | 84428                         | GC/G                                                          | TAAGAAAGCGAGGGTG<br>ATGC    | GAAAGCTGAAGTTGGT<br>TCGC   | 60.4                             | 668                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_852315 | scaffold674                             | 852315                        | TAAAAAAAAA/TAAAAAAAAA                                         | TTGATATTCTAACACAG<br>CGAGCA | TTCCAATTTTCAATCAC<br>TTTGC | 59.9                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                               | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                                                                                             |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold674_P4_9082  | scaffold674                             | 9082                          | CTTTTTTTTT/CTTTTTTTTT                                                                                                       | CATGGGTCGTGACTG<br>TTTG  | TTGGACCGATCTAACA<br>AGCC | 60.0                             | 340                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold674_P4_92319 | scaffold674                             | 92319                         | TAAAAAAAAA/TAAAAAAAAA                                                                                                       | TGTCAGTTGCTGGCAT<br>TAGC | ATCACCAACACCAGT<br>GCAA  | 60.0                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold675_P4_15473 | scaffold675                             | 15473                         | TATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAA/TATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAA | TGGCATGCTTGTGTAC<br>GAAT | TTGAGTTATCTCCCCAA<br>CCG | 60.1                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold675_P4_15562 | scaffold675                             | 15562                         | TATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAA/TATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAA          | TGGCATGCTTGTGTAC<br>GAAT | TTGAGTTATCTCCCCAA<br>CCG | 60.1                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold675_P4_81863 | scaffold675                             | 81863                         | CTTTTT/CTTTTT                                                                                                               | TATCAGAGTTCTCCCC<br>ACCG | AAACATGACGAGGGCA<br>TTTA | 60.1                             | 895                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold675_P4_81930 | scaffold675                             | 81930                         | TT/TTGAAAAT                                                                                                                 | TATCAGAGTTCTCCCC<br>ACCG | AAACATGACGAGGGCA<br>TTTA | 60.1                             | 895                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold675_P4_82372 | scaffold675                             | 82372                         | T/TC                                                                                                                        | TAAATGCCCTCGTCAT<br>GTTT | CCCCTTTCCACGGCTA<br>TTAT | 58.1                             | 444                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold675_P4_89761 | scaffold675                             | 89761                         | A/AT                                                                                                                        | AGATGCGCTTGCTTTT<br>TCAT | GCTAAATCACCGCAA<br>GAGG  | 60.0                             | 400                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold675_P4_90564 | scaffold675                             | 90564                         | CATAATAATAA/CATAATAATAATA                                                                                                   | TCTTGATTTGGCTGCC<br>ACTA | ATCAGGTCGTGTGTTG<br>GTCA | 59.4                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold676_P4_14215 | scaffold676                             | 14215                         | CG/C                                                                                                                        | GATGAAATCGAGGACC<br>AGGA | TTTCATCTGGACTTTTC<br>GGG | 60.0                             | 823                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold676_P4_14755  | scaffold676                             | 14755                         | TC/TCTCC                                                      | TCCAGATGAAATCGAG<br>GACC  | CTTTTCGGGCAATTTTC<br>GTA | 60.0                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold676_P4_161888 | scaffold676                             | 161888                        | TAAAAAAA/TAAAAAA                                              | AACCCTAAACAACCCA<br>ACACA | CGGGTGATTTTCGTAC<br>CACT | 59.2                             | 737                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold676_P4_55025  | scaffold676                             | 55025                         | TAAAAAAA/TAAAAAAA                                             | CAAACCACAAAATG<br>GACC    | AACCTCAAACCCAAAAC<br>CTT | 60.1                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold676_P4_69502  | scaffold676                             | 69502                         | AG/A                                                          | TGAAATCTAGCGCGGA<br>ACTT  | CTGTGTATCGGGTTCC<br>TCGT | 60.0                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold676_P4_72988  | scaffold676                             | 72988                         | TAA/TAAA                                                      | CTTTTCGGCGATTTT<br>GTA    | TCCTGATGAAATCGAG<br>GACC | 60.1                             | 162                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold676_P4_84081  | scaffold676                             | 84081                         | CTTTT/CTTT                                                    | CACGAAACCCGAAACA<br>CTTT  | GCCATCGTCTAATCCG<br>AAAA | 60.0                             | 146                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold676_P4_84534  | scaffold676                             | 84534                         | GCAC/GCACAAACAC                                               | TTTTCGGATTAGACGA<br>TGGC  | GATGAAATCGAGGACC<br>AGGA | 60.0                             | 796                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6760_P4_1141  | scaffold6760                            | 1141                          | ATTTTT/ATTTTT                                                 | AAATGTGTCCATCTCA<br>GCCC  | TCAAAACTCAAGGGG<br>CAAT  | 59.9                             | 545                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6760_P4_908   | scaffold6760                            | 908                           | CTTCATTTT/CTT                                                 | TGTTTTCAAAGGGG<br>TCAG    | GGGCTGAGATGGACAC<br>ATTT | 59.9                             | 621                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold678_P4_19770  | scaffold678                             | 19770                         | TCTT/TCTTACTT                                                 | GATCTATGAGGACAG<br>GCCA   | TATCACCTATCAGAGC<br>GGGG | 60.0                             | 490                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold678_P4_39763 | scaffold678                             | 39763                         | TAGTTATTAAGTTATT/TAGTTATT                                     | AGGAGTTTGAGCATCG<br>CATT | ATCCCACCCCTAAAC<br>CAAG     | 59.8                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold678_P4_40998 | scaffold678                             | 40998                         | TAAAAAAAA/TAAAAAAAAA                                          | GAACAGCTTTGAGGGC<br>AATC | CGATCACCACGTGACA<br>CTTC    | 59.8                             | 849                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold678_P4_42464 | scaffold678                             | 42464                         | TAAAAA/TAAAAA                                                 | GCGCACAATAGATGGG<br>TTTA | TTTTCCAACGAGTCCA<br>CCTC    | 58.7                             | 816                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold678_P4_55317 | scaffold678                             | 55317                         | ATTTTTTTTT/ATTTTTTTTT                                         | AGGCCCTCTAAACCA<br>ACAT  | GATCTTGCCTTTTGGG<br>ATCA    | 59.8                             | 410                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold678_P4_81722 | scaffold678                             | 81722                         | TAAAAA/TAAAAA                                                 | AGGAAGCCCAAGTTCC<br>AAAT | AGAAAGTGTTGACGGG<br>TTGG    | 59.9                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6782_P4_1068 | scaffold6782                            | 1068                          | GA/GAGAAA                                                     | GACGTTCTTTGCGGTA<br>CCAT | CAATGTCAACCACACA<br>TTTTG   | 60.0                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6782_P4_1089 | scaffold6782                            | 1089                          | GAAAAA/GAAAAA                                                 | GACGTTCTTTGCGGTA<br>CCAT | CAATGTCAACCACACA<br>TTTTG   | 60.0                             | 428                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6782_P4_1165 | scaffold6782                            | 1165                          | CG/CAG                                                        | GACGTTCTTTGCGGTA<br>CCAT | TTTAAATTGCTGCTAAG<br>ATTGGT | 60.0                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6782_P4_544  | scaffold6782                            | 544                           | AC/A                                                          | ACTCACCCACATCCA<br>ACAT  | ATGGTACCGCAAAGAA<br>CGTC    | 60.1                             | 337                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6782_P4_758  | scaffold6782                            | 758                           | ATTTTTTT/ATTTTTTT                                             | GACGTTCTTTGCGGTA<br>CCAT | TCAAACGCTCACACAC<br>ACAA    | 60.0                             | 292                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                       | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                                     |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold6790_P4_1414  | scaffold6790                            | 1414                          | C/CAAA                                                                                                                                              | TCCTTGACCCCAATTC<br>GTAG | TTTTGGGGTTTAGGGT<br>GTCA | 59.9                             | 356                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6790_P4_2258  | scaffold6790                            | 2258                          | ACC/ACCC                                                                                                                                            | TTCAAATTGGCCTTGT<br>CCTC | CATAGACCAACGAGGG<br>GAGA | 60.1                             | 317                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6790_P4_704   | scaffold6790                            | 704                           | ACATCATC/ACATCATCATC                                                                                                                                | TAGTTATGCTGAGGG<br>ACGG  | CTACGAATTGGGGTCA<br>AGGA | 60.1                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6790_P4_910   | scaffold6790                            | 910                           | TATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TATAATAATAA | TAGTTATGCTGAGGG<br>ACGG  | TGCAAGTACATTCCCG<br>ATCA | 60.1                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold681_P4_25444  | scaffold681                             | 25444                         | TAAA/TAA                                                                                                                                            | ACGTTAAGGCATGAGT<br>TGGG | CATAGTTGTGTGGTGC<br>GTCC | 60.0                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold682_P4_183807 | scaffold682                             | 183807                        | CTTTTTTTTT/CTTTTTTTTTT                                                                                                                              | GATGGGGGTAAACATG<br>ATGC | TCGTCAACCTTGACAC<br>AAAG | 60.0                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold682_P4_302365 | scaffold682                             | 302365                        | A/AGAGAGAT                                                                                                                                          | GCTGCAAAAGTCAACG<br>TCAA | CACCCCTGAACCTTGG<br>AGGA | 60.0                             | 177                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold682_P4_491190 | scaffold682                             | 491190                        | ATTTTTTTTT/ATTTTTTTTT                                                                                                                               | AACTCACACCCTCGT<br>TCAT  | GCCATGTCCAAACCAT<br>TCTT | 59.4                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold682_P4_498670 | scaffold682                             | 498670                        | T/TC                                                                                                                                                | GGTTTCGAATCAACGA<br>GGAA | CTTGGGAAGTGGAGAG<br>CAAG | 60.1                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold682_P4_506392 | scaffold682                             | 506392                        | GATATATATATATATATATATATA<br>TATATATAT/GATATATATATATAT<br>ATATATATATATATATATATATAT                                                                   | AGGGAGGTTTGTGTT<br>GACG  | TTTAATGTGTTGCGGG<br>TGAA | 60.0                             | 408                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold682_P4_539867 | scaffold682                             | 539867                        | CT/CTTT                                                       | TCGCCATTGTA CTG            | CCATGCCTCCAATCAA<br>AAGT | 60.0                             | 886                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold682_P4_540074 | scaffold682                             | 540074                        | AG/A                                                          | TGATTTTGCTCGTTTGA<br>TGC   | CCATGCCTCCAATCAA<br>AAGT | 59.8                             | 247                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold682_P4_540419 | scaffold682                             | 540419                        | TGAG/TGAGAG                                                   | ACTTTTGATTGGAGGC<br>ATGG   | TAATATGGGGAGAGGG<br>GAGG | 59.9                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold682_P4_540592 | scaffold682                             | 540592                        | GTTTTTTTTTTT/GTTTTTTT                                         | ACTTTTGATTGGAGGC<br>ATGG   | TAATATGGGGAGAGGG<br>GAGG | 59.9                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold682_P4_540642 | scaffold682                             | 540642                        | T/TC                                                          | ACTTTTGATTGGAGGC<br>ATGG   | GAAGCAAAACCAGGGA<br>ATGA | 59.9                             | 886                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold682_P4_540845 | scaffold682                             | 540845                        | A/AT                                                          | AAGGACTGGTTCACCA<br>GCAG   | GAAGCAAAACCAGGGA<br>ATGA | 60.3                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold682_P4_540957 | scaffold682                             | 540957                        | GAAA/GAAAA                                                    | CCTCCCCTCTCCCCT<br>ATTA    | GAAGCAAAACCAGGGA<br>ATGA | 60.1                             | 241                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold682_P4_541607 | scaffold682                             | 541607                        | AT/ACGT                                                       | TAAGACACCGCTGCCT<br>TCTT   | TGTATCGCAAAGCAATA<br>GCG | 60.0                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold682_P4_64518  | scaffold682                             | 64518                         | TTATATATAT/TTATATAT                                           | TCCCCTTTGCTTCTTG<br>TGG    | AATTACCGCCAATTAC<br>ACC  | 60.1                             | 688                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold682_P4_88286  | scaffold682                             | 88286                         | CAATAATAATAATAATAA/CAATAATA<br>ATAATAATAATAA                  | AGCCGAGTGAATATCA<br>AAATGA | GTGAATGGAAGACGTC<br>GGTT | 58.7                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                       | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                                                     |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold683_P4_15318  | scaffold683                             | 15318                         | GC/GCC                                                                                                                                                              | TAAGCCTTTGGAGGAC<br>GAAA  | CCCTAGGCTTATTCTTG<br>CCC | 59.8                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold683_P4_20681  | scaffold683                             | 20681                         | TAA/TAAA                                                                                                                                                            | GAAGGATGAAAATGGG<br>GGTT  | TTGGAAAGGCTGAAAT<br>CTGG | 60.0                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold683_P4_25448  | scaffold683                             | 25448                         | AT/ACTTT                                                                                                                                                            | GCAATCGATTCCAACA<br>GGTC  | TGTTGCTCCTCACGAA<br>TCTG | 60.5                             | 183                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold684_P4_40548  | scaffold684                             | 40548                         | CATATATATATATATATA/CATATA<br>TATATATATATATATA                                                                                                                       | AGGAAGAGTGGAGTTG<br>CGAA  | TTAATTTAAGGCGTTTC<br>GGG | 60.0                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6842_P4_1766  | scaffold6842                            | 1766                          | ATTT/ATTTT                                                                                                                                                          | TCCGATTATTTTCGAGG<br>TCGT | CCGTGCATGACGTTTA<br>TCAT | 59.5                             | 570                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6846_P4_1083  | scaffold6846                            | 1083                          | CAATAATAATAATAATATTAATA<br>ATAATATTAATAATGATAATGATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAATCATAATAATAATAATA<br>ATAATA/CAATAATAATAATAATTA<br>ATAATAATAATAATCATAATCAT | TCCTCTTCTGTCGAT<br>CGTT   | CTCATCAACGGCTCCT<br>CTTC | 59.8                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6846_P4_1369  | scaffold6846                            | 1369                          | GACGACGACCA/GA                                                                                                                                                      | TTTTCTTTCTTCCAC<br>ACA    | CTCATCAACGGCTCCT<br>CTTC | 58.2                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6846_P4_522   | scaffold6846                            | 522                           | T/TC                                                                                                                                                                | TGCATTGGTATATGGG<br>GGTT  | CGATCGACAGGAAGAG<br>GAAG | 59.9                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6846_P4_948   | scaffold6846                            | 948                           | CATT/CATTAATT                                                                                                                                                       | TCCTCTTCTGTCGAT<br>CGTT   | CGTCGTCGTCGTCATC<br>ATTA | 59.8                             | 599                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold686_P4_105035 | scaffold686                             | 105035                        | TATGCATGCA/TATGCA                                                                                                                                                   | GCGAAAAATGGGTTTG<br>AGTC  | AATCGGGGTGTTACAT<br>CTGC | 59.6                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                           | Forward primers (5'-3')        | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                                         |                                |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold686_P4_108971 | scaffold686                             | 108971                        | GATATATATATATATATATATA/GA<br>TATATATATATATATATATATA                                                                                                     | GGGAGAAGGAGGAAG<br>AATGG       | CTTGGGAAGTGGAGAG<br>CAAG   | 60.0                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold686_P4_134728 | scaffold686                             | 134728                        | ATATTATTATTATTATTATTATTA<br>TTATT/ATATTATTATTATTATTATTA<br>TTATTATT                                                                                     | TGAGAAATGCACTCTT<br>CCCAT      | CATCCGCCTCTAAAGT<br>GAGC   | 59.7                             | 506                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold686_P4_180622 | scaffold686                             | 180622                        | GATATATATATATATATATATGTA<br>TATATATATATATATATATATATA<br>CATATATATATATATA/GATATATATA<br>TATATATATATATGTATATATATA<br>TATATATATATATATACATATATA<br>TATATATA | AATTTTACCGTGCAACT<br>CGC       | TCATCACAATGCAAAAT<br>CGAC  | 60.1                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold686_P4_183469 | scaffold686                             | 183469                        | AT/ATT                                                                                                                                                  | TGGATTAAATCATTCCC<br>CCA       | ATCCCTGTTGATTGCT<br>TCG    | 60.0                             | 617                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold686_P4_183725 | scaffold686                             | 183725                        | TACAAAGAACTAGAAAACAAAGAAC<br>TAGAAAAACA/TACAAAGAACTAGAA<br>AACAA                                                                                        | TTACGAAGCAAATCAA<br>CAGGG      | GTGGCATAGTATCGTG<br>GCCT   | 60.1                             | 332                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold686_P4_186665 | scaffold686                             | 186665                        | GAAA/GAAAA                                                                                                                                              | TTTGGGCTGAAGCCAT<br>AAAC       | TGGAGTTTCTTCTTCCT<br>CATCC | 60.1                             | 338                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold686_P4_226597 | scaffold686                             | 226597                        | ACTCTCTCT/ACTCT                                                                                                                                         | ATTGATGGGAAGCAAT<br>CTGG       | TGGTTGCCAAACCAGT<br>GTAA   | 59.9                             | 386                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold686_P4_230657 | scaffold686                             | 230657                        | GTATATATATAT/GTATATATATATAT                                                                                                                             | CCGCGAGTAAATCCGA<br>TAAA       | TTTGATTTTGGCTCGT<br>AGG    | 60.1                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold686_P4_81421  | scaffold686                             | 81421                         | GATAAATAAATAAATAAATAAATAA<br>TAAATA/GATAAATAAATAAATAAATA<br>AATAAATAAATAAATA                                                                            | TTGCTCTACGTATCT<br>CCCCG       | GCTTTTAACCTTCGATT<br>GTGC  | 60.2                             | 808                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold686_P4_95535  | scaffold686                             | 95535                         | CAAAAAAAAAAAAA/CAAAAAAAAAA                                                                                                                              | CCACTTGTGTACTAAC<br>AACTCAAAGA | CTTGCCAGACTGGTTG<br>GATT   | 58.9                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                                     | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                                                                   |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold6873_P4_1457  | scaffold6873                            | 1457                          | T/TA                                                                                                                                                                              | TACCCAATCTTGTGCA<br>ACCA  | CCTAGGGTCGACGAAA<br>ATGA   | 60.0                             | 575                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold688_P4_2385   | scaffold688                             | 2385                          | GAAT/GAT                                                                                                                                                                          | AGGTCATTTCCGTCCT<br>TCCT  | GACACGAACACACCTC<br>ATGG   | 59.9                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold692_P4_62843  | scaffold692                             | 62843                         | CATATATATATATATATATATATATA/<br>CATATATATATATATATATATATATA<br>TA                                                                                                                   | TGGAGATGAGCAATTT<br>TCCC  | GAAAGAATTGCGGCGA<br>TAGT   | 60.0                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold696_P4_196380 | scaffold696                             | 196380                        | CATATATATATATATATATATATAT/C<br>ATATATATATATATATATATAT                                                                                                                             | AAATGGAGGAAGGAGG<br>GAGA  | TATTTTGGATTTTGGCT<br>CGG   | 60.0                             | 437                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold696_P4_25713  | scaffold696                             | 25713                         | GTTATTATTATTATTATTATTATT<br>ATTATTATTATTGTTAGTGTTATTAT<br>TATTATTATTATTGTTATTATTATTAT<br>TGTTATTATTATTATTATT/GTTATTA<br>TTATTATTATTATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTATT | TTGGAATTGGAATTGG<br>AAGG  | TTCAATTGAGTTGCGA<br>CGAC   | 59.7                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold696_P4_25880  | scaffold696                             | 25880                         | ATTTTTTT/ATTTT                                                                                                                                                                    | TTGGAATTGGAATTGG<br>AAGG  | TTCAATTGAGTTGCGA<br>CGAC   | 59.7                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6980_P4_22077 | scaffold6980                            | 22077                         | AATATATATATA/AATATATATATATA                                                                                                                                                       | GCCAATTCTATCCCTC<br>ACCTC | CCGATGTTTGAGGGGT<br>ATT    | 59.9                             | 859                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold6981_P4_1263  | scaffold6981                            | 1263                          | CG/C                                                                                                                                                                              | AGAGCGCTTTGCAAAA<br>GAAG  | TTCGTAATGGACGGGA<br>TGAT   | 59.9                             | 175                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7_P4_215103   | scaffold7                               | 215103                        | A/AC                                                                                                                                                                              | TTGATCCTTGCAGTCA<br>CTCG  | TGGCACTCCGATTAAC<br>ATGA   | 60.0                             | 805                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_105940 | scaffold702                             | 105940                        | AAC/AACAC                                                                                                                                                                         | AGCTCGAAAGTGACCC<br>AAGA  | TTTCCACTGTGAGCTAT<br>TCCAA | 60.0                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                      | Forward primers (5'-3')      | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------|------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                    |                              |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold702_P4_115828 | scaffold702                             | 115828                        | ATGTGT/ATGTGTGT                                                                                    | CCACACTGCGGTGCTA<br>GTAA     | AATTACGCCAATTAC<br>ACC        | 59.9                             | 375                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_154351 | scaffold702                             | 154351                        | ATTTTTTTTT/ATTTTTTTTT                                                                              | TCGATTATGCGTAGGG<br>AAGG     | CTGAAAAGGTTTTGCA<br>ACCG      | 60.1                             | 763                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_181516 | scaffold702                             | 181516                        | CTTT/CTTTT                                                                                         | TTTTTGATGATGCACA<br>CTCTCATT | TCCAACAATAATTTAA<br>ACCTTACAA | 59.9                             | 430                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_216004 | scaffold702                             | 216004                        | GA/G                                                                                               | CTGTTTGGCGTCGAA<br>TTAT      | TATTTCTCCCCTCGTT<br>GGT       | 60.0                             | 630                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_223066 | scaffold702                             | 223066                        | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTAT/TTTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTAT | GGACGAAATCAGGAAG<br>AAAAA    | CCTGAGTGTGGCCTAC<br>GATT      | 58.3                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_249855 | scaffold702                             | 249855                        | TAA/TA                                                                                             | TTGGATGCACAAGATT<br>GGTT     | AGGTCATTTTCGTCCTC<br>CCT      | 59.0                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_255829 | scaffold702                             | 255829                        | AGG/AGGG                                                                                           | AATTGGCCTTGAAAA<br>GCCT      | TTTGGTCATTTTCGTCC<br>TCC      | 60.1                             | 441                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_273004 | scaffold702                             | 273004                        | AG/A                                                                                               | ATTGGTTAAAAACCCC<br>CGAT     | AGGTCATTTTCGTCCTC<br>CCT      | 59.4                             | 454                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_275210 | scaffold702                             | 275210                        | TAAAAA/TAAAAA                                                                                      | GGACAAGAATATGCCT<br>TGGG     | AGGTCATTTTCGTCCTC<br>CCT      | 59.4                             | 336                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_49940  | scaffold702                             | 49940                         | ATATTATTA/ATATTA                                                                                   | GTTTTCGAATCAACGA<br>GGGA     | TTTGCTCGAAGGCTT<br>TTTA       | 60.1                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                                             |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold702_P4_50496 | scaffold702                             | 50496                         | TATAA/TA                                                                    | GGTACAGAGCGGGTC<br>CACTA  | AGGGCTGAACGAATAT<br>GGTG  | 60.1                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_55303 | scaffold702                             | 55303                         | CAAAAAAAAA/CAAAAAAAAA                                                       | GCATCTGCACATGAAA<br>AACAA | CAAACCCAATTTGATCC<br>GAC  | 59.7                             | 865                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_55997 | scaffold702                             | 55997                         | CTACATACATACATACGTACA<br>TACATAC/CTACATACATACAT<br>ACATACATACGTACATACATAC   | GGGGTCCATCACATTT<br>GTTC  | CCATGTTAGGTTTGAA<br>CCAGG | 60.0                             | 114                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_59657 | scaffold702                             | 59657                         | ATTTTTTTT/ATTTTTTTT                                                         | TAGCCACATAGGCAAC<br>CACA  | CGTGCATATTTGAGGT<br>GGTG  | 60.1                             | 225                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_62322 | scaffold702                             | 62322                         | TATTCTAATTCTAATTCTAATTCTAA<br>TTCTAATTCT/TATTCTAATTCTAATT<br>CTAATTCTAATTCT | GGGCTTATGGTGATC<br>TTGT   | TGTGCCTCAAGCAATC<br>TGTC  | 60.0                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_664   | scaffold702                             | 664                           | C/CA                                                                        | AGCGCAGAATGTTCTT<br>GACA  | CCAAACGATTTCCCTT<br>CAA   | 59.6                             | 691                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold702_P4_99680 | scaffold702                             | 99680                         | ATTTTGCATAGTTTTTGCATAGT/AT<br>TTTGCATAGT                                    | CGCTCGATAACCCCAA<br>AATA  | ATTACCGACATTGCAG<br>AGGG  | 59.9                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7038_P4_1268 | scaffold7038                            | 1268                          | TTATATATATATATATATATATATATA<br>TAT/TTATATATATATATATATATATA<br>TATATATAT     | GGTGCTTGTTAAGTTG<br>TGCCT | CCAACTCACCTTTCTTT<br>ACCG | 59.3                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7048_P4_512  | scaffold7048                            | 512                           | GT/G                                                                        | ATGCGTGTGTTGTGTC<br>TTGG  | AGGGAGGACGAAATG<br>ACCT   | 60.4                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold705_P4_17000 | scaffold705                             | 17000                         | TAAA/TAAAA                                                                  | AGGGTCTTTCGATCCT<br>CGAT  | AGTCCGCGCTAGATT<br>TCAA   | 60.0                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                                 |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold705_P4_30569  | scaffold705                             | 30569                         | CAAAAAAAAA/CAAAAAAAAA                                         | GGTCCTCGATTTCATC<br>TGGA  | AGGGGTACGAAAATAT<br>CCCG        | 60.0                             | 619                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold705_P4_34777  | scaffold705                             | 34777                         | A/ATATTGTTATT                                                 | GGTTTGACTGCATAAC<br>CAAGA | GTACTTCATAACGAAGA<br>CAAATTAACA | 57.7                             | 608                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold705_P4_45291  | scaffold705                             | 45291                         | CGGG/CGG                                                      | TTTCATCTGGTCTTTTC<br>GGG  | CGATCCATTTTTGTCTGTG             | 60.0                             | 215                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold707_P4_106321 | scaffold707                             | 106321                        | CAAAAAAAAA/CAAAAAAAAAAA<br>AA                                 | TTGGAAAAGCCACCT<br>ACAC   | TTTCAATAATGCATGC<br>GGA         | 60.0                             | 455                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold707_P4_121772 | scaffold707                             | 121772                        | GAAA/GAA                                                      | TTCTAAGCAGGGGCC<br>TAAT   | TGCTGCTTTGGTTCAAA<br>ATG        | 60.1                             | 149                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold707_P4_136483 | scaffold707                             | 136483                        | C/CA                                                          | TTTTGAGGACTTTTCG<br>GTTG  | TTGGTCGTTTGAGCCT<br>TTCT        | 60.1                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold707_P4_71570  | scaffold707                             | 71570                         | AT/A                                                          | CAACTGCGAGAGTCCA<br>AACA  | CATGCCGTTTATCTTTC<br>AACA       | 60.0                             | 230                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7081_P4_2451  | scaffold7081                            | 2451                          | A/AC                                                          | TTAATGAGGGGCTGAA<br>TTGG  | AAGCGTACCTGTGGGA<br>ATTG        | 59.9                             | 259                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7081_P4_2734  | scaffold7081                            | 2734                          | ATTTT/ATTTT                                                   | CAATTCCCACAGGTAC<br>GCTT  | TGGGGGTTAAAGGGAT<br>TAGG        | 60.0                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold709_P4_1585   | scaffold709                             | 1585                          | CTTTT/CTTTT                                                   | ATGTTTTCTTTGGGTT<br>GCG   | CGTTTTTCAAAGCGAG<br>GGTA        | 60.0                             | 211                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold709_P4_4010   | scaffold709                             | 4010                          | GTTTT/GTTTTTTT                                                | ACTCAAATGATGTTGG<br>CGCT   | CATGAGGAAACAATTG<br>TGCAG   | 60.7                             | 788                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold709_P4_7022   | scaffold709                             | 7022                          | TAACAACAA/TAACAA                                              | ATCGCCATAATTTGGA<br>ATGC   | TGAATTGATGATTGAGA<br>ACCG   | 59.8                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold71_P4_37235   | scaffold71                              | 37235                         | ATTT/ATTTT                                                    | CCCTCATATTCAAAACA<br>ATCCC | GGCCATTCTCAGGAAT<br>TTCA    | 59.6                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7107_P4_12825 | scaffold7107                            | 12825                         | AA/AAAGA                                                      | GGGGACTAAAATTGGG<br>GAGA   | TGCAGGCAATCAATGA<br>AAGA    | 60.1                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7107_P4_13331 | scaffold7107                            | 13331                         | TAAAA/TAAAAA                                                  | GACTCATTCAATGCAC<br>CCAA   | TGCGATTGTTGTGGTT<br>GTTT    | 59.5                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7107_P4_13380 | scaffold7107                            | 13380                         | TTTTGAAAATTTTGAA/TTTTTGAA                                     | GACTCATTCAATGCAC<br>CCAA   | TGCGATTGTTGTGGTT<br>GTTT    | 59.5                             | 627                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7107_P4_14328 | scaffold7107                            | 14328                         | GTAT/GT                                                       | ATGCATTGTGAGGGGA<br>AAAT   | CGGGATGCGACCTTCT<br>ATTA    | 59.2                             | 365                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7107_P4_14640 | scaffold7107                            | 14640                         | AAATAATAATAATAATAAT/AAAT<br>AATAATAATAATAATAAT                | TAATAGAAGGTCGCAT<br>CCCG   | TGTGTCAAACGAAATG<br>ATGTG   | 60.1                             | 368                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7107_P4_15792 | scaffold7107                            | 15792                         | CAAAATCATCTAAAAATCATC/CAA<br>AATCATC                          | TCACTCGGTTGCATCA<br>CATT   | GGAGGTTCTAGCCCTT<br>ATAGCTT | 60.1                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7107_P4_16409 | scaffold7107                            | 16409                         | CTATATATATATATATATA/CTATATA<br>TATATATATATATATA               | GGGGCTAGAACCTCCT<br>ACAA   | CCATTTGCATGATTCCA<br>CAC    | 58.3                             | 946                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                   |                             |                          |                                  |                                               | Sequence<br>components<br>of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold7107_P4_16449 | scaffold7107                            | 16449                         | TTTCAT/TTTCATCTTCAT                                                               | TCCAATGCTTACAATCC<br>TCTCTC | CCATTTGCATGATTCCA<br>CAC | 59.7                             | 508                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold7107_P4_25673 | scaffold7107                            | 25673                         | TAAAAAAAA/TAAAAAAAAAAAA                                                           | CATCCGATGCACATTTT<br>GTC    | ATACGGCGCGTTCTAC<br>ATCT | 59.9                             | 476                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold711_P4_204653 | scaffold711                             | 204653                        | GATATATATATATATATA/GATATATA<br>TATATATA                                           | AATGTGAATCCCACCA<br>GGAA    | TTTACAGCGCTTGTCCT<br>CAA | 60.2                             | 796                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold711_P4_3553   | scaffold711                             | 3553                          | AATTATTATTATTAT/AATTATTATTA<br>TTATTAT                                            | CCTAGGAAAGCGATCA<br>CCTG    | CACGTCATTTGTCTTTG<br>GCA | 59.8                             | 453                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold711_P4_36212  | scaffold711                             | 36212                         | CT/CTCAGCATT                                                                      | CGGGAGACAAGAAGCT<br>CTTC    | CCTTTGCACAAGCTTC<br>ACA  | 60.0                             | 256                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold711_P4_46613  | scaffold711                             | 46613                         | AATATATATATATATATATATATAT<br>ATA/AATATATATATATATATATATAT<br>ATATATATATATATATATATA | CACACCGCATTGACTT<br>TTTG    | TTCATACATGCCTCGC<br>GTTA | 60.1                             | 868                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold711_P4_97599  | scaffold711                             | 97599                         | CGGG/CGGGG                                                                        | AACTGTCTCGTTGGT<br>CCTTCT   | TTGCGTAAAGGCATG<br>CTAA  | 59.3                             | 338                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold7148_P4_4428  | scaffold7148                            | 4428                          | AAATAATAATAATAATAATAATA<br>ATAATAATAA/AAATAATAATAAAT<br>AATAATAATAATAATAATAATAA   | CCTTATTAATGGCTTCC<br>GCA    | AGAGGCAACAAGAAC<br>CGAA  | 60.1                             | 607                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold716_P4_112534 | scaffold716                             | 112534                        | GTTTTT/GTTTT                                                                      | CCTCTTGACTCTACAG<br>CCCG    | GTTGCCAAGTCCGCA<br>TAAT  | 60.0                             | 277                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold716_P4_117351 | scaffold716                             | 117351                        | CATATATATATATATATATATATA<br>TAT/CATATATATATATATATATAT<br>ATATATAT                 | AGGAGGTTTGTGTTTG<br>ACGG    | GCTGTTAGCCAGTTT<br>TTGG  | 60.0                             | 612                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)        | Forward primers (5'-3')  | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------|--------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                      |                          |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold716_P4_163516 | scaffold716                             | 163516                        | C/CA                                                                 | TCCCAACCCAAATAAA<br>CCAA | TTTACAGCGCTTCTCC<br>CAAT      | 60.0                             | 744                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold716_P4_189823 | scaffold716                             | 189823                        | TAAA/TAAAA                                                           | AAGCTTGTGCAAAGGG<br>AAAA | TGGTTTTGATGGGACC<br>AAAT      | 59.9                             | 113                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold716_P4_23644  | scaffold716                             | 23644                         | GCA/GCATAACCA                                                        | CCACAATCTTGGCAAA<br>ACCT | GATTGCCACCGGTAAG<br>AGAA      | 60.0                             | 620                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold716_P4_241616 | scaffold716                             | 241616                        | CTTTTTTT/CTTTTTT                                                     | CCAACCACAACAAATT<br>CCC  | CTTCCACCTCCTTTTC<br>CAA       | 60.1                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold716_P4_365986 | scaffold716                             | 365986                        | TTAATAATAATAATAATAATAAT<br>AATAA/TTAATAATAATAATAATA<br>ATAATAATAATAA | TGGATGCAAAAGATTG<br>GTTG | TTGGGTTCCAATTCTG<br>CTC       | 59.5                             | 969                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold716_P4_66387  | scaffold716                             | 66387                         | CAAAA/CAAAAA                                                         | ATGGTGGTGAGCAACT<br>TTCC | TTCGCAACTCCACTCTT<br>CCT      | 60.0                             | 136                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7187_P4_901   | scaffold7187                            | 901                           | A/ATAAC                                                              | TTTTAGGTTTGAGGTT<br>CGGG | AATTATTTATATTTATT<br>TGCAACTC | 59.1                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold719_P4_123762 | scaffold719                             | 123762                        | TAAAA/TAAA                                                           | AGGTCATTTTCGTCCT<br>CCCT | TTATCCAATGGCACAA<br>AGA       | 59.9                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold719_P4_15306  | scaffold719                             | 15306                         | TAAAA/TAAAAA                                                         | TGCATCCAACAGGTGT<br>GTTT | TTGATTGTCAATTTCT<br>ATTGTG    | 60.0                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold719_P4_20457  | scaffold719                             | 20457                         | AAATAATAATAATAATAA/AAATAATA<br>ATAATAA                               | TGCTTATACCCATTGG<br>TCCC | TGAGAACTTTTCCGCT<br>GCT       | 59.6                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold719_P4_78505  | scaffold719                             | 78505                         | T/TA                                                          | ATAACCAATCTTGCGC<br>ATCC  | GGAGAACGAAAATGAC<br>CGAA   | 59.9                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7196_P4_616   | scaffold7196                            | 616                           | ATTTT/ATTT                                                    | GATTGGATGGAAGTCA<br>GGGA  | GTTATTCATAGCCTCC<br>GCCA   | 59.9                             | 818                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7196_P4_842   | scaffold7196                            | 842                           | GTAGGATGATCAGATTAGGATGAT/<br>GTAGGATGAT                       | GCCCTCAGATGAGAGT<br>CAGG  | GTTATTCATAGCCTCC<br>GCCA   | 59.9                             | 285                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7197_P4_1691  | scaffold7197                            | 1691                          | AAA/AAAA                                                      | CACACACACCTTTTGG<br>ATGC  | AGGTCATTTTCGTCCTC<br>CCT   | 60.0                             | 551                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold720_P4_205887 | scaffold720                             | 205887                        | ATTTTTTTTT/ATTTTTTTTTT                                        | CCTAAATGCGTTACAC<br>TTGGC | TCATTTGGAAATTTGAG<br>TGATG | 59.7                             | 449                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold720_P4_330129 | scaffold720                             | 330129                        | ATTTT/ATTT                                                    | GGTTTGAGAGGCGATG<br>TGAT  | AGCAACTTTTCCTTCTG<br>CCA   | 60.1                             | 329                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold720_P4_333511 | scaffold720                             | 333511                        | CA/CATA                                                       | CGCTGTTAAAAATCGG<br>GTGT  | CTCATTTGATGCCTGCT<br>TGA   | 60.0                             | 709                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold720_P4_360540 | scaffold720                             | 360540                        | TA/TCA                                                        | CACCGGAAGAAATTGA<br>TCGT  | CCAGCCTGAGTCCTCT<br>TTTG   | 59.9                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold720_P4_370256 | scaffold720                             | 370256                        | GTT/GTTT                                                      | TTGCCCTTAACGGAAT<br>CCAC  | GGTGGGTGTAGGGAGT<br>GAGA   | 59.9                             | 336                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold720_P4_370691 | scaffold720                             | 370691                        | ATTGATTTTGATTTTGATTTT/ATTGA<br>TTTTGATTTT                     | TCTCACTCCCTACACC<br>CACC  | CAATTCACAATTGCACC<br>GTC   | 60.0                             | 625                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold720_P4_372071 | scaffold720                             | 372071                        | T/TTA                                                         | ACCAACATTTTCAGGCT<br>CACC | TAGAGCGCCAAACCCT<br>AATG  | 60.0                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold721_P4_191166 | scaffold721                             | 191166                        | GA/GAA                                                        | CGGAGGACGAAAATGA<br>CCTA  | TGTGCATCCCATAGGT<br>GTGT  | 60.1                             | 473                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7210_P4_7073  | scaffold7210                            | 7073                          | GA/G                                                          | TTTTCGTCCTCCCTAG<br>GCTT  | TTGGATGCACATGATT<br>GGTT  | 60.2                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold724_P4_104152 | scaffold724                             | 104152                        | CAAAA/CAAA                                                    | TCGCACTTCAATATGCT<br>TCG  | GGATGACATGTTGATT<br>GTTGG | 60.0                             | 304                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold724_P4_108519 | scaffold724                             | 108519                        | ATATTATTATTATTATTAT/ATAT<br>TATTATTATTATTATTAT                | GCGGTACTGGCATTGA<br>GCAT  | TTGAAAGGCCTGAGCC<br>TAGA  | 60.1                             | 792                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold724_P4_129064 | scaffold724                             | 129064                        | TTTATTATTATTATTATTATTATT<br>AT/TTTATTATTATTATTAT              | CCCAAGCGGTACTGAC<br>ATTT  | CTGGCCTGGAAGCCTA<br>TTTA  | 60.0                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7279_P4_558   | scaffold7279                            | 558                           | AA/AAAGGGTGTGGTCGA                                            | GGAATCGAGAGCTCCA<br>AGTG  | TCTCAACGCCAGTTA<br>GCTT   | 60.0                             | 523                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold728_P4_22885  | scaffold728                             | 22885                         | CTCAGTTTCA/CTCAGTTTCAGTTTC<br>A                               | AAGGTAACTTGCAGC<br>CAGC   | GAATTGAACAATGGAT<br>GGGG  | 59.5                             | 279                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold728_P4_32793  | scaffold728                             | 32793                         | TC/T                                                          | ATGGAGACGAGTGAAT<br>TCGG  | TGAAGAAGAGTTGGGA<br>AACGA | 60.1                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold728_P4_40630  | scaffold728                             | 40630                         | TAAAGAAA/TAAAGAAAGAAA                                         | TAActAAGCTGCTTGC<br>GGGT  | TTGGAAGGAGCCCTTA<br>CCTT  | 60.0                             | 666                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                       |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold7280_P4_1708  | scaffold7280                            | 1708                          | AC/ACC                                                                | GTTTCGTACCCCTCGA<br>CAAA   | TCCAGATGAAATCGAG<br>GACC   | 60.0                             | 311                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7293_P4_13170 | scaffold7293                            | 13170                         | AG/A                                                                  | TGCCTCTGGATTGGTT<br>GAAT   | AATCTATCCACCCGGA<br>AACC   | 60.5                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7293_P4_13675 | scaffold7293                            | 13675                         | T/TGAGCA                                                              | GGTTCCGGGTGGATA<br>GATT    | TGTGCAGATTGATGGT<br>TGAAG  | 60.0                             | 522                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7293_P4_15472 | scaffold7293                            | 15472                         | TT/TTAGAAAAGTGATAGT                                                   | TTCATGCCAGCAACTC<br>TTTG   | TGCTTTGCTATGCACC<br>AGTC   | 60.0                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7293_P4_20198 | scaffold7293                            | 20198                         | TC/T                                                                  | TTGCTGCCTTCTCCTG<br>TTTT   | ATGATGCACTTTGGGC<br>CTAC   | 60.0                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7299_P4_551   | scaffold7299                            | 551                           | AATATATATATATATAAATATATAT<br>ATA/AATATATATATATATATATAA<br>ATATATATATA | CACCAAACTTAATTTT<br>CCCTTT | TGATTCTATGCATCGT<br>ATTTTG | 59.7                             | 459                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_23555  | scaffold731                             | 23555                         | ATTGATATTTGATATTGATATTTGA<br>/ATTGATATTTGATATTTGA                     | GCCTCCATGATACCAT<br>CTCC   | AACATGCGATTGAGTG<br>GTGA   | 59.3                             | 197                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_239927 | scaffold731                             | 239927                        | AATATATATATATATATATATATAT<br>ATATAT/AATATATATATATATATA<br>TATATATATAT | AAACCGTTGATTCATC<br>GAAA   | TCAAAATTTTAGCCCC<br>CTT    | 58.1                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_313013 | scaffold731                             | 313013                        | AAA/AGAAGGAA                                                          | TCAAAATTTTCCGCTG<br>CTT    | AACTGTCTCAACTCTC<br>GGGC   | 59.8                             | 192                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_322781 | scaffold731                             | 322781                        | T/TCAAATTCATTAAAA                                                     | ATCCCCGATTCCTCTC<br>AAGT   | AATTCCTACTGGATGC<br>ACGC   | 59.9                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                       | Forward primers (5'-3')  | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------|--------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                     |                          |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold731_P4_323181 | scaffold731                             | 323181                        | GATAAATCAATAT/GATAAATCAATA<br>TAAATCAATAT                                           | GCAGGAATCCTCGTAC<br>CTCA | CTGCGAATTGCGTGAA<br>AGTA       | 60.2                             | 296                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_323712 | scaffold731                             | 323712                        | T/TCTTCCGA                                                                          | TACTTTTCACGCAATTG<br>CAG | TTTATTTTCCGATTGCC<br>TCG       | 60.0                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_324476 | scaffold731                             | 324476                        | CAA/CAAAA                                                                           | TGTGATATGGTTGCGA<br>AGGA | CAACCATCCCGTTTGG<br>TATC       | 60.1                             | 650                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_324511 | scaffold731                             | 324511                        | A/ACGAGA                                                                            | TGTTTGGAAGACCGAA<br>AACC | CAACCATCCCGTTTGG<br>TATC       | 59.9                             | 257                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_324642 | scaffold731                             | 324642                        | T/TA                                                                                | TGTTTGGAAGACCGAA<br>AACC | CAACCATCCCGTTTGG<br>TATC       | 59.9                             | 257                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_32852  | scaffold731                             | 32852                         | GTATATATATATATATATATATAT<br>ATATATATATATAT/GTATATATATAT<br>ATATATATATATATATATATATAT | GTATTAGGTGCCGTG<br>GAGA  | AAAATATATAAAACTC<br>GCCATTTGAA | 60.1                             | 815                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_335005 | scaffold731                             | 335005                        | A/AGTGGA                                                                            | CTATCAATAACCCAGC<br>CGGA | TGGATCAGATCGAGTT<br>GGAA       | 59.9                             | 857                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_339474 | scaffold731                             | 339474                        | GT/GTTTCTCTT                                                                        | TGTGCAAACGTCATTG<br>GATT | CCTCAGATGAGAGGCA<br>GGAC       | 60.0                             | 544                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_342154 | scaffold731                             | 342154                        | CAAAAAA/CAAAA                                                                       | AAATGGAGGAGAAGGA<br>GGGA | ACCCAATTACTGGAGA<br>TGCG       | 60.0                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_347933 | scaffold731                             | 347933                        | ATT/ATTT                                                                            | TAAGCCCAATCGATT<br>CCAA  | CTCGTGTTTCGTCGTG<br>AGAA       | 60.4                             | 438                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold731_P4_354401 | scaffold731                             | 354401                        | AC/ACGCTGTTTAGC                                               | GCCCTCAGATGAGAGT<br>CAGG  | GGTGAAATGGTAGACA<br>CCCG | 59.9                             | 483                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_354972 | scaffold731                             | 354972                        | T/TATAATCATAC                                                 | ATAACCTTAGCGCATT<br>CCCA  | CCTCCCGTAAGATCCA<br>ACAA | 59.6                             | 308                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_366076 | scaffold731                             | 366076                        | GAA/GAAA                                                      | TCTCGCGGATTTTCAT<br>AACC  | CCATCCATTTCCGTATT<br>GCT | 60.0                             | 100                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_369468 | scaffold731                             | 369468                        | AC/ACAAATTC                                                   | ATTTTCCAAAGGGTCT<br>CGG   | AAATCCAATCTCTCCCG<br>CTT | 60.3                             | 421                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold731_P4_46491  | scaffold731                             | 46491                         | ATT/AT                                                        | CGATTTGGCAAGTTAC<br>AGGG  | TACATCCCACACAG<br>GGT    | 60.5                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold735_P4_15341  | scaffold735                             | 15341                         | CTTTTT/CTTTT                                                  | GCTGTGTGTTTGTCC<br>AATG   | TCGATAGAGGTGTTGG<br>GGTC | 60.0                             | 361                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold735_P4_192011 | scaffold735                             | 192011                        | CTTTTTTTTT/CTTTTTTTTT                                         | AACTCAACCCAACATT<br>GAACA | TGGTGATGTGGCAATC<br>ATT  | 58.0                             | 824                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7355_P4_17568 | scaffold7355                            | 17568                         | TAAAA/TAAAAA                                                  | AGTAAACGCGGAAAA<br>AGGT   | GCATCAAGACGACGAA<br>CAAA | 60.0                             | 756                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7355_P4_18760 | scaffold7355                            | 18760                         | A/ATC                                                         | ATTTTGCTAGGGGAG<br>AGGA   | GAGTGGGCTGATGCAA<br>AAAT | 60.0                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7355_P4_8922  | scaffold7355                            | 8922                          | TAAAAAAA/TAAAAA                                               | TGTATTTGATCGACG<br>GCTG   | AAAAGGGAATAGGGTG<br>GGTG | 59.7                             | 239                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold7355_P4_9362 | scaffold7355                            | 9362                          | ATTTTTTTTTTT/ATTTTTTTTTTT                                     | AGAGAAACGCTCCTCT<br>TCCC | TTGCATACCCCTTTTCA<br>CAT | 60.0                             | 266                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7355_P4_9486 | scaffold7355                            | 9486                          | AGGGGG/AGGGG                                                  | AGAGAAACGCTCCTCT<br>TCCC | CAGTGACATGACTCCC<br>AACG | 60.0                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7355_P4_9558 | scaffold7355                            | 9558                          | AATA/AATATA                                                   | AGAGAAACGCTCCTCT<br>TCCC | CAGTGACATGACTCCC<br>AACG | 60.0                             | 683                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7364_P4_2154 | scaffold7364                            | 2154                          | CAT/C                                                         | TCAATTTGGGTTTAGG<br>GTGC | TGTAGTGGCATGTTTG<br>GCAT | 59.8                             | 497                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7364_P4_4397 | scaffold7364                            | 4397                          | ATT/ATTTT                                                     | TGCTTCACAAGCTCCA<br>TTTG | AAACGCAATCCTTGAG<br>TTCG | 60.0                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7377_P4_545  | scaffold7377                            | 545                           | CT/CTT                                                        | TTTCTTCCCAACCTTCA<br>TCG | GCCGTTGGAACCTCAT<br>CATT | 60.0                             | 816                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold738_P4_10670 | scaffold738                             | 10670                         | GAAAA/GAAAAA                                                  | GTACCACCCCAAAAA<br>ATGG  | CATCAGGACTTTTGGG<br>GCTA | 59.9                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold738_P4_2137  | scaffold738                             | 2137                          | T/TC                                                          | TGAATATCGCCGAAA<br>AGTC  | TTTCATAGCAGACGAG<br>GGCT | 60.0                             | 292                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold738_P4_5098  | scaffold738                             | 5098                          | ATTTTT/ATTTT                                                  | TCGGGTGGTACTTAA<br>TCGC  | ATCTGACGTGGAAC<br>GAAC   | 60.0                             | 274                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold74_P4_17446  | scaffold74                              | 17446                         | C/CA                                                          | AGGTCATTTTCGCCT<br>CCCT  | TTGGATGCACAAGATT<br>GGTT | 59.9                             | 168                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold743_P4_14244  | scaffold743                             | 14244                         | AACACACA/AACACA                                               | TGCTTGATTGCTTGAG<br>TTCC | GTACCCTGATTGCCCT<br>CTGA  | 59.0                             | 321                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold7448_P4_21480 | scaffold7448                            | 21480                         | GAAA/GAAAA                                                    | AGGATCTCCCGATTCT<br>CGAT | TTCCGGGTCAGATTTC<br>AAAC  | 60.0                             | 287                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold7470_P4_2428  | scaffold7470                            | 2428                          | TCCC/TCC                                                      | TGTGCATCCGATAGGT<br>GTGT | GGGAGAATGAAATGA<br>CCGA   | 60.0                             | 760                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold7477_P4_2293  | scaffold7477                            | 2293                          | TAAA/TAA                                                      | TTGGTGGATTGAGAC<br>CACA  | ACTTCCTTTGCACATT<br>TGG   | 59.9                             | 652                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold7477_P4_6564  | scaffold7477                            | 6564                          | TTTG/TTTGTTG                                                  | CCTGCAGAAAGCAAAA<br>CACA | ACCTTGGGAAGGAGGA<br>GAAA  | 60.0                             | 590                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold7477_P4_6861  | scaffold7477                            | 6861                          | GCCCCC/GCCCCC                                                 | TGCAAAAGAGCACTGA<br>CACA | GGGAAAAGCATTTTTG<br>CGTA  | 59.2                             | 260                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold7480_P4_797   | scaffold7480                            | 797                           | ATGTT/ATGTTGTT                                                | ATGAACCTAACCCAAA<br>CCCC | AAAATCCAACAATCTCC<br>CCC  | 59.9                             | 569                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold7489_P4_558   | scaffold7489                            | 558                           | TAAAA/TA                                                      | AACCACAACAATGCCA<br>ACAA | TTTTGCTTTTGTGCCA<br>ACC   | 59.9                             | 539                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold7489_P4_828   | scaffold7489                            | 828                           | GTATATATATATATATA/GTATATA<br>TATATATATA                       | GGTTGGACCAAAAAGC<br>AAAA | TCACCTTCTCATCACAA<br>CAGC | 60.0                             | 602                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold749_P4_1624   | scaffold749                             | 1624                          | CTATATATATATATATATATATAT<br>AT/CTATATATATATATATATAT           | CTTGGGAAGTGGAGAG<br>CAAG | GAGGAGGGAGGGATT<br>TGAG   | 60.0                             | 536                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                               | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                             |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold750_P4_210452 | scaffold750                             | 210452                        | CATATATATATATATATATATATATATATATATATATATAT/CATATATATATATATATATATATATATATATATATATAT                           | AATCATCGCTTCCAAG<br>ATGG    | TTTGAGAAAGTGATGGG<br>AGGG | 60.0                             | 352                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold750_P4_264392 | scaffold750                             | 264392                        | GTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTAT/GTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTAT | CGTCGCCCAATAAAAGT<br>CCTA   | TTTGTTAGCATTTGCAA<br>GGGT | 60.1                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold750_P4_273596 | scaffold750                             | 273596                        | AC/A                                                                                                        | ATCGCCTCTTCAACCA<br>AGAA    | GATGATGGAAAAGGAG<br>GCAA  | 59.8                             | 678                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold750_P4_31851  | scaffold750                             | 31851                         | GAAAAAAAA/GAAAAAA                                                                                           | TGAGTTTCTATGCAAG<br>GGCA    | TTCATGAAGACACCGG<br>AACA  | 59.4                             | 273                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold750_P4_32900  | scaffold750                             | 32900                         | TA/T                                                                                                        | ATGCTCCATGTTTGCT<br>TAGG    | TCCTTTGCTAGCCCTTT<br>TGA  | 60.1                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold750_P4_38979  | scaffold750                             | 38979                         | AT/A                                                                                                        | CACTGATAACGCGACT<br>AATTTGA | ACCGCCACAAATGATA<br>AAGC  | 59.3                             | 748                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold750_P4_5643   | scaffold750                             | 5643                          | TAAA/TAA                                                                                                    | TCGGGAACACACAC<br>AACA      | ACAACGCGATTTC<br>AAAC     | 60.0                             | 504                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold750_P4_59023  | scaffold750                             | 59023                         | ATTGTTGTTGTT/ATTGTTGTTGTTGTT                                                                                | CGTAGCATCAGCAACC<br>TTCA    | TCCCTCTTTTGTTTTTC<br>CCA  | 60.0                             | 989                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold750_P4_59256  | scaffold750                             | 59256                         | TATGTTCTGCTAATGT/TATGT                                                                                      | TGTTACACCCAAAG<br>CAAA      | TCCCTCTTTTGTTTTTC<br>CCA  | 59.1                             | 373                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold750_P4_59806  | scaffold750                             | 59806                         | A/AG                                                                                                        | AAAGTTGTACCGTCG<br>GAAC     | TGTCTTGAAGGCTGAT<br>TTGC  | 60.0                             | 401                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                            | Forward primers (5'-3')     | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------|-----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                          |                             |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold750_P4_911    | scaffold750                             | 911                           | GAAAAAAAA/GAAAAAAAA                                                                                      | TGGCCAGCTGTATATT<br>TCACC   | TTTTTCTTAACACAAGC<br>CAACA   | 60.0                             | 299                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7502_P4_559   | scaffold7502                            | 559                           | ATTATATAT/A                                                                                              | GTTGGTTCCTAGCAC<br>CGTA     | TATCCAATCTTGTGCGT<br>CCA     | 60.0                             | 806                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold752_P4_131814 | scaffold752                             | 131814                        | GTATATATATATATATAT/GTATATAT<br>ATATATATATAT                                                              | GTTGGTTCCTAGCAC<br>CGTA     | ATTGCCAGAGGTGTGT<br>GAGT     | 60.0                             | 754                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold752_P4_209358 | scaffold752                             | 209358                        | TAATAAATAAATAAATAAATAAATAA<br>ATAAATAAATAAATAAATAAATAAATAA<br>ATAAATAAATAAATAAATAAATAAATAA<br>AAATAAATAA | TCTGCTAACGGGTCGT<br>TTCT    | TCCCTTTTAGATAAACA<br>TGTGCAA | 59.9                             | 577                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold752_P4_269557 | scaffold752                             | 269557                        | A/AC                                                                                                     | AACGACACAATTTTACT<br>CATCGT | TAAGGTTGTCTGGGGA<br>GGTG     | 57.8                             | 368                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold752_P4_505163 | scaffold752                             | 505163                        | TTTTATTTTATTTATTTTAT/TTTTATT<br>TTATTTATTTTATTTATTTTAT                                                   | AGCCATTGCAGTCTTC<br>GTCT    | TCGTGTCTCAAACTCA<br>AGGAA    | 60.0                             | 854                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold752_P4_99344  | scaffold752                             | 99344                         | ATTT/ATTTT                                                                                               | TTGCATGTAAGCAATC<br>GTCC    | GCAAGATCGCACTCTT<br>GTCA     | 59.7                             | 730                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7528_P4_11099 | scaffold7528                            | 11099                         | ATTTT/ATTTT                                                                                              | AAACAATCGTGTGCAT<br>CCAA    | CCAAGGGAGAACGAAA<br>ATGA     | 60.0                             | 273                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7528_P4_15298 | scaffold7528                            | 15298                         | T/TC                                                                                                     | CCAAGGCTTATTCCTA<br>TCCA    | GGCAGGACGAAAATGA<br>CCTA     | 59.9                             | 817                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold753_P4_276343 | scaffold753                             | 276343                        | TAAAAAAAA/TAAAAAAAA                                                                                      | TTAACCCGGTTTTGATT<br>TGC    | TACGTATCTCCCGATG<br>CGAT     | 59.8                             | 743                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                     |                            |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold753_P4_334129 | scaffold753                             | 334129                        | AATATATATATATAT/AATATATAT<br>ATATATATAT                             | AGTGAGACGCTACTCG<br>GCAT   | TTTAAACCGTGGTTTGA<br>AACTT    | 60.0                             | 204                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7565_P4_3129  | scaffold7565                            | 3129                          | CAAAAA/CAAAA                                                        | GGTCCTCGATTTCATC<br>TGGA   | AAAAATCGCATGAAAC<br>GTCC      | 60.0                             | 200                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7569_P4_558   | scaffold7569                            | 558                           | GAA/GA                                                              | ACTACCCATTCTGCT<br>GTGG    | AGATGAAAAATGGCTTT<br>GGC      | 60.0                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold758_P4_13400  | scaffold758                             | 13400                         | AATATATATATATATATATA/AA<br>TATATATATATATATATA                       | CTCGTCCAATCCCT<br>TTTT     | CGATTTTACGTGAATAT<br>ACGAACAC | 60.3                             | 603                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold758_P4_22430  | scaffold758                             | 22430                         | TA/T                                                                | TCACATTAAGTCAAAAC<br>ACACA | TCACCACAAATTCGAT<br>GACA      | 57.8                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold758_P4_26328  | scaffold758                             | 26328                         | TTATATATATATATATATATATA<br>TATA/TTATATATATATATATATAT<br>ATATATATATA | TTTGGCTCGAAGGCTT<br>TTTA   | GTTGGTTCCCTAGCAC<br>CGTA      | 60.0                             | 600                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold758_P4_3569   | scaffold758                             | 3569                          | CTATATATATATATATATATATAT<br>ATA/CTATATATATATATATATATA<br>TATATATA   | CATGATCCTCCTACTC<br>CCGA   | CAACAAGGTTGGTGT<br>GCTG       | 60.0                             | 348                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7617_P4_656   | scaffold7617                            | 656                           | CAAAA/CAAAA                                                         | TCCAATGAGCACACAA<br>CCTT   | GTGCGTTTGAGACATT<br>TGGA      | 59.1                             | 712                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7657_P4_660   | scaffold7657                            | 660                           | CACAACAA/CACAA                                                      | AGGGAGGACGAAAATG<br>ACCT   | GGTGTGTTTGTGTCGT<br>TGGA      | 59.9                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold766_P4_12390  | scaffold766                             | 12390                         | ATTTTT/ATTTTTTT                                                     | TTTGCAACTTTAGC<br>GTGAA    | TGAAAATGAAGTCAATG<br>TGAATGA  | 59.5                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                   |                               |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold766_P4_144590 | scaffold766                             | 144590                        | GAAAAAAAAA/GAAAAAAAAAAAAA                                         | CTCCTAAGGGTGGCCT<br>TACC      | CAATTGAGACCTTGTC<br>GGCT  | 60.0                             | 590                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold766_P4_164185 | scaffold766                             | 164185                        | CATCAAAAA/CATCAAAAAATCAAAA<br>A                                   | CTGAGTCGAACCCCGT<br>ACAT      | AGCAGCAAAACAGTGAA<br>AGCA | 60.0                             | 656                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold766_P4_67907  | scaffold766                             | 67907                         | ATTTTTTTTT/ATTTTTTTTTTT                                           | TTAGCAAGAAGGGCAG<br>CAAT      | TCAAGTTTGGGAGAAG<br>TCCG  | 60.0                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold766_P4_79566  | scaffold766                             | 79566                         | CTT/CT                                                            | CAGCGAGTTCATCCTC<br>TTCC      | CCTCAGATGAGAAACC<br>CCAA  | 60.0                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold768_P4_560    | scaffold768                             | 560                           | T/TG                                                              | CCATGAGAGTCGAAAT<br>CGGT      | TCCCACAGATCCACATT<br>CAA  | 60.1                             | 188                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold769_P4_1084   | scaffold769                             | 1084                          | T/TAAC                                                            | AAATGAACCAATTTAAT<br>GAGCTACC | CCCTCCCAAAACACCC<br>TTAT  | 59.0                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold769_P4_2786   | scaffold769                             | 2786                          | TGGCAGCAG/TG                                                      | ACGTACACGTCAGCGT<br>TTTG      | CCCAATTCTCAATCCCA<br>CTT  | 59.8                             | 147                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold769_P4_29353  | scaffold769                             | 29353                         | AGC/AGCCCACTAATATGC                                               | GCACTCTCATTTCATCC<br>CACA     | CCACATGTCATTTAACC<br>CTGC | 59.6                             | 370                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold769_P4_3496   | scaffold769                             | 3496                          | A/ATAC                                                            | TCCAAGAAAACAGTTT<br>CCGA      | TGAATGGTTTATTGAG<br>CTGGA | 58.3                             | 588                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold769_P4_5414   | scaffold769                             | 5414                          | AATATATATATATATATATATATAT<br>ATATAT/AATATATATATATATATATA<br>TATAT | TCACTCGCGTTAATTTT<br>GATG     | GCGAGTGAATACATGT<br>GCCA  | 58.8                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                         |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold769_P4_5924   | scaffold769                             | 5924                          | AATATATATATATATAT/AATATATAT<br>ATATATATATAT                             | TGGCACATGTATTCAC<br>TCGC | TGTTGTTATTTGTGGC<br>GGAA | 60.7                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold769_P4_5960   | scaffold769                             | 5960                          | ATATTATTATTATTATT/ATATTATTA<br>TTATT                                    | TGGCACATGTATTCAC<br>TCGC | TGTTGTTATTTGTGGC<br>GGAA | 60.7                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold769_P4_91398  | scaffold769                             | 91398                         | GAAAAAAAAA/GAAAAAAAAA                                                   | AGATGAATTTTCAGCC<br>ACCG | CCCGATTTCGTGCATC<br>TATT | 60.1                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7697_P4_589   | scaffold7697                            | 589                           | G/GA                                                                    | CTAGCCCTCGTCTGTT<br>CCAG | AATCCGTATTTTCGCAC<br>CAG | 60.0                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold772_P4_112502 | scaffold772                             | 112502                        | CATATATATATATATATATATATA<br>T/CATATATATATATATATATATAT<br>ATATATATATATAT | AGGGAGGTTTGTGTT<br>GACG  | CCGGGTTGCTTTTCA<br>GATA  | 60.0                             | 791                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold772_P4_11892  | scaffold772                             | 11892                         | TAAA/TA                                                                 | GGCACACTCCGTAA<br>ATTC   | TTTTTCGCACACCAATG<br>AGA | 59.4                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold772_P4_211515 | scaffold772                             | 211515                        | TCT/TCTTACAACCTCCCT                                                     | AATGGAGGAAGGAGG<br>GAGAA | ACGTTTCCAAGTTCTG<br>GTGG | 60.0                             | 452                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold772_P4_213642 | scaffold772                             | 213642                        | AGG/AGGG                                                                | ACTTGAGGGCGAAGAA<br>CAAA | TTGGATGACCTACGAC<br>TCCC | 59.9                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold772_P4_39391  | scaffold772                             | 39391                         | CAA/CAAA                                                                | CAGGTGTATTCGCTTG<br>GGTT | GCCAAAACTGTTTCAG<br>GGAA | 60.0                             | 396                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold774_P4_3829   | scaffold774                             | 3829                          | GAAAATGACC/GAAAATGACCAAAAT<br>GACC                                      | TGGATGCACAAGATTG<br>GCTA | AGGTCAATTTTCGTCTC<br>CCT | 60.2                             | 468                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                 |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold775_P4_110824 | scaffold775                             | 110824                        | TAAA/TAA                                                        | GCCGAATCGATTTGT<br>CAGT   | GGAGGGTTTTGGTTTG<br>GAAT | 60.1                             | 521                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold775_P4_116393 | scaffold775                             | 116393                        | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATA<br>TATAT | TTGGTATTGAACTCGG<br>AGGC  | ATCCGGTAAAAATCTCC<br>GCT | 60.1                             | 649                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold775_P4_142437 | scaffold775                             | 142437                        | TATTATTAT/TATTATTATAATTATTA<br>T                                | CAACAAAAATCTCATGT<br>GGCA | CATGACAGTGGTGTGC<br>GATA | 59.6                             | 448                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold775_P4_226154 | scaffold775                             | 226154                        | CAA/CAAA                                                        | TATGCAGCCATAAATG<br>CCAA  | GCCGAATAAACCTC<br>ACAA   | 60.1                             | 345                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold775_P4_381546 | scaffold775                             | 381546                        | A/AATGC                                                         | TGTTTTGCTGAACATC<br>GCTC  | GGGTGATGAGGACTCA<br>GGAA | 60.0                             | 431                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold775_P4_388602 | scaffold775                             | 388602                        | CATATATATATATATAT/CATATAT<br>ATATATATATATAT                     | CTTCGCGAAATAAAGC<br>TTGG  | TTGGTATTGAACTCGG<br>AGGC | 60.0                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold775_P4_409996 | scaffold775                             | 409996                        | CAGCGCTTTTCCACAAAGCGCTTT/<br>CAGCGCTTT                          | ACGAGCTTCCTTCCAC<br>AAGA  | GTCACATAGCGCTTGC<br>ACAT | 60.0                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold775_P4_446063 | scaffold775                             | 446063                        | TTATATATATATAT/TTATATATATAT<br>ATAT                             | TTTTGCAAGATCTGCC<br>ACTG  | TGGAAGGATCCGGAAC<br>TATG | 60.0                             | 867                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold776_P4_224423 | scaffold776                             | 224423                        | T/TTCCCTA                                                       | TGGGATACGTAGGAGC<br>AAGG  | TGTCCTGAAAAATGA<br>GTCG  | 60.1                             | 310                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7765_P4_977   | scaffold7765                            | 977                           | ATTTTTTTTT/ATTTTTTTTTTTT                                        | AGATGGCTGCAGCTCA<br>AAGT  | TTTCCAAGAGGTTTTG<br>GGTC | 60.2                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                       |                           |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold779_P4_14847  | scaffold779                             | 14847                         | AC/A                                                                  | CGCATTATTTGCAATG<br>CCTA  | GTGGTTCCGTGGATGA<br>AATA    | 59.7                             | 866                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold779_P4_1487   | scaffold779                             | 1487                          | TATTAT/TATTATCATTAT                                                   | CCTTATTTTCGACGCTTT<br>TGC | TGTGATACGTTGCTAG<br>TCTTGCA | 59.9                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7800_P4_12006 | scaffold7800                            | 12006                         | CTATATATATATATATATATATAC/<br>TATATATATATATATATATATATAT<br>ATATATA     | TGGAGCCAACCTAGA<br>AGAA   | ACCAAACTGGGGACA<br>AACA     | 59.8                             | 804                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold783_P4_104485 | scaffold783                             | 104485                        | ATT/A                                                                 | CAAATCGATTGCCTGA<br>AGGT  | CCCGTGATAGGCAGTA<br>CGTT    | 60.1                             | 703                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold783_P4_104775 | scaffold783                             | 104775                        | CGGGG/CGGG                                                            | GTGCAGTCTCTCACGG<br>ACAA  | CCCGTGATAGGCAGTA<br>CGTT    | 60.0                             | 154                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold783_P4_120194 | scaffold783                             | 120194                        | CTATATATATATATATATATATAT<br>ATAT/CTATATATATATATATATAT<br>ATATATATATAT | TTGGATTTTGGTTCAG<br>AGGC  | ACCGTAGTTTGGTGGT<br>GAGC    | 60.1                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold783_P4_128797 | scaffold783                             | 128797                        | TTTA/T                                                                | GGAAGTTTCGTGGAAA<br>ACGA  | ATTCCAAACCAAAACCC<br>TCC    | 60.1                             | 813                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold783_P4_31156  | scaffold783                             | 31156                         | CATATATATATATATATATATATA<br>TATATA/CATATATATATATATATA<br>TATATATATATA | TTTGGGTGTTTGAGTG<br>TCCA  | CACATTTTCTTCTCACG<br>TCCA   | 60.0                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7842_P4_20001 | scaffold7842                            | 20001                         | CAA/CAAA                                                              | AAAGGGTGATGACGAT<br>TTCAG | TTCTTTCTCAGCCTCTA<br>TGCG   | 59.0                             | 571                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_12153  | scaffold787                             | 12153                         | TAAAAAAAAA/TAAAAAAAAA                                                 | CGAGGCAAAGGTTTGA<br>GAAG  | CAAAGCAATTTTGTAGA<br>GGGA   | 60.0                             | 685                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold787_P4_129918 | scaffold787                             | 129918                        | AAATAATAATAATAATAATAATA<br>ATAATA/AAATAATAATAATAATA<br>ATAATA | AGAATCCACAACGCAACACA    | AAGGCACGACATCATCATCA    | 60.2                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_136185 | scaffold787                             | 136185                        | TAAAAAAAA/TAAAAAAAA                                           | GGTAAACCCATTGGTCCCT     | GTGTATATACGCGCACCCAA    | 59.9                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_140503 | scaffold787                             | 140503                        | TC/TCCCTCTTTCTAGATCAC                                         | GGAAACCTGAAATGCTCA      | AATCAATGCCACCAAGAAGG    | 60.1                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_149556 | scaffold787                             | 149556                        | ATTTTT/ATTTT                                                  | CGGGATGGTGGCATAATATC    | AGCAGGGTTTCTCCCAAAT     | 60.0                             | 343                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_288311 | scaffold787                             | 288311                        | ATTTTTTTTT/ATTTTTTTTT                                         | GGGACTTAATTGTCCCGGTT    | TCACAATGGTGTCTTTGCACT   | 60.1                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_289233 | scaffold787                             | 289233                        | TAAAAAAAA/TAAAAAAAA                                           | CAAGCTATTCTTTGCCGACAT   | CGACATTCAAACATGACCTT    | 59.4                             | 621                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_305395 | scaffold787                             | 305395                        | TTAAGTA/TTA                                                   | CTTGATGGTCGGATTGTGTG    | AATCCACTTACACCGCCAAG    | 60.0                             | 306                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_306110 | scaffold787                             | 306110                        | GAAAAAAAA/GAAAAAAAA                                           | TGAAGTTGAACCTTGACCA     | GTGCTCTCCCTTTGTCTGTC    | 59.1                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_32833  | scaffold787                             | 32833                         | TAAAAAAAA/TAAAAAAAA                                           | GCTTTCAGCATCGAGGTAG     | TCCAAAAGATATGCCCGAC     | 60.0                             | 553                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_334329 | scaffold787                             | 334329                        | ATTTTTTTTT/ATTTTTTTTT                                         | CTTCCTCTGTGCCACATCCT    | TTCATTCTGTCTGCTTTGG     | 60.3                             | 598                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold787_P4_348087 | scaffold787                             | 348087                        | TTATATATATATAT/TTATATATATAT                                   | GAGGGGATGGTGAGA<br>GTGAA | GCAGACATCACATGGA<br>AGGA | 60.0                             | 595                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_349729 | scaffold787                             | 349729                        | ATAATTAATTAATTAATTAAT/ATAAT<br>TAATTAATTAAT                   | GGTTCAGTTCGGTTTT<br>TCCA | CAAGACAAGAGGGAGT<br>GGGA | 59.9                             | 917                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_349982 | scaffold787                             | 349982                        | TCATATATACAG/T                                                | GGGTGGTGGAGAAAA<br>GTGAA | CAAGACAAGAGGGAGT<br>GGGA | 59.9                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_353218 | scaffold787                             | 353218                        | A/AT                                                          | CCCCCTCTTAGGCGTA<br>CTTC | TACCTCCGTCACCAA<br>AAAC  | 60.1                             | 529                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_365234 | scaffold787                             | 365234                        | TAAAAAAAAA/TAAAAAAAAA                                         | CAGTCACTTAGGCAAC<br>CAGC | AGTTTTCCCAAGCAA<br>GGTT  | 59.4                             | 796                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_460508 | scaffold787                             | 460508                        | CATTTTATTT/CATTTTATTTTATTT<br>ATTT                            | TATGGGAAGGAAATGT<br>GGGA | TCACTCGCAACGAGAA<br>GTTG | 60.1                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_460684 | scaffold787                             | 460684                        | CAT/CATAT                                                     | TATGGGAAGGAAATGT<br>GGGA | TCACTCGCAACGAGAA<br>GTTG | 60.1                             | 601                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_462837 | scaffold787                             | 462837                        | GGTGGCCATTCCCTAGTG/GGTGG<br>CCATTCCCTAGTGGCCATTCCCTAG<br>TG   | ACCACCCTTTAACGTTT<br>TGC | GTTACTCCACGTGAC<br>ACCC  | 59.0                             | 282                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_464479 | scaffold787                             | 464479                        | ATTTTTTTTT/ATTTTTTTTT                                         | AGCCGTAGTCAATCCG<br>ACAG | TGGTTTTGTTGTCCCAT<br>GTC | 60.3                             | 537                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold787_P4_469394 | scaffold787                             | 469394                        | CAGG/C                                                        | GGCGGTTGCTAAAGTA<br>GTGC | ACGATCTTCTCCACG<br>ATGC  | 59.9                             | 331                                           | INTERGENIC                                        | --                                  | --                    | --  |

[illegible]



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold794_P4_138143 | scaffold794                             | 138143                        | GA/G                                                          | CTGTCAAACCGGTTCTGTT        | TGCTTGCAGTGCTTCA<br>TCTT | 60.0                             | 378                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold794_P4_138803 | scaffold794                             | 138803                        | AA/AATGCTTA                                                   | CAGAAATGGGTGCCAAAAA        | GCGGAAACATTAGCAAGACC     | 60.8                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold794_P4_55949  | scaffold794                             | 55949                         | GAAAAAAAAA/GAAAAAAAAA                                         | ACCTTGTGTGTTTTGGCTGG       | CACAAAAGCCCAACACCTT      | 60.0                             | 586                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold794_P4_68927  | scaffold794                             | 68927                         | AG/AGG                                                        | TGAAGATCCAAGAACAACCCA      | GGAACACGAAAGCCACTACC     | 60.5                             | 760                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold796_P4_26479  | scaffold796                             | 26479                         | GTT/GTTT                                                      | TCATTTTCGTCTCTCTTGG        | GCCTATTGGATGCACAGGAT     | 60.0                             | 470                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold797_P4_15287  | scaffold797                             | 15287                         | CAAAAA/CAAAAAA                                                | GGTGATTTTTATGATGTGCTAGTTTT | CCCTTTCAATCCCCTTTT       | 59.0                             | 689                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold7976_P4_703   | scaffold7976                            | 703                           | GA/GAA                                                        | GGGGAGCATCTGATGTGTT        | AGAGGCTACTGACTTGGCA      | 59.9                             | 548                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold798_P4_1261   | scaffold798                             | 1261                          | A/AT                                                          | ACAGCGGAAGAGTTTCTCCA       | GATTGGCAACACAGGACT       | 60.0                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold798_P4_12704  | scaffold798                             | 12704                         | GTT/GTTT                                                      | GCGTTTAGGGGTAAAGGTC        | TTGCCATTGACTTGCA<br>CAAT | 58.6                             | 706                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold798_P4_16927  | scaffold798                             | 16927                         | T/TC                                                          | ATGCAATGCGTATATGCCAA       | TAAATCGTGTTGACCCGTGA     | 59.9                             | 233                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)                | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                               |                            |                            |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| scaffold799_P4_20961  | scaffold799                             | 20961                         | TAAAAAAAAA/TAAAAAAAAA                                                         | TCGTCTGATAGACGGC<br>TGAA   | ATATTGGTTTAAACGGC<br>GCT   | 59.5                             | 873                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold80_P4_182397  | scaffold80                              | 182397                        | GAAAAAAAAA/GAAAAAAAAA                                                         | GAATCGTGAGCGTGT<br>GAGA    | CCAGCACAAATTTATTC<br>TCCG  | 60.0                             | 485                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold80_P4_264906  | scaffold80                              | 264906                        | ATTTTT/ATTTTT                                                                 | GTTGCTGGGGATTGTC<br>ATCT   | CCATGTGGTGATGCTA<br>CCAG   | 59.9                             | 671                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold80_P4_271823  | scaffold80                              | 271823                        | AATAT/AATATAT                                                                 | AAATGAAAGCCGTTCA<br>AAAATC | AACAAATGTGTGCAAAA<br>TGACA | 59.5                             | 419                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold80_P4_318973  | scaffold80                              | 318973                        | TTATATATATATATATATATATATA<br>TATATAT/TTATATATATATATATATA<br>TATATATATATATATAT | TGTGCACTTGGGTGCGA<br>GATA  | ACCCCACCTCTCTCTT<br>CCAT   | 60.3                             | 462                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold80_P4_386609  | scaffold80                              | 386609                        | ACC/AC                                                                        | GGAGGTCTTTTACAAC<br>GCTCTT | TGGAGATGATTTGCAA<br>TGGA   | 59.0                             | 692                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold80_P4_43513   | scaffold80                              | 43513                         | AGGG/AGG                                                                      | CCGAGCCAAATCCAA<br>AATA    | TTCTCGGGCTAAATC<br>ATGG    | 59.9                             | 352                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold801_P4_141880 | scaffold801                             | 141880                        | CAAAAAA/CAAAAAA                                                               | AAGCCCCAAGAAGCAA<br>ACAA   | AAAGGGCAACACAG<br>TGTC     | 59.9                             | 120                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold801_P4_152306 | scaffold801                             | 152306                        | ATTTTTTTTT/ATTTTTTTTT                                                         | TCCCCATTCTCTTCTC<br>ACC    | TGGTGGTCTTGTGGT<br>TTCA    | 59.1                             | 778                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold801_P4_152885 | scaffold801                             | 152885                        | TAATAAATAAATAAT/TAATAATAA<br>ATAAATAAAT                                       | TGAAACCAACAAGACC<br>ACCA   | TTATCCCCCTCCTCTCT<br>GCT   | 60.0                             | 552                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold801_P4_156769 | scaffold801                             | 156769                        | ATTTTTTTTTTTTT/ATTTTTTTTTTT                                   | GAGACGGGCTCAACAA<br>AATC  | TTTCGCAAATTCACAT<br>TCATC | 59.7                             | 659                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold801_P4_160078 | scaffold801                             | 160078                        | TAA/TAATAACAA                                                 | ACTAGATGGTCGCATC<br>CTGG  | CACACGTTTGTTTTATG<br>GCAA | 60.1                             | 717                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold801_P4_165990 | scaffold801                             | 165990                        | CAA/CAAAA                                                     | ATCGCGGTCACCACTT<br>AAAC  | TCGAAAAGAAATCGAG<br>ACCG  | 60.0                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold801_P4_192338 | scaffold801                             | 192338                        | ATTTTTTTTT/ATTTTTTTTTTT                                       | TGTGCAGATAAATGGC<br>CAAA  | GAGCTGTGTCTTGGA<br>ATCA   | 60.1                             | 792                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold801_P4_201715 | scaffold801                             | 201715                        | CTTTTTTTTTTT/CTTTTTTTTTTTT                                    | TGCACCTTCTTCATTG<br>GGT   | TGAAGCAAAACGTGCA<br>AAAG  | 60.5                             | 320                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold801_P4_202304 | scaffold801                             | 202304                        | TAAAAAAAA/TAAAAAAAA                                           | TGCTTCTTTTGCACGTT<br>TTG  | AGACGTCTTTCTTTTGC<br>GGA  | 60.0                             | 837                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold801_P4_207271 | scaffold801                             | 207271                        | CAAAAAAAAA/CAAAAAAAAAA                                        | TCACAACTTGCTTATTT<br>GCCA | TCATTCTTCCTGCAC<br>TCCT   | 59.4                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold801_P4_211563 | scaffold801                             | 211563                        | AGAGTA/AGAGTACGAGTA                                           | GAATACCGCCTAAGGA<br>CTTGC | GTTGGTTTCAATTACA<br>CCCG  | 60.1                             | 639                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold801_P4_260922 | scaffold801                             | 260922                        | GTATATATATATATATAT/GTATATAT<br>ATATATATATATATAT               | TCGTCCGTAAAAGATA<br>CCGC  | GGACCAAAATTGAGC<br>AACAA  | 60.1                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold801_P4_260992 | scaffold801                             | 260992                        | CATAT/CAT                                                     | TCGTCCGTAAAAGATA<br>CCGC  | GGAGGACCAAAATTG<br>AGCA   | 60.1                             | 661                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold801_P4_27220 | scaffold801                             | 27220                         | CTTTTTTT/CTTTTTTT                                             | CCAAGTCTCCAACTT<br>CCCA     | GACCGTGATGATTCC<br>AAGC  | 60.1                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold801_P4_4383  | scaffold801                             | 4383                          | CCTC/CC                                                       | ATGGTGGTGAGCAACT<br>TTCC    | TATTTTGGATTTTGGCT<br>CGG | 60.0                             | 626                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold801_P4_46766 | scaffold801                             | 46766                         | GTTTTTTTTTT/GTTTTTTTTT                                        | AGGCGTGAAAAAGTTG<br>ATGA    | GATCAAGCCCAAAGG<br>TCAA  | 58.4                             | 350                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold801_P4_55129 | scaffold801                             | 55129                         | ATTTTTTT/ATTTTTTT                                             | TTTGC GTTACGAATTTG<br>ATGA  | CCGGCTTGGTCCTTA<br>TTTT  | 59.2                             | 171                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold801_P4_75364 | scaffold801                             | 75364                         | GTTATTATTATTATTAT/GTTATTATT<br>ATTAT                          | TGCATTCCATTCCCCTT<br>TTA    | ACTAAAACCTATTCGG<br>GGCG | 60.3                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold801_P4_75899 | scaffold801                             | 75899                         | CAAAAAAAAAAAAA/CAAAAAAAAAA<br>A                               | CGCCCCGAATAGGTTT<br>TAGT    | ACCGAATGCATCCTTG<br>TTTC | 60.3                             | 550                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold801_P4_89006 | scaffold801                             | 89006                         | TAAAAAAAAAAAA/TAAAAAAAAA                                      | GGCAATTAATGCATCT<br>AGAAGGT | GGGACGTACACAAGAG<br>GGAA | 58.7                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8054_P4_1926 | scaffold8054                            | 1926                          | AT/A                                                          | TGTTAATCCAATGCCG<br>ATGA    | GAATTTGGGATTTCAAC<br>CGA | 59.9                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold806_P4_81468 | scaffold806                             | 81468                         | AAATCGATT/AAATCGATTAGCCAAT<br>CGATT                           | CGTTCCTGAGGGAATT<br>GTGT    | TTGATTCAATCGATTG<br>GCA  | 60.0                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold809_P4_24118 | scaffold809                             | 24118                         | AATATATATATATATATATATA/AA<br>TATATATATATA                     | AAACAGTTATTTGTGG<br>CGGC    | ATTTGTTGGCATTTTGT<br>GGC | 60.0                             | 782                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                  | Forward primers (5'-3')        | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------|--------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                |                                |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold81_P4_91419   | scaffold81                              | 91419                         | A/AC                                                                                                           | TGAGGAGAAACAAAAT<br>GGGG       | ATGGAAGGGTCGTTGA<br>CATT  | 59.9                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold811_P4_125062 | scaffold811                             | 125062                        | AATATATATATATATATATATA/AA<br>TATATATATATATATATATATATAT<br>A                                                    | TTGGTATTGAACTCGG<br>AGGC       | GGTTTTGCATGCATGT<br>TGAG  | 60.1                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold811_P4_214933 | scaffold811                             | 214933                        | CTTTTTTTTT/CTTTTTTTTT                                                                                          | TCAATAATTACATCTGT<br>GGTCCCTT  | TTTCCCGACTTGGTCC<br>TTTA  | 60.0                             | 309                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold811_P4_290807 | scaffold811                             | 290807                        | TATAATAATAATAATAATAATAAA<br>TAATAATAATAATAATAATAAA/TA<br>TAATAATAATAATAATAATAATAA<br>ATAATAATAATAATAATAATAATAA | AAAATTATTCTACCACA<br>AGGAACACA | TCTGACCCGGAAATCG<br>TAAC  | 59.3                             | 478                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold811_P4_56559  | scaffold811                             | 56559                         | GATATATATATATATATATATAT/G<br>ATATATATATATATATATATATAT                                                          | TTTAACGTGTCGCGTC<br>TTTG       | GAATAAAATGCACCGG<br>CACT  | 59.9                             | 748                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_104865 | scaffold812                             | 104865                        | ATTTTT/ATTTT                                                                                                   | CCCATTGGTATGGGTG<br>ACTT       | TCCACGGCAAAACTA<br>AATC   | 59.5                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_202037 | scaffold812                             | 202037                        | ATTTTTTTTTTT/ATTTTTTTTTTT                                                                                      | AAATAGGGGGACCAAT<br>TTCG       | GCTTACCCAACAAAAC<br>GGAA  | 60.0                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_204592 | scaffold812                             | 204592                        | GAAAA/GAAAAA                                                                                                   | TTTTATGCCGAGGGAG<br>AATG       | CATGGAGAAAACTCTT<br>ACGGG | 60.0                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_213139 | scaffold812                             | 213139                        | TTTTATTTTA/TTTTATTTTATTTTA                                                                                     | GCGCACAAAGTCAAGA<br>ATGA       | TAGTTGGACGTCTTG<br>TCCC   | 60.0                             | 224                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_213627 | scaffold812                             | 213627                        | ATTTTTTTTT/ATTTTTTTTTTT                                                                                        | GGGACAAGACGTCCAA<br>CCTA       | TGTGAATGCCTAAGTG<br>GCTG  | 60.0                             | 694                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                  | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold812_P4_215247 | scaffold812                             | 215247                        | TGG/TG                                                                         | AGAAGGAACAACGAGA<br>ACGC  | TGTCCTTCTCATTGGG<br>AACC   | 59.5                             | 178                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_245558 | scaffold812                             | 245558                        | GAAAAAAAA/GAAAAAAAAA                                                           | CAAAGTCTTCACACAC<br>CGACA | TGTTGACTCCAGTCAC<br>CGAG   | 59.8                             | 736                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_255112 | scaffold812                             | 255112                        | ATTTTTTTTT/ATTTTTTTTT                                                          | CCAAACTGGGGAGAA<br>ACAA   | CCACAAATCTTTTGCAT<br>TTGA  | 59.9                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_259804 | scaffold812                             | 259804                        | A/ACGTATTT                                                                     | TTGTGCAAGGAGAATA<br>CCAAA | TTGCTATTTTGTTCG<br>TTCAAGC | 58.3                             | 374                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_311738 | scaffold812                             | 311738                        | AATTATTATTATTATTATTATT<br>TATTATT/AATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT | TTGTTTGTGGGCAC<br>GTTA    | GGATGCGACCATCTAC<br>TGCT   | 60.0                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_348098 | scaffold812                             | 348098                        | CAAAAAAAAA/CAAAAAAAAA                                                          | ATATAGGTCGGGAAAG<br>CCCT  | TCGTCTGGTCACTTTCT<br>CTGG  | 58.9                             | 732                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_350314 | scaffold812                             | 350314                        | GAAAAAAAA/GAAAAAAAAA                                                           | ACACCACGACGACGTA<br>CAAA  | AATGGTTCTCACTATCG<br>CCG   | 60.1                             | 239                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_356184 | scaffold812                             | 356184                        | CTTTTTTTTT/CTTTTTTTTT                                                          | CTCGTTGACGGATGCA<br>CTAA  | ACCCATTTTCTCGTGT<br>TGC    | 59.9                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_407862 | scaffold812                             | 407862                        | ATTTATCATTTATGTTTTAT/ATTTAT<br>CATTTATGTTTATCATTTATGTTTT<br>AT                 | TTGTGCAAAGACATGG<br>GAAA  | TCAACTGTTGCACCTTC<br>GAG   | 60.1                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_471428 | scaffold812                             | 471428                        | AT/ATT                                                                         | TCTGATGCGTTTCTTG<br>ATGC  | TTGGTGTGTCGAGTTG<br>GGTA   | 60.0                             | 580                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                     | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                   |                              |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold812_P4_482198 | scaffold812                             | 482198                        | GTAATAATAATAATAATAATAAT<br>AA/GTAATAATAATAATAATAATA<br>ATAATAA                                                    | AAATGTCACACTTGCC<br>ATAAAGTT | TGAGCAATTGACTTTT<br>CATTTTT | 59.0                             | 249                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_525957 | scaffold812                             | 525957                        | AT/A                                                                                                              | TCGACTTGTCATCGC<br>TTTG      | CACTCCAGTGCTGAGG<br>GAAT    | 60.0                             | 215                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_526031 | scaffold812                             | 526031                        | TGG/TG                                                                                                            | TCGACTTGTCATCGC<br>TTTG      | CACTCCAGTGCTGAGG<br>GAAT    | 60.0                             | 215                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold812_P4_540816 | scaffold812                             | 540816                        | TTATATATATATATAT/TTATATAT<br>ATATATATATATAT                                                                       | GTAAGTGAAGCGCTT<br>TCGC      | TTGCAATCTCATCACT<br>CGG     | 60.0                             | 916                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold820_P4_15078  | scaffold820                             | 15078                         | A/AG                                                                                                              | TCATCATGGGCTTACG<br>ACCT     | GGCCAAACCCATTAA<br>ACCT     | 60.5                             | 343                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8200_P4_1090  | scaffold8200                            | 1090                          | TTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAAT/TT<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAAT                | GGAAAAATCCATGTTCC<br>TTCG    | CCACGTGGGATATGAC<br>ATGA    | 59.4                             | 729                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8200_P4_526   | scaffold8200                            | 526                           | T/TTC                                                                                                             | CCAACTCATGCACCCC<br>TAGT     | TTTGATTTTGATGTGG<br>GACA    | 60.0                             | 388                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8226_P4_1846  | scaffold8226                            | 1846                          | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTATTAT<br>T | TGATGAGATGGAAGAC<br>CGAA     | TTTTATGTGGCAAGAT<br>CCC     | 59.2                             | 821                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold824_P4_4509   | scaffold824                             | 4509                          | T/TG                                                                                                              | GAGGACGAAAATGACC<br>CAAA     | ATTTCCATCCTTCCTTG<br>GCT    | 59.9                             | 112                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold824_P4_6128   | scaffold824                             | 6128                          | CA/C                                                                                                              | CACCCAGTTTGTAGG<br>GTAA      | CGATTGTGTTGTGACA<br>GGG     | 59.8                             | 191                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                               |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold829_P4_10973  | scaffold829                             | 10973                         | T/TA                                                          | TTTATTTGACAACTCGT<br>TTTTGTT  | GAGCGAATTGAGAAAC<br>GAGG      | 57.1                             | 799                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold829_P4_8235   | scaffold829                             | 8235                          | CTTTT/CTTTTT                                                  | TGTTTGAAATATGACG<br>CGGA      | TTTCGGTCCATTTTAGT<br>CGG      | 60.1                             | 583                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8301_P4_5927  | scaffold8301                            | 5927                          | AGTTAGTTTTTTTATTGTTAGTTTT<br>T/AGTTAGTTTTTT                   | ATGTCGCGTCTTCATC<br>AACC      | ACAATTTATCCGTGTCG<br>CGT      | 61.1                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold831_P4_49277  | scaffold831                             | 49277                         | A/AC                                                          | TTGGATGCACAAGATT<br>GGTT      | AGGTCATTTCCATCCTC<br>CCT      | 59.0                             | 667                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8314_P4_1258  | scaffold8314                            | 1258                          | CTTTTTTT/CTTTTTTT                                             | AATTTAGCTCATTGCTG<br>CCG      | TACCTCCTTTGGAAGC<br>ATGG      | 60.4                             | 353                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8314_P4_868   | scaffold8314                            | 868                           | CAAAAAAAAAAAAA/CAAAAAAAAA<br>AA                               | TGAATGGTTGCATGGT<br>TATCA     | GTGGGAAGTGGTAGAG<br>TGCG      | 59.8                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8314_P4_898   | scaffold8314                            | 898                           | TATAT/TATATGAATAT                                             | TGAATGGTTGCATGGT<br>TATCA     | TGGTGTGAATTTCTTGT<br>GGG      | 59.8                             | 658                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8315_P4_17784 | scaffold8315                            | 17784                         | TATATATATATATATATAT/TATATAT<br>ATATATATATATATATATAT           | AGGGTCTCCAAGTCCT<br>CGAT      | TTTTAGGGCTAGTTGTA<br>CACATGAA | 60.1                             | 377                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8315_P4_18988 | scaffold8315                            | 18988                         | T/TTTA                                                        | AAAAATTTATATTGCGT<br>CAATTTGG | GTGCTGGCCATAGGAA<br>ATGT      | 59.6                             | 565                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8315_P4_20409 | scaffold8315                            | 20409                         | ATT/AGTTTTT                                                   | TTTCCAAC TCGGGAGT<br>AATTG    | TGGAAGAATGTTTAA<br>GGTTTTGA   | 59.1                             | 777                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')       | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                               |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold8315_P4_20462 | scaffold8315                            | 20462                         | GTTT/GTT                                                      | AAAAGGATATTCAACTC<br>TCCAAAAA | CGATTTTGCTACACAAA<br>ATTTC   | 58.7                             | 759                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8378_P4_1029  | scaffold8378                            | 1029                          | GA/G                                                          | GGAGTCGCCACCAAAA<br>TCTA      | GCCACTCAATTCTCAAC<br>CGT     | 60.1                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8378_P4_1988  | scaffold8378                            | 1988                          | C/CG                                                          | AGCAACCACTCGCTTC<br>AAAT      | CAATATTGCTAGGCGC<br>AACA     | 59.9                             | 458                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold841_P4_37303  | scaffold841                             | 37303                         | AT/ATT                                                        | TTTGTGCTCACCTTATT<br>GATGA    | AAAATGGACAATTGGC<br>TTGC     | 58.3                             | 651                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8412_P4_961   | scaffold8412                            | 961                           | TAAAAAAAA/TAAAAAAAAA                                          | TTTTCACATTTCAAAAG<br>CATGA    | TCACATCTTCCTTATGT<br>CCGC    | 58.3                             | 342                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold842_P4_16087  | scaffold842                             | 16087                         | TG/T                                                          | TGGGTACGGTCATTTG<br>TGAA      | TCACTCTCTCGAAAAC<br>CCT      | 59.8                             | 702                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold842_P4_20647  | scaffold842                             | 20647                         | TA/TAA                                                        | TGATTCCTGTAACACC<br>CCAA      | AACCAAACACACAAGG<br>AAATATGA | 58.8                             | 332                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold843_P4_1852   | scaffold843                             | 1852                          | GCC/G                                                         | TTTCGGTCCATTTTGGC<br>TTC      | TCCTGGTCCTCGATTT<br>CATC     | 60.1                             | 283                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8442_P4_1501  | scaffold8442                            | 1501                          | C/A/C                                                         | AACCAAACGGTGCAAT<br>CACA      | AGCCTAGGGTGGACGA<br>AAAT     | 60.0                             | 676                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8445_P4_5721  | scaffold8445                            | 5721                          | TAA/TA                                                        | CATCTACGCGTGTGTT<br>CGTAA     | TGCATAAAATCACCATG<br>CCA     | 59.8                             | 206                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold845_P4_111245 | scaffold845                             | 111245                        | ACGAAT/A                                                      | GGCTCGGTAGGTATCC<br>GTAA  | TTATATTAGTGCGGGC<br>GTGG  | 59.1                             | 166                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_115589 | scaffold845                             | 115589                        | TATT/TATTAATT                                                 | AACGGAAATCGGATGA<br>AATG  | AAAGCAATGAGCATGA<br>TCCC  | 59.8                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_116005 | scaffold845                             | 116005                        | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                 | GGGATCATGCTCATTG<br>CTTT  | TTTTGACCAAAAAGTTT<br>GCTG | 60.0                             | 691                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_11900  | scaffold845                             | 11900                         | TATATTTAAA/TATATTTAAATAATAA<br>TATTTAAA                       | GCTTCTTTGAGATACC<br>GTGCC | TGTGAACACGACCTCT<br>CCCT  | 61.1                             | 535                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_121811 | scaffold845                             | 121811                        | CAATTAATTAATTAAT/CAATTAATTA<br>AT                             | GCGTGTGGGTGATTAG<br>GACT  | GAAAGCGATTGGGAAA<br>ATCA  | 60.0                             | 763                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_126825 | scaffold845                             | 126825                        | TG/T                                                          | TGCGGATTGTAGTCAT<br>TGGA  | AACAGAAGCAAACCGA<br>CCTC  | 60.1                             | 678                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_132751 | scaffold845                             | 132751                        | CAAATAAAT/CAAATAAATAAAT                                       | AGTGTGTTTGGGTTG<br>GGAG   | TCGATTTGACATTGCG<br>TGT   | 59.9                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_132810 | scaffold845                             | 132810                        | GA/GAAATTCTAA                                                 | AGTGTGTTTGGGTTG<br>GGAG   | TCGATTTGACATTGCG<br>TGT   | 59.9                             | 526                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_133006 | scaffold845                             | 133006                        | T/TTATTAA                                                     | CCACCAAAAACCAACC<br>AACT  | GGCCTAACCTGGAAGC<br>CTAT  | 59.7                             | 730                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_149135 | scaffold845                             | 149135                        | TAAGTTA/TAAGTTATCGATTCAACA<br>AAGTTA                          | TCAAACGGTGGTGTC<br>AAAA   | AATTGGAACGACCCG<br>AAAA   | 60.0                             | 640                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold845_P4_162524 | scaffold845                             | 162524                        | TAAAAAAAAA/TAAAAAAAA                                          | AATGCTTTGAAAAGGC<br>AACG | AAGAGCAAGAGCGCAG<br>AGAC      | 60.2                             | 364                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_170397 | scaffold845                             | 170397                        | GATATAATATATAATATATA/GATATA<br>ATATATA                        | ATTTGGTGCGCATGAT<br>AAGA | TTTACAAGGGTATTTTT<br>GTGATTAC | 59.1                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_170625 | scaffold845                             | 170625                        | ATTT/ATTTT                                                    | ATTTGGTGCGCATGAT<br>AAGA | AAAAATGAGGTGGGT<br>AGAAATTA   | 59.1                             | 777                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_17115  | scaffold845                             | 17115                         | ATTT/ATT                                                      | AAATAATCAAGGCAC<br>GCAC  | TGGTATCTGGGGTTGA<br>GGAC      | 60.0                             | 482                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_171604 | scaffold845                             | 171604                        | ATTTTTTTT/ATTTTTTT                                            | TGTCGGCAATCATGCA<br>ATTA | CAACGGGTAACTTGAA<br>ACAGG     | 61.0                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_175162 | scaffold845                             | 175162                        | AA/AATTA                                                      | AAAGGGCTCCTGCAGG<br>TAAT | TGATTAATTTTGAACG<br>GCA       | 60.1                             | 435                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_17551  | scaffold845                             | 17551                         | TGGGGGG/TGGGGG                                                | GTCCTCAACCCAGAT<br>ACCA  | AAAAAGTGCGAAAGTG<br>GCA       | 59.8                             | 104                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_175667 | scaffold845                             | 175667                        | TCACACACACAC/TCACACACAC<br>AC                                 | TGCCGTTGCAAAATTA<br>ATCA | CATGTTCCGACCACGT<br>ATTG      | 60.1                             | 835                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_17586  | scaffold845                             | 17586                         | CTTTTTTT/CTTTTTT                                              | GTCCTCAACCCAGAT<br>ACCA  | TTTGTAGCTTCCTCACT<br>TGG      | 59.8                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_19068  | scaffold845                             | 19068                         | T/TC                                                          | TGTCCAACAATTTGAC<br>GGTT | CGCATTTTCGTTCTATC<br>ATTAGC   | 58.9                             | 991                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')         | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                                 |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold845_P4_19378  | scaffold845                             | 19378                         | AAAATTTGTAAAT/AAAAT                                           | CAATATGACACTTTTCG<br>TGCG | TTCTCGGTCAACAACA<br>CCAA        | 59.2                             | 483                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold845_P4_19791  | scaffold845                             | 19791                         | ATTTTTTTT/ATTTTTTTTT                                          | TCGATGTCAACGTTGG<br>TGTT  | AAGAAAAATGCCAAGC<br>TAACAAA     | 60.0                             | 318                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold845_P4_2172   | scaffold845                             | 2172                          | TTA/TCTTTAGTA                                                 | CAACATTTTGGGTGCA<br>TTTG  | TGGTTATTTTGCATGTA<br>GCGA       | 59.8                             | 657                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold845_P4_22031  | scaffold845                             | 22031                         | ATT/ATTT                                                      | CCCTGAAATGCACAAC<br>AAGA  | TTGTGGTGGCTAAAA<br>GCCT         | 59.7                             | 651                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold845_P4_22323  | scaffold845                             | 22323                         | CAA/CAAA                                                      | AGGCTTTTAGCCACCA<br>ACAA  | AATGTGGGAAAAACAA<br>TGCC        | 59.7                             | 226                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold845_P4_23284  | scaffold845                             | 23284                         | GA/GAA                                                        | CAAACCTAAGCTCCAT<br>CCCT  | CATGAGTACCAATCAT<br>GCCAA       | 59.3                             | 407                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold845_P4_23562  | scaffold845                             | 23562                         | CT/C                                                          | TCGATCAACCTAGATT<br>GGCA  | TCTGAACACTATCGTAT<br>CATGTTTCTT | 59.2                             | 655                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold845_P4_24715  | scaffold845                             | 24715                         | AAATACTGAATA/AAATA                                            | TGCGGTTTAAGATTGG<br>AACA  | GTTGGGTCTTGTGGGA<br>ATGT        | 59.2                             | 203                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold845_P4_266300 | scaffold845                             | 266300                        | GTTTTTT/GTTTTTTTT                                             | GCGATTCATCATTCTC<br>CGTT  | GGAGAGGCAGAAGAG<br>GTGTG        | 60.0                             | 495                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold845_P4_281210 | scaffold845                             | 281210                        | TCCCC/TCCC                                                    | TGCAAAGATCAATCTT<br>GGGTT | GTGGGTTACGTCCAGT<br>CCTC        | 59.6                             | 806                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                         | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                       |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold845_P4_314352 | scaffold845                             | 314352                        | CAATAAATAAATAAATAAATAA<br>ATAAATAAATAAATAAATAA/C<br>AATAAATAAATAAATAAATAA<br>TAAATAAA | ACAAGAAATGACCGAC<br>AGGG   | CACCGAAAAACCAAG<br>AAGG   | 60.0                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_31762  | scaffold845                             | 31762                         | GAAAAAAAA/GAAAAAAAAA                                                                  | TTTTGTCTATCAGCGG<br>GGAC   | AGAGAATGTGGCCTTC<br>ACAA  | 60.1                             | 776                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_32097  | scaffold845                             | 32097                         | AC/A                                                                                  | TTATGGGGGAGGAAGT<br>TTGA   | CCCACATGTCAGCAT<br>AAAT   | 59.4                             | 878                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_331956 | scaffold845                             | 331956                        | TG/TGG                                                                                | TTGCTTGAAAGGAAA<br>ATCG    | GGGGCCAAATAATGTT<br>GCTA  | 60.2                             | 802                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_37680  | scaffold845                             | 37680                         | ATTT/ATTTTT                                                                           | GCAGTGTTAGGATGAA<br>ACCACA | CCCATGCAAGTTTAAT<br>GGAGA | 60.0                             | 484                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_38901  | scaffold845                             | 38901                         | CAAAATAAAATAAAAT/CAAAATAAA<br>ATAAAATAAAATAAAAT                                       | GGTGCAAAATGAGAAGC<br>ACAA  | AAAAGCATGCTGTCAA<br>CCG   | 59.8                             | 584                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_39649  | scaffold845                             | 39649                         | TTT/TTTCTT                                                                            | TGAAACGTTGAAAATG<br>GCAC   | TTGTTATCGCAGGGGA<br>AATC  | 59.6                             | 251                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_39704  | scaffold845                             | 39704                         | GAAAAA/GAAAAA                                                                         | TGAAACGTTGAAAATG<br>GCAC   | TTGTTATCGCAGGGGA<br>AATC  | 59.6                             | 251                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_41535  | scaffold845                             | 41535                         | TAAAA/TAAAA                                                                           | GCATTGCAACTTTGT<br>GTGC    | ACTTGGTGGGTCATGG<br>AAAA  | 60.3                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_41593  | scaffold845                             | 41593                         | TAAA/TAAAA                                                                            | GCATTGCAACTTTGT<br>GTGC    | ACTTGGTGGGTCATGG<br>AAAA  | 60.3                             | 397                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold845_P4_47867 | scaffold845                             | 47867                         | GAAAA/GAAAAA                                                  | AAGGGAAAAGGGTGTG<br>TGTG    | AATGCGACGTTTGATT<br>ATCG    | 59.9                             | 999                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_48050 | scaffold845                             | 48050                         | ATT/A                                                         | TTGATAGGGATTGGAA<br>TAAACAA | TTTTGTGTTGGTGCGA<br>CATT    | 57.6                             | 427                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_48945 | scaffold845                             | 48945                         | A/AG                                                          | TTTCGAACATTGGTTGT<br>GCT    | GCAAAAAGGGGAGTGG<br>TGTA    | 59.2                             | 935                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_59954 | scaffold845                             | 59954                         | G/A/G                                                         | CGTTTTGAAACTTTCGT<br>GTTT   | AAGTTTCGAATGTGGG<br>GATG    | 57.0                             | 460                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_64302 | scaffold845                             | 64302                         | CT/CTGT                                                       | TGGATTCGTGTCCATC<br>TGAA    | ACAATTGCGCAAATTCC<br>TCT    | 60.0                             | 610                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_81876 | scaffold845                             | 81876                         | GAAAAAAAA/GAAAAAAAA                                           | GGTTTTTGTTTGAAT<br>GTGG     | AAAAGGGAGGGGCAAT<br>CTAA    | 60.1                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_84201 | scaffold845                             | 84201                         | G/GT                                                          | TTTTTCAAGTCACGCCA<br>CAC    | AAACCAGTTTTTGAAT<br>GCG     | 59.7                             | 260                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold845_P4_94960 | scaffold845                             | 94960                         | TTTATT/TTTATTATT                                              | ACATGGGTCAAGCCCA<br>TTAG    | TGACTGATGTTAAGTAT<br>GCCCCG | 59.8                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8479_P4_1013 | scaffold8479                            | 1013                          | GTTTTTT/GTTTTTTTT                                             | GGGGCATGTTTGTTT<br>AGTTT    | CCCTCCCGAACATATC<br>ATCA    | 60.1                             | 815                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8479_P4_813  | scaffold8479                            | 813                           | AA/AATTTTTA                                                   | GGGGCATGTTTGTTT<br>AGTTT    | AAGTAGTCTTTGGGAA<br>ACGGC   | 60.1                             | 662                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold848_P4_149214 | scaffold848                             | 149214                        | ATAATAATA/ATAATAATAGTAATAAT<br>A                              | ACGGAGGTGACGATGT<br>AAGG | GTGGACAACATATCCG<br>GACC | 60.0                             | 453                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold848_P4_226354 | scaffold848                             | 226354                        | GTCT/GT                                                       | TTTTGGCGTAGTGTGT<br>GCTC | CAGCAAACGTTCTCCG<br>TTTT | 59.9                             | 678                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold848_P4_24049  | scaffold848                             | 24049                         | CTTTTTTTT/CTTTTTTTTTT                                         | CAAACGAAAATGCAAG<br>CTCA | GCTACGCACCCAAGAA<br>GCTA | 60.0                             | 883                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8493_P4_17800 | scaffold8493                            | 17800                         | ATTTTTTTT/ATTTTTTTTTT                                         | TGCACAGTCAATAGGC<br>TTCG | TGCGGGAGACATTGAT<br>GATA | 60.0                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8493_P4_18046 | scaffold8493                            | 18046                         | ATTTT/ATTT                                                    | TGCACAGTCAATAGGC<br>TTCG | TGCGGGAGACATTGAT<br>GATA | 60.0                             | 547                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8493_P4_18958 | scaffold8493                            | 18958                         | GAAAAAAAAA/GAAAAAAAAA                                         | TTGGGCCCCATGAAAT<br>AATA | AAAAGCCTCATTGGAA<br>GCCT | 60.0                             | 373                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8493_P4_9496  | scaffold8493                            | 9496                          | A/AT                                                          | CGACCATGATTTAACG<br>ACCA | GTTTTCAAGAGGTGGC<br>CTTG | 59.4                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold855_P4_30893  | scaffold855                             | 30893                         | ATT/ATTT                                                      | AGGCCGTGATGTTTT<br>GAAC  | GCATCATATGTGTGGG<br>CAAG | 60.0                             | 268                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold855_P4_31194  | scaffold855                             | 31194                         | ACCC/ACC                                                      | CTCGTACGCTTTTGGT<br>GTGA | GTAGGGGGTAGAAAAC<br>CCCA | 59.9                             | 556                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold855_P4_31470  | scaffold855                             | 31470                         | TTAATATCC/T                                                   | AATTGGATACCCCTTTT<br>GGC | GTAGGGGGTAGAAAAC<br>CCCA | 60.0                             | 384                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                                |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold8565_P4_6875  | scaffold8565                            | 6875                          | GTTTTTTTTT/GTTTTTTTTT                                         | TGACCAAAATCCATCC<br>CTTC       | TTTACAGCGCTTGTTCC<br>AAA    | 59.7                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8586_P4_1534  | scaffold8586                            | 1534                          | GTTTTTTTTTTTT/GTTTTTTTTTTT                                    | TTCCACATTACCACTC<br>GATACG     | CCCAACAATAAGAGGC<br>ATGT    | 59.9                             | 357                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold859_P4_19948  | scaffold859                             | 19948                         | A/ATTATTT                                                     | TTTAAGTAGACTGCCTT<br>ATCGTGTTT | AACTGGAAGTCAACAG<br>GTATGGA | 59.0                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold859_P4_22608  | scaffold859                             | 22608                         | ATTTTTTTTTTT/ATTTTTTTTTT                                      | CGCGACTTTCAAAAC<br>ATGA        | GCTCTTCATGTCCAAC<br>AGCA    | 59.8                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold859_P4_27190  | scaffold859                             | 27190                         | CT/CTATT                                                      | TGGAGGTAAACTCAA<br>GCCG        | ACTTGCATCCTCTGCA<br>TCC     | 60.2                             | 579                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold859_P4_52290  | scaffold859                             | 52290                         | GTTTTTTTTTTT/GTTTTTTTTTTTT                                    | TTGGCTCCCAAATTA<br>ACG         | CGACGCTTGATCGTTA<br>ATTG    | 59.9                             | 612                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold859_P4_95458  | scaffold859                             | 95458                         | C/CAA                                                         | GTAAAGGGTCACCAAC<br>CGAA       | GCCCTCAGATGAGAGT<br>CAGG    | 59.8                             | 714                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold862_P4_34938  | scaffold862                             | 34938                         | GTTT/GTT                                                      | CGGAACCCGAAACAA<br>GTTA        | CGGAACCCGAAAAACA<br>GTTA    | 60.0                             | 919                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8620_P4_950   | scaffold8620                            | 950                           | GTCCTAATTCCTAATT/GTCCTAATT                                    | AGCCAAGGGAGGATGA<br>AAAT       | TTAACCAACCTTGTGC<br>CTCC    | 59.9                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold864_P4_135809 | scaffold864                             | 135809                        | T/TAGA                                                        | TGTGAGGTGGTAGGG<br>GAGTC       | GACTTGATGCATCTTTG<br>CGA    | 60.0                             | 398                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                         |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold8646_P4_2561  | scaffold8646                            | 2561                          | ATT/AAATTT                                                              | CTTCCTCACAAATGAT<br>GCGA | ATTGTAATAGGAGGC<br>CGCT  | 59.8                             | 621                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8646_P4_2745  | scaffold8646                            | 2745                          | TAAAAA/TAAAAAA                                                          | AGTCTACGACGAAGCG<br>TTCC | TCCATAGGAGGTCGAT<br>GGTC | 59.5                             | 532                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8646_P4_6918  | scaffold8646                            | 6918                          | GATATATATATATATATATATATA<br>TA/GATATATATATATATATATATA<br>TATATATATATATA | TCCATTTGCTTCTGCCT<br>CTT | CGAAGAAAATGAAAAC<br>GGGA | 60.0                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold866_P4_116963 | scaffold866                             | 116963                        | AATATATATATAT/AATATATATAT<br>ATATATAT                                   | AAGAATTTAATGCGTTG<br>CGG | GTTGGTCCCTAGCAC<br>CGTA  | 60.1                             | 471                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold866_P4_142556 | scaffold866                             | 142556                        | TAAAA/TAAAAA                                                            | GCAGCGGTTCCAAAAT<br>AGAG | GGTGGCATAGTATCAC<br>GCCT | 59.8                             | 571                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold866_P4_142956 | scaffold866                             | 142956                        | CTT/CT                                                                  | GGATCCCCAATCGATA<br>ACCT | CTGTTGAGCCTTAGGG<br>CAAG | 60.0                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold866_P4_36277  | scaffold866                             | 36277                         | ACCC/ACC                                                                | GAACAACAAGTGGGAT<br>GCCT | TGTGAAAAATGAACAC<br>CCCA | 60.0                             | 360                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold868_P4_25892  | scaffold868                             | 25892                         | ATA/ATATGCCTA                                                           | TTCGTTGCACATGTTT<br>GGTT | TCATTTTCGTCTCTTT<br>GGG  | 60.0                             | 464                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold869_P4_26934  | scaffold869                             | 26934                         | CAAAAA/CAAAAAA                                                          | GCACTGCCCCAAGAAT<br>TTTA | GTGGAGATCACTCGGG<br>TTGT | 60.1                             | 209                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold87_P4_167740  | scaffold87                              | 167740                        | GNNNNNNNNN/GNNNNN                                                       | GAAACAAGCGATCAAG<br>AGCC | GTCGACCTTGTTTTG<br>CATT  | 60.0                             | 412                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold87_P4_374332 | scaffold87                              | 374332                        | CAAAAAAAAA/CAAAAAAAAA                                         | ATGGTTAGGTACGTGCAAAA    | CAAGCTCGTCTAGTTCCGTT    | 57.3                             | 898                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold87_P4_386465 | scaffold87                              | 386465                        | GAAGAGAAAG/GAAGAGAAAGAGAAAG                                   | CAAAGAAGCACCAACAAGCA    | CACCCATCCAAATCGTTCT     | 60.0                             | 447                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold87_P4_468940 | scaffold87                              | 468940                        | TT/TTCGGAT                                                    | GAGAATGGCAGCCCAAATA     | TCGGTATTTGCCATGAGACA    | 60.0                             | 533                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold87_P4_506525 | scaffold87                              | 506525                        | TGA/T                                                         | GCGTGTTCCACGTGATAATG    | TGAGTGCTCGTGATTTGAGC    | 60.0                             | 796                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold87_P4_521197 | scaffold87                              | 521197                        | TAAAAAAAAA/TAAAAAAAAA                                         | TCTTGTGCATGAATCCCAAA    | CATACGTCGTGGGACTGTTG    | 60.0                             | 528                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold87_P4_571525 | scaffold87                              | 571525                        | GAAAAAAAA/GAAAAAAAA                                           | AAACGCAATCCTTGAGTTCG    | AGATTGCCTTTTCGGGTTTT    | 60.2                             | 211                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold87_P4_587649 | scaffold87                              | 587649                        | ATTTTTTT/ATTTTTTTT                                            | GGGTCCACTTCTACCCATT     | GTGCAGACAATTGGAGGGT     | 60.1                             | 501                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold87_P4_594427 | scaffold87                              | 594427                        | CAGATA/CA                                                     | TGACCGATTTGGTGACTGAA    | TTGGTGATCATGATGCTGGT    | 60.1                             | 555                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold87_P4_597245 | scaffold87                              | 597245                        | TAAAAAAAAA/TAAAAAAAAA                                         | TAAGCCAAATAACCCCTCC     | TCTCCCATCCTCTCATCAC     | 60.1                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold870_P4_11315 | scaffold870                             | 11315                         | ACTTTTCTTT/ACTTTTCTTTCTTT                                     | CGAAACATTTGCAAGAGAAGA   | CATTGCCACAACATTGCTAA    | 58.2                             | 503                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                  | Forward primers (5'-3')     | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                                |                             |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold870_P4_32135  | scaffold870                             | 32135                         | CTTTTTTT/CTTTTTTTTTTT                                                                                                                          | CATGAGGCCACCACT<br>TTTT     | TCGTGGTTTTCTTGGG<br>AGAC    | 60.0                             | 407                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold870_P4_39934  | scaffold870                             | 39934                         | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTAT/TTTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTAT                                       | AGAGGCCAAACAAGAAC<br>CGAA   | GGTGAGCCACCTTCAT<br>TTGT    | 59.9                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold870_P4_55397  | scaffold870                             | 55397                         | AACAAATATCTAGATTTACAAATA<br>TCTAGATATTTACAAATATCTAGATA<br>TTT/AACAAATATCTAGATTTTACAA<br>ATATCTAGATATTTACAAATATCTAG<br>ATATTTACAAATATCTAGATATTT | TTGGAAGGAGCCCTTA<br>CCTT    | ATCTGCCATTGAATTA<br>CGG     | 60.1                             | 527                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold870_P4_82445  | scaffold870                             | 82445                         | GT/GTT                                                                                                                                         | TGGTGGTGCAATTCAC<br>ATCT    | TTTCACCGTCATGCTTT<br>TTG    | 60.0                             | 540                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold873_P4_105352 | scaffold873                             | 105352                        | TAAAAAAAA/TAAAAAAAA                                                                                                                            | TTCTCCTGAAGCTGT<br>CGGT     | TCCGGTACATAAAGCG<br>TTCC    | 60.0                             | 289                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold873_P4_18275  | scaffold873                             | 18275                         | GATATATATATATATATAT/GATAT<br>ATATATATATATATATAT                                                                                                | TGTTGGGTCCACAAAG<br>AGAG    | TGTTGTTCTCCTCTGAC<br>ACAATG | 58.7                             | 402                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold873_P4_18311  | scaffold873                             | 18311                         | GAAAAAA/GAAAAA                                                                                                                                 | TGTTGGGTCCACAAAG<br>AGAG    | TGTTGTTCTCCTCTGAC<br>ACAATG | 58.7                             | 402                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold873_P4_18746  | scaffold873                             | 18746                         | AATATATATATATATATAT/AAT<br>ATATATATATATATATATATAT                                                                                              | CATTGTGTCAGAGGAG<br>AACAACA | TTTCTTCCCACCTT<br>GTG       | 60.2                             | 628                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold873_P4_308551 | scaffold873                             | 308551                        | CCCAA/CCCAACCAA                                                                                                                                | ATTGGGGCACCCCTTT<br>ATTC    | AGGTTTTCAACCTAGC<br>GGGT    | 60.0                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold873_P4_344880 | scaffold873                             | 344880                        | GGTTGT/GGTTGTTGT                                                                                                                               | GCCCTTCTTCTTTTCCT<br>GGT    | ATAATGGCGTTCGGAT<br>TGAC    | 59.7                             | 310                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                             | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                                           |                           |                           |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold873_P4_76909  | scaffold873                             | 76909                         | ATTTTTTT/ATTTTTTTT                                                                                                                                        | CAGTTGCAAATTGTGA<br>CCGT  | CAAGGCAAGCACACAT<br>AATCA | 59.6                             | 503                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold8734_P4_1079  | scaffold8734                            | 1079                          | TAAA/TAAAA                                                                                                                                                | CTGTGACACCCTAAAT<br>CCCA  | GATCTATGAGGACAGG<br>GCCA  | 58.4                             | 798                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold8734_P4_801   | scaffold8734                            | 801                           | TAA/TAAA                                                                                                                                                  | TTGGGCGAAAATGGAT<br>AAAG  | CCCCGCTCTGATAGGT<br>GATA  | 59.9                             | 802                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold876_P4_108685 | scaffold876                             | 108685                        | GATATATATATATATATATATATA<br>TAT/GATATATATATATATATATAT<br>ATATATATATATAT                                                                                   | TGCAAAATTGTCGTGAA<br>AACA | TCATCTCACCCCTTACC<br>TCG  | 58.7                             | 482                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold876_P4_119606 | scaffold876                             | 119606                        | AATATATATATATATATATATATAT<br>ATATATATAT/AATATATATATATATA<br>TATATATATATATATAT                                                                             | AAGAGCGCTGGAAAAG<br>ACCT  | ATGTGAATCCCACCAG<br>GAAA  | 60.5                             | 582                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold876_P4_147256 | scaffold876                             | 147256                        | CATATATATATATATATATATAT/CAT<br>ATATATATATATATATATATATATAT                                                                                                 | AAGATCAAGCAATGCC<br>AACC  | TCAATTTGTCAACCGAT<br>CCC  | 60.1                             | 233                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold876_P4_369643 | scaffold876                             | 369643                        | A/AC                                                                                                                                                      | AACGTACTGCCTATCA<br>CGGG  | GGTAAGGGCTCCTTCC<br>AAAC  | 60.0                             | 836                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold876_P4_426612 | scaffold876                             | 426612                        | CTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAATA<br>TAATAATAATAATAA/CTAATAATAAT<br>AATAATAATAATAATAATAATAATA<br>TAATAATAATAATAATAATAATAATA<br>ATAATAA | CCTGCTCCTCCAAGTC<br>AGTC  | TACAAACGCAATCCGA<br>ACAA  | 60.0                             | 647                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold876_P4_5309   | scaffold876                             | 5309                          | T/TA                                                                                                                                                      | CCCTTTTGTCTTCTTGT<br>GGC  | TTCGGTTCTTGTTTGGC<br>TCT  | 59.7                             | 382                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold876_P4_5429   | scaffold876                             | 5429                          | TTTATTATTATTATTATTATTATT<br>ATTATT/TTTATTATTATTATTATTAT<br>TATTATTATTATTATT                                                                               | AGAGGCAACAAGAAC<br>CGAA   | TACGGCATAACAATTG<br>CAGC  | 59.9                             | 566                                           | INTERGENIC                                           | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                              | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                            |                            |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold8803_P4_7473  | scaffold8803                            | 7473                          | ATTTTTTTTT/ATTTTTTTT                                                                       | AAGATTAAAGGGTGGT<br>GTTGGA | AGTTTGTAAACCGTGC<br>GTTC      | 59.7                             | 249                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8803_P4_7526  | scaffold8803                            | 7526                          | GATATATATATATATA/GATATATATA<br>TATATATA                                                    | AAGATTAAAGGGTGGT<br>GTTGGA | AGTTTGTAAACCGTGC<br>GTTC      | 59.7                             | 249                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold882_P4_318763 | scaffold882                             | 318763                        | CAAAAAAAAA/CAAAAAAAAA                                                                      | TCGCTAACCACAACT<br>TGGA    | GAAACTCCAAGGATG<br>GCAA       | 59.3                             | 834                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold882_P4_318842 | scaffold882                             | 318842                        | ATTTTTTTTT/ATTTTTTTTTT                                                                     | AAAGGATTCATAGGCC<br>GAAT   | GAAACTCCAAGGATG<br>GCAA       | 57.6                             | 697                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold882_P4_38532  | scaffold882                             | 38532                         | GATAATAATAATAATAATAATAA<br>TAATAATAATAATAATA/GATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATA | AAAGGCCAAGGTGATT<br>GAGA   | TGGGAAGCTTTCAGAG<br>CCTA      | 59.7                             | 725                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold882_P4_432656 | scaffold882                             | 432656                        | GTT/GT                                                                                     | TGAATGAGCTTGATTG<br>TGCC   | CATGGTAGCTCCCGAC<br>ATTT      | 59.8                             | 127                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold882_P4_438894 | scaffold882                             | 438894                        | CATATATATATATATATATATATA<br>TA/CATATATATATATATATATATATA<br>TATATATA                        | AATTGAAATTTGGCTC<br>GGA    | ATGGAGGAAGGAGGGA<br>GAAA      | 59.5                             | 417                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold882_P4_446893 | scaffold882                             | 446893                        | GTTT/GTTTT                                                                                 | TGGTTGGTTTTTGTTG<br>TGAA   | TCACGGGCAACACAA<br>TTTA       | 59.8                             | 644                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold882_P4_486809 | scaffold882                             | 486809                        | CTTTAATTGTTTAATTGT/CTTTAATT<br>GT                                                          | CACCAATGCGTTTGAT<br>GTTC   | AAACCATCCTCCGTGA<br>ACTTT     | 60.0                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold882_P4_639280 | scaffold882                             | 639280                        | CTTTTTTTTT/CTTTTTTTTTT                                                                     | AGGAATGACCAAAACG<br>TTCG   | CACTTGATTATTGAAA<br>CACAAAGGT | 60.0                             | 881                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold882_P4_70530  | scaffold882                             | 70530                         | CAAAAA/CAAAAA                                                                 | CACATCAACAGCAGCC<br>TTGT  | TGATGTTGCCTCTGTTT<br>TGC  | 59.9                             | 385                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold882_P4_95047  | scaffold882                             | 95047                         | AATATATATATATATATATA/AATATA<br>TATATATATATATATA                               | CGTTGGTGATAGTCGT<br>GGTG  | TGTGATTTTACGCGTAT<br>CCAA | 60.0                             | 894                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold882_P4_99112  | scaffold882                             | 99112                         | GTATATATATATATATATATATATAT<br>ATAT/GTATATATATATATATATATAT<br>ATATATATATATATAT | AACCGATGTTTCGATCC<br>ACTC | CACCCCTCGTTGCTTG<br>TACT  | 59.9                             | 518                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8825_P4_968   | scaffold8825                            | 968                           | TAAAAA/TAAAAA                                                                 | AATCGATTGGCATCAA<br>CACA  | CCAGTCAAGCATTCCC<br>ATCT  | 59.9                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold8836_P4_981   | scaffold8836                            | 981                           | GAAATAAAAA/GAAA                                                               | CAACACAACAAGAACG<br>AGCAA | TCCAAGTAGGCTCTGCC<br>CAAT | 59.9                             | 288                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold884_P4_132657 | scaffold884                             | 132657                        | CAAAA/CAA                                                                     | TTGCCACATCCAAAAT<br>GCTA  | AGTGCCAGAGTCGGGA<br>ATTA  | 60.1                             | 739                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold886_P4_101914 | scaffold886                             | 101914                        | TT/TTAGACGTGACACAT                                                            | TGATGGAGGAAGAGAT<br>GCAG  | TGATGTGGCCCATTTA<br>ACAA  | 58.9                             | 694                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold886_P4_172563 | scaffold886                             | 172563                        | AATATATATATATATATATATATAT/A<br>ATATATATATATATATATATATATA<br>T                 | AAGCCGACAATTTGTTT<br>TTCT | TCATTCTGATTTGGG<br>GGTA   | 57.9                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold886_P4_52860  | scaffold886                             | 52860                         | AATATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATATA<br>TATATATATAT     | CACCGTTTGTCACTTT<br>CCAG  | TCGGATTCTCGAGCAA<br>TTTA  | 59.2                             | 320                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold89_P4_101242  | scaffold89                              | 101242                        | TAAAAAAA/TAAAAA                                                               | TGTGTAACCTCGTGCGT<br>TTCG | CGGGGTATATGGAATG<br>GTGT  | 60.9                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                                   |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold89_P4_212189 | scaffold89                              | 212189                        | ATTTTTTTT/ATTTTTTT                                                | CAACCCAGCAGCCAA<br>TAAT  | GCATAGGTGCACATGA<br>AAGG | 60.0                             | 377                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold89_P4_234540 | scaffold89                              | 234540                        | AATATATATATATATATATATATAT/A<br>ATATATATATATATATATATATATATA<br>TAT | AGCAATACACACACAA<br>CGCA | CCGTGGTCGTAAACC<br>GTAT  | 58.8                             | 476                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold89_P4_24707  | scaffold89                              | 24707                         | AAC/A                                                             | ATGATGGAGAAGAAGC<br>GTGC | ATTCCGCTTATTCGA<br>GGAC  | 60.1                             | 562                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold89_P4_58905  | scaffold89                              | 58905                         | ATATTTATTTATTTAT/ATATTTATTT<br>ATTTATTTAT                         | CATCAAAGACCCACAG<br>TTGC | TCAATCTCCCTTTGAG<br>CAC  | 59.1                             | 546                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold891_P4_10627 | scaffold891                             | 10627                         | GAAAAAAAAAAAAA/GAAAAAAAAAAAA<br>AA                                | ACCAGGAAAAGAAGAA<br>GGGC | AAAGCGCTTGTGTAA<br>ACGC  | 59.7                             | 677                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold892_P4_26717 | scaffold892                             | 26717                         | ATT/ATTT                                                          | TCAAGCTTCCTCTCCA<br>CACA | AATTAATATCCACGCA<br>CGC  | 59.5                             | 255                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold892_P4_29801 | scaffold892                             | 29801                         | CAAAAA/CAAAAA                                                     | GAAGCCATGAAACCT<br>TCCA  | ATGCAAAACATTTCCAC<br>CTC | 60.1                             | 392                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold892_P4_38411 | scaffold892                             | 38411                         | AATATATATATATATATAT/AATATAT<br>ATATATATATATATAT                   | GTAATGGCAGGTAGA<br>GGCG  | ACCACTAACTCGGTGC<br>CAAC | 59.7                             | 826                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold892_P4_44352 | scaffold892                             | 44352                         | TAAAAAAAA/TAAAAAA                                                 | CTGAGTTGCGACGAGA<br>GTTG | TTGGAAGGAGCCCTTA<br>CCTT | 59.8                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold892_P4_63033 | scaffold892                             | 63033                         | TAAAAAAAA/TAAAA                                                   | TCCCAACCCAAATAAA<br>CCAA | CTCAACATGCATGCAA<br>AACC | 60.0                             | 515                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)                | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                       |                                  | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------|----------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                               |                           |                          |                                  |                                               | Sequence components of <i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| scaffold893_P4_10885  | scaffold893                             | 10885                         | A/AG                                                                          | GAGATTGTGGCCAATT<br>CGAT  | CTCTCACCCAAGAAGA<br>TCGC | 59.9                             | 395                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold895_P4_104837 | scaffold895                             | 104837                        | GAC/GACAACAAC                                                                 | TCCCATCAACCATAGC<br>CTTC  | TCGAATGGCGGTTCC<br>TTAG  | 59.9                             | 720                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold895_P4_140163 | scaffold895                             | 140163                        | TTATATATATATATATATATATATA<br>TATATATAT/TTATATATATATATATA<br>TATATATATATATATAT | CGAGGCACGTTGAAGA<br>AAAT  | ACGCCAAAGGTAGCAA<br>TTCA | 60.2                             | 439                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold895_P4_91931  | scaffold895                             | 91931                         | GATAATAATAATAATAATAATAA<br>TA/GATAATAATAATAATAATAAT<br>A                      | TTGCTCCTACGTATCC<br>CCAG  | CTCAATCGTGGGTGAC<br>CTTT | 60.1                             | 370                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold895_P4_93605  | scaffold895                             | 93605                         | GTTATTATTATTATTATTATTATT<br>ATTATTATT/GTTATTATTATTATTAT<br>TATTATTATTATTATT   | AGAGGCCAAACAAGAAC<br>CGAA | GAAGCCGAGAAAACGA<br>CTTG | 59.9                             | 399                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold896_P4_22295  | scaffold896                             | 22295                         | G/GA                                                                          | GAAAAACAAGACCCGC<br>GATA  | TCACCCCTTGATCCTCT<br>CAC | 60.1                             | 433                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold896_P4_47144  | scaffold896                             | 47144                         | TAAA/TAAAA                                                                    | AGGGAGAGCAGAAAATG<br>ACCT | TGTGCATCAAATAGGC<br>GTGT | 59.9                             | 259                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold896_P4_63807  | scaffold896                             | 63807                         | GTTTTTTTTTTT/GTTTTTTTTTTT                                                     | ACTCCTCCACAAGCCT<br>CTGA  | CTCCCCCTTTTGGCAT<br>AAT  | 60.0                             | 894                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold900_P4_12737  | scaffold900                             | 12737                         | GCAC/GCACTAGAACAC                                                             | CCATTTTGTCTCTG<br>CAT     | AAGGCCAATGCCACAT<br>AAAG | 59.9                             | 604                                           | INTERGENIC                                  | --                               | --                    | --  |
| scaffold901_P4_141337 | scaffold901                             | 141337                        | CAAACCCTAAA/CAAACCCTAAACCC<br>TAAA                                            | TTGATCATAGCATTTG<br>GGCA  | TGGAAACCGAAACCA<br>ATTC  | 60.0                             | 651                                           | INTERGENIC                                  | --                               | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold901_P4_23860  | scaffold901                             | 23860                         | TTT/TTTATT                                                    | TCAAGCCACATAATTG<br>GTCC    | CGTGAGGCTGTTGGGA<br>TATT | 58.4                             | 591                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold9024_P4_1748  | scaffold9024                            | 1748                          | GA/GAA                                                        | TGACCAAAATGTTTCAG<br>CCAA   | GCCATGGTTTATTGTG<br>GTCC | 60.1                             | 489                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold9059_P4_539   | scaffold9059                            | 539                           | ATT/ATTT                                                      | TTAGGGCTCATACGAT<br>TCGG    | GGAAAATTAGCCACGG<br>ATCA | 60.1                             | 443                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold907_P4_4218   | scaffold907                             | 4218                          | TAAAAAAAAA/TAAAAAAAAA                                         | AAACACACCTTTTGAT<br>GCC     | AGGTCAATTCGTCCT<br>CCCT  | 59.8                             | 382                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold909_P4_21317  | scaffold909                             | 21317                         | T/TA                                                          | CCCACAAAAATAGAC<br>CGAA     | TGCTTGATTGCTTGAG<br>ATCC | 59.9                             | 429                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold909_P4_6745   | scaffold909                             | 6745                          | TA/TAA                                                        | TTTCATCTGAACCTTTC<br>GGG    | TAGGGTGGTACGAAAA<br>TCGC | 60.0                             | 365                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold9125_P4_1875  | scaffold9125                            | 1875                          | ATTTTTTTTT/ATTTTTTTTT                                         | GTCTTCCCTTGTCAG<br>ACCA     | ATCGAGTATCGGGAGA<br>CCCT | 59.9                             | 462                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold913_P4_123805 | scaffold913                             | 123805                        | TTGT/TT                                                       | ACGTCGCGTGACTTAT<br>GAGA    | TGAGAACTTTTCCGCT<br>GCT  | 59.5                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold913_P4_140774 | scaffold913                             | 140774                        | CAT/CATAT                                                     | TTGAGTTATGGCTAAT<br>GAAGTCA | AGCGAGCCGCTCAATT<br>AGTA | 60.0                             | 269                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold913_P4_216659 | scaffold913                             | 216659                        | CTATATATATATATA/CTATATATATA                                   | TCAGTTCTACCCGGAT<br>ACGC    | AAATTGCAGGGATGTG<br>AACC | 61.2                             | 328                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                          |                                  | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------|----------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                       |                            |                           |                                  |                                               | Sequence components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs |
| scaffold913_P4_251490 | scaffold913                             | 251490                        | TG/T                                                                  | ACTCGCAAATCAAACC<br>AAGC   | TGACTCACTTGCCTTC<br>ACG   | 60.3                             | 481                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold913_P4_251734 | scaffold913                             | 251734                        | ATTTT/ATTTTTT                                                         | AGCGTGAAAGGCAAGT<br>GAGT   | CCCATGCAAGGTATGC<br>TTTT  | 60.1                             | 441                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold913_P4_251896 | scaffold913                             | 251896                        | C/CA                                                                  | AGCGTGAAAGGCAAGT<br>GAGT   | CCCATGCAAGGTATGC<br>TTTT  | 60.1                             | 441                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold913_P4_252195 | scaffold913                             | 252195                        | T/TG                                                                  | ATGCGTCCCCAAGATTC<br>TGTT  | ATGGGATTGACTTGCT<br>CTGG  | 59.6                             | 668                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold913_P4_256760 | scaffold913                             | 256760                        | CATATATATATATATATATATATA<br>TATAT/CATATATATATATATATAT<br>ATATATATATAT | TGTTGCGATCGAGGAA<br>GTAA   | AAACACCGAAACAAGC<br>AAGC  | 59.4                             | 344                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold913_P4_282492 | scaffold913                             | 282492                        | ATTTT/ATT                                                             | TTGGATTTCATACCCAC<br>ACATC | AAAATCCGTTGGAAATT<br>TTGG | 59.6                             | 466                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold913_P4_387877 | scaffold913                             | 387877                        | T/TA                                                                  | TCATGTTCTCCAGCT<br>GCTA    | TTTGCCAGACCACCT<br>TTAC   | 59.5                             | 380                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold913_P4_412532 | scaffold913                             | 412532                        | T/TG                                                                  | TATGCTGACCACTACC<br>GCAA   | GGTCCATGGAGCAAAC<br>CTAA  | 60.3                             | 905                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold913_P4_9223   | scaffold913                             | 9223                          | AATATATATATATATATAT/AATAT<br>ATATATATATATAT                           | TGTTTGAATCGATGAA<br>GTGAA  | TGTGCGAATGTGGTTT<br>TTGT  | 58.3                             | 622                                           | INTERGENIC                                     | --                               | --                    | --  |
| scaffold914_P4_118122 | scaffold914                             | 118122                        | CATATATATATATA/CATATATATA<br>TATATATA                                 | TGCAAATTGAACCAAC<br>CAAA   | TGCCCCTAGACACCAG<br>TACC  | 59.9                             | 591                                           | INTERGENIC                                     | --                               | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)      | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                    |                           |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold916_P4_110560 | scaffold916                             | 110560                        | TAAA/TAA                                                           | GAGTGTGGTGGCAAT<br>TGTG   | GCAACGGTTTGATGTT<br>GATG      | 60.0                             | 675                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_134889 | scaffold916                             | 134889                        | TT/TTAT                                                            | AAATGTGGTCTCGGTT<br>TTGC  | TTGTTTTGTGAGTTTGA<br>ATGATGTT | 60.0                             | 770                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_255185 | scaffold916                             | 255185                        | AATATATATATATATATATATATAT<br>A/AATATATATATATATATATATAT<br>ATATA    | ACACGTTTAAGGCGTC<br>GTTC  | TCAGTCCTTAAATGAAA<br>TGCCA    | 60.2                             | 606                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_363659 | scaffold916                             | 363659                        | TAAAATTAAAAATTAAAAATTAAAA/<br>TAAAATTAAAAATTAAAAATTAAAA<br>TTAAAAA | CCACCCTCTACCATGC<br>AACT  | TGTTTTCCATGTGTGC<br>CACT      | 60.0                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_429531 | scaffold916                             | 429531                        | ATTTTTTTTT/ATTTTTTTT                                               | TGCGTTCAATTTAAAG<br>GTGTG | TCGCCTCAAAACATCAA<br>GAA      | 60.0                             | 321                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_4344   | scaffold916                             | 4344                          | GAAAAA/GAAAAA                                                      | TGTTGACGAATGTCCA<br>TGAAA | CCTCCAAAACCAACTA<br>CCA       | 60.0                             | 181                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_470919 | scaffold916                             | 470919                        | TTTATTATTATTATTATTATTATT<br>ATT/TTTATTATTATTATTATTAT<br>TATT       | TGATTAACACCATGCC<br>GTGT  | TTACAAGCAGGGAAAA<br>TGCC      | 59.8                             | 564                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_4805   | scaffold916                             | 4805                          | T/TACAATA                                                          | TGGTAGTTGGGTTTTG<br>GAGG  | TTATGACATGCATCCA<br>TCC       | 59.8                             | 907                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_4868   | scaffold916                             | 4868                          | GTTTTTTTT/GTTTTTTTTT                                               | TGGTAGTTGGGTTTTG<br>GAGG  | TTATGACATGCATCCA<br>TCC       | 59.8                             | 907                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_499308 | scaffold916                             | 499308                        | ATAAAT/ATAAATTATCTAAAT                                             | CCGTACGTAGTAAGCC<br>CCAA  | ACGAACCCATTGTTGC<br>ATTT      | 60.0                             | 855                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                              |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold916_P4_5303   | scaffold916                             | 5303                          | A/AT                                                          | TGTCTCTTTACGCCG<br>CAAT      | CTAGGCATTGCAACAG<br>GGAT | 60.8                             | 738                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_7772   | scaffold916                             | 7772                          | AG/A                                                          | TGTCCTTCTGTTCAATC<br>AAATACC | TGGTGGTGCATAGTTG<br>GTGT | 59.4                             | 636                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_7870   | scaffold916                             | 7870                          | TTGAAAAATGAAAA/TTGAAAA                                        | TGTCCTTCTGTTCAATC<br>AAATACC | TGGTGGTGCATAGTTG<br>GTGT | 59.4                             | 636                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_8185   | scaffold916                             | 8185                          | TT/TTCGATTAAT                                                 | ACACCAACTATGCACC<br>ACCA     | ATAGGCCCCAATTAAC<br>CCAC | 59.9                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_8308   | scaffold916                             | 8308                          | ATT/AT                                                        | ACACCAACTATGCACC<br>ACCA     | ATAGGCCCCAATTAAC<br>CCAC | 59.9                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_9278   | scaffold916                             | 9278                          | CTTT/CTTTT                                                    | TCACATAGGGATTGCC<br>AACA     | TCCCACCACATTCAATC<br>CTT | 59.9                             | 769                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_9500   | scaffold916                             | 9500                          | ATCTT/A                                                       | CCCATATGGTTTGGGA<br>ATCA     | TCCCACCACATTCAATC<br>CTT | 60.4                             | 257                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold916_P4_9949   | scaffold916                             | 9949                          | AAG/A                                                         | AGGATTGAATGTGGTG<br>GGAA     | GCAGAAAAATAAGGC<br>GATG  | 60.2                             | 354                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold918_P4_49291  | scaffold918                             | 49291                         | CAAA/CAAAA                                                    | TAGCGAGGACGAAAA<br>GACC      | CGTCCTCCCTGGGTTT<br>ATTC | 60.2                             | 820                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold919_P4_183431 | scaffold919                             | 183431                        | ATGTTGTT/ATGTT                                                | TGGCAAATACCGATTG<br>ACAA     | TGCTTCCATCCTTTATT<br>GGC | 59.9                             | 559                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                              |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold919_P4_301815 | scaffold919                             | 301815                        | TTTACTTACTT/TTTACTT                                           | CCTTGGAAGAACCTTG<br>GTGA     | AATCTGGAAGCGACAA<br>ATGG   | 60.1                             | 741                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold919_P4_431669 | scaffold919                             | 431669                        | AATATATATATATATATA/AATATATA<br>TATATATATATA                   | TTTGGGCTGACTATAG<br>TGTGATAA | CTTTGCATGCATATTGA<br>GAACA | 57.9                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold919_P4_525779 | scaffold919                             | 525779                        | AATATATATATATATATATAT/AAT<br>ATATATATATATATATATATATAT         | TTTGAATATGAGAGTTT<br>GGCTTG  | TACGACTGCTGAAGCT<br>CCCT   | 58.4                             | 332                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold919_P4_582534 | scaffold919                             | 582534                        | ATT/A                                                         | ACAAGGCACAAAATGC<br>ATCA     | TTGACTCTGCAAATTCG<br>TCG   | 60.1                             | 376                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold919_P4_724282 | scaffold919                             | 724282                        | GCCC/GCC                                                      | CCAAAAAGTGCAGAAA<br>GGGA     | TGGGATGCAGTTGAAA<br>ATGA   | 60.2                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold919_P4_73303  | scaffold919                             | 73303                         | GCTTCTTCTTCTC/GCTTCTTCTTC<br>TTCTTC                           | CACCCTCGCTTAGAAA<br>AACG     | TTTGAGACCAATGGT<br>GACA    | 59.9                             | 878                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold919_P4_83832  | scaffold919                             | 83832                         | AAAAAAATAAAAAA/AAAAAAATA<br>AAAAAATAAAAAA                     | GTTTGAAAGTTGTCCGC<br>GTCT    | GACACTTGCGCCCTA<br>TAAA    | 60.3                             | 479                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold92_P4_108844  | scaffold92                              | 108844                        | AG/AGAAGACATGG                                                | GGTACGAAAATCGCCA<br>GAAA     | TTCGAACAAGATGAGG<br>GACC   | 60.1                             | 725                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold92_P4_45246   | scaffold92                              | 45246                         | ATATTATTATTATTATT/ATATTA<br>TTATTATTATTATTATTATT              | TGCAATAAAACCATAT<br>ACGAAGA  | TGTTTGAAGTGCATAAC<br>GAAGA | 57.9                             | 438                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold9236_P4_1447  | scaffold9236                            | 1447                          | ACCC/ACC                                                      | GGAGGACGAAAATGAC<br>CAAA     | TCCCTTGCTTAATCGT<br>GTC    | 59.9                             | 307                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')     | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|-----------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                   |                             |                            |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold924_P4_151267 | scaffold924                             | 151267                        | AATATATATATATATATATAT/AATAT<br>ATATATATATATATATATATATAT                           | GACCTAAGTTCATGAA<br>GTGCAAA | CAGACCCCAACAAGA<br>AGAA    | 58.4                             | 506                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold924_P4_195853 | scaffold924                             | 195853                        | TTATATATATATATATATATATATATA<br>TAT/TTATATATATATATATATATATA<br>TATATATATAT         | CGACTGTATCCCTCCA<br>CGAT    | TTCATTCGGGGCTTAC<br>TACG   | 60.0                             | 516                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold924_P4_202228 | scaffold924                             | 202228                        | TTATATATATATATAT/TTATATATAT<br>ATAT                                               | AGGAAGAGTGGAGTTG<br>CGAA    | CAGGTTTGATGCAACC<br>ATTG   | 60.0                             | 689                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold924_P4_222190 | scaffold924                             | 222190                        | CCT/CCTACCTTTCTCT                                                                 | GCTTTTAGCACCTTGCA<br>CACG   | TTGTGTTTGGTGTTG<br>CGAT    | 59.7                             | 742                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold924_P4_250687 | scaffold924                             | 250687                        | ATTTTT/ATTTTT                                                                     | TGAAAAACGCTGCATC<br>TCAG    | GGAAAGGAATTGGTGG<br>GAAT   | 60.1                             | 525                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold9247_P4_528   | scaffold9247                            | 528                           | GATATATATATATATATATATAT/G<br>ATATATATATATATATATAT                                 | CAACCATTCAGCCTTG<br>GTTT    | CGTTTGTGCAATATCTG<br>CTCA  | 60.0                             | 562                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold929_P4_10600  | scaffold929                             | 10600                         | C/CT                                                                              | TCCTGGTCCTCGATTT<br>CATC    | GCGTTTCGAGTTTCGG<br>ATTA   | 60.0                             | 659                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold93_P4_141155  | scaffold93                              | 141155                        | CAA/CAA                                                                           | TCGATTGGCTTAAAC<br>CAGG     | AGAATTTACGAGCAGC<br>GGAA   | 60.1                             | 617                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold93_P4_265293  | scaffold93                              | 265293                        | TAAAAAAAAA/TAAAAAAAAA                                                             | AAATGTCCCAGTGAA<br>GTCG     | CTCCTTGAGTTTGTAGA<br>CACGA | 60.0                             | 589                                           | INTERGENIC                                           | --                                  | --                    | --  |
| scaffold93_P4_401190  | scaffold93                              | 401190                        | AATTATTATTATTATTATTATTATT<br>TATTATTATTATT/AATTATTATTATT<br>ATTATTATTATTATTATTATT | GCACCTAAAAGGGCAT<br>GAAA    | GGCGTTACCTCTTGTC<br>ATCG   | 60.1                             | 627                                           | INTERGENIC                                           | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold93_P4_514638  | scaffold93                              | 514638                        | AATATATATATATATATAT/AATATAT<br>ATATATATATATAT                 | CTGGCGTGACTAGGTG<br>TCAA   | TTCATTAAAGGGGGCT<br>GAAA  | 59.9                             | 622                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold93_P4_662816  | scaffold93                              | 662816                        | TC/T                                                          | AACGAGTGAAGAAAA<br>GAGCA   | GCGCTGTAAATGTGC<br>AAAA   | 59.1                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold93_P4_6723    | scaffold93                              | 6723                          | GTTTTT/GTTTT                                                  | GGATCGTAATCCGTGG<br>GTAA   | GAGAGAGCGATCATCA<br>AGGC  | 59.6                             | 415                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold9303_P4_1186  | scaffold9303                            | 1186                          | CT/CTT                                                        | AAGACCACATCATTGT<br>GTCACC | TGTTTGTCGCGTCTTA<br>ATTTT | 59.8                             | 439                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold931_P4_100445 | scaffold931                             | 100445                        | AATA/AATATA                                                   | CCCTTCAAGTCCAAAG<br>TCCA   | CATATTGAAGGGGGCT<br>CAAA  | 60.1                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold931_P4_100930 | scaffold931                             | 100930                        | A/AC                                                          | TTTGAGCCCCCTTCAA<br>TATG   | GATTCTCCTTGGGGAT<br>GGAT  | 59.9                             | 616                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold931_P4_116282 | scaffold931                             | 116282                        | GTTTTTTTTTTTTTTT/GTTTTTTTTT<br>TT                             | TCAGTTGCAATTCCTT<br>CCC    | TAAACCGATTGGGA<br>GTCG    | 60.1                             | 519                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold931_P4_116416 | scaffold931                             | 116416                        | ATTT/ATTTCCCTAGATGCTCTTT                                      | CGACTCCCAATCGGT<br>TTTA    | TTGGGCTGATGCAATA<br>AACA  | 59.9                             | 260                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold931_P4_116537 | scaffold931                             | 116537                        | ATT/ATTT                                                      | CGACTCCCAATCGGT<br>TTTA    | TTGGGCTGATGCAATA<br>AACA  | 59.9                             | 260                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold931_P4_117076 | scaffold931                             | 117076                        | CAAA/CAA                                                      | TGCCACAACCAATCTT<br>CATC   | AGACAGTGGGTGTTCC<br>AAGC  | 59.5                             | 391                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold931_P4_118275 | scaffold931                             | 118275                        | GAAAA/GAAAAA                                                  | TGCTCTGACTCATTCAA<br>CCG | CACCAACAATTGGCAT<br>CAAG     | 60.0                             | 725                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold931_P4_125652 | scaffold931                             | 125652                        | TAAAA/TAAAAA                                                  | TCACAAACTGTCGAG<br>ACGC  | CTCTCAAATTCCTCCC<br>ACA      | 60.0                             | 432                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold931_P4_154829 | scaffold931                             | 154829                        | GAAA/GAAAA                                                    | ACAGCAAACCGTCACA<br>AACA | AAGGGTGAGAGAGCGT<br>TTGA     | 60.2                             | 502                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold931_P4_180349 | scaffold931                             | 180349                        | GATATATATATATATA/GATATATA<br>TATATATA                         | TCGTCCCATGTAATT<br>GTCA  | TGGATACCCAAAAACC<br>ATTCA    | 59.8                             | 281                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold931_P4_180540 | scaffold931                             | 180540                        | T/TG                                                          | TCGTCCCATGTAATT<br>GTCA  | CACTCATTGCTTGAAG<br>AGTGCT   | 59.8                             | 486                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold931_P4_181299 | scaffold931                             | 181299                        | G/GTT                                                         | GTAGAGTGCCAACGAC<br>ACCA | TGAAGTATTGATTGGAT<br>CGTGC   | 59.8                             | 665                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold931_P4_19252  | scaffold931                             | 19252                         | GTTTTTT/GTTTTTTT                                              | AGAACGGTTGCCAGAG<br>AAGA | TGGGATGCAACATCTT<br>TTGA     | 60.0                             | 811                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold931_P4_246666 | scaffold931                             | 246666                        | TTATATATATATATATATATAT/TT<br>ATATATATATATATATAT               | GGGTGTCACATCACCC<br>TTTT | GCGGAAGACTTTATAG<br>TGAAAGGA | 59.7                             | 191                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold931_P4_80806  | scaffold931                             | 80806                         | CTTTTT/CTTTT                                                  | GCCCTCAGATGAGAGT<br>CAGG | TTGCTGGACATTCTGC<br>TTTG     | 59.9                             | 836                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold931_P4_85447  | scaffold931                             | 85447                         | CTGTT/CTT                                                     | GCGATTCATCATTCTC<br>CGTT | TGCAGACTGTTTGTT<br>CGAG      | 60.0                             | 372                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                     | Forward primers (5'-3')        | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                                                   |                                |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold9314_P4_649   | scaffold9314                            | 649                           | TC/TCATTAC                                                                                                                                                        | TAAGTTGTCTGGGGA<br>GGTG        | GTTTGGGATCGGAATT<br>GAAA     | 60.0                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold933_P4_2760   | scaffold933                             | 2760                          | GTCGCATATATGTGTCTCGCGTATA<br>TGTGTCTC/GTCGCGTATATGTGTC<br>TC                                                                                                      | CGTGGTGGTTTGATGT<br>TGAG       | GGCGCTAGCAACTCTA<br>TTGG     | 60.0                             | 615                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold933_P4_3249   | scaffold933                             | 3249                          | TA/TAA                                                                                                                                                            | TTGTCTCTTGGACATTC<br>CCC       | TTTTCCAGTGCACCTTG<br>TGA     | 59.9                             | 548                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold933_P4_4208   | scaffold933                             | 4208                          | GTTTTTTTTT/GTTTTTTTTT                                                                                                                                             | TCAAACCCAGTGGTCT<br>CCTT       | AGTCCGATGAAGGGTC<br>ACAG     | 59.5                             | 654                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold933_P4_4502   | scaffold933                             | 4502                          | ATTTTTTTTT/ATTTTTTTTT                                                                                                                                             | TCATTTTAAATTCCTT<br>ACAAAAACCA | AGTCCGATGAAGGGTC<br>ACAG     | 58.7                             | 569                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold933_P4_5878   | scaffold933                             | 5878                          | CAAAAAAAAA/CAAAAAAAAA                                                                                                                                             | AGCACTCGTGGTCCCT<br>TTAC       | TTTCTGATTGGATCAT<br>TTAGTTTT | 59.2                             | 463                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold937_P4_169841 | scaffold937                             | 169841                        | CTAATAATAATAATAATAATAAT<br>AATAATAATAATTAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ACAATAACAATAACAATAATAATA<br>AATAATAATAATAATAATAATAA<br>TATCTAATAATAATAATAATAATA | CCAATGTGGGACTTCA<br>ACAA       | ATGTCTACCAGGTTGG<br>TGCC     | 59.4                             | 609                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold937_P4_190077 | scaffold937                             | 190077                        | CTTTTTTTTT/CTTTTTTTTT                                                                                                                                             | TTGCGTTACGGATTG<br>ATGA        | TGTCCCTCACTCAACTA<br>TTCG    | 60.1                             | 279                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold9371_P4_631   | scaffold9371                            | 631                           | TTTT/TTTTGTTTT                                                                                                                                                    | GCGGCTGAAAGAGAGA<br>GAGA       | AAAGATTCCGGTACA<br>CACCA     | 60.0                             | 687                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold939_P4_1093   | scaffold939                             | 1093                          | ATTT/ATT                                                                                                                                                          | GTGACGTTGGGGGAG<br>TTAAA       | TCGAGCCTTATGGCAA<br>GATT     | 59.8                             | 317                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                     |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold939_P4_1155   | scaffold939                             | 1155                          | GTTTCTTTGTTT/GTTTCTTTGTTT<br>TTTCTTTGTTT                            | GTGACGTTGGGGAG<br>TTAA     | TCGAGCCTTATGGCA<br>GATT   | 59.8                             | 317                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold9411_P4_2892  | scaffold9411                            | 2892                          | TTAACT/TT                                                           | GGATATGTCAGAAAAG<br>GAACGG | GAAGCATCTCCAACAG<br>CTCA  | 59.8                             | 393                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold9411_P4_3721  | scaffold9411                            | 3721                          | TAAAA/TAAAA                                                         | TGAAGTGTGCTCTTC<br>GCAC    | TTTTTCCATTTGCGTC<br>TATTT | 60.2                             | 536                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold9411_P4_3911  | scaffold9411                            | 3911                          | AATA/AATATATA                                                       | TGAAGTGTGCTCTTC<br>GCAC    | GAAAGCCATTTTACC<br>CCAT   | 60.2                             | 840                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold943_P4_141649 | scaffold943                             | 141649                        | AATATATATATATATATATATAT/A<br>ATATATATATATATATATATAT                 | AAACCGGTAAATCTC<br>CGCT    | TATTTTGATTTTGCT<br>CGG    | 60.0                             | 703                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold943_P4_163051 | scaffold943                             | 163051                        | ATTT/ATT                                                            | TGGCAAATCGATTGAA<br>ACAA   | GTGCCAGTCGATTGCC<br>TAAT  | 60.1                             | 516                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold943_P4_187129 | scaffold943                             | 187129                        | TC/TCCC                                                             | ACCAGGACATGCAAGT<br>TTCC   | TTGCTCGTTACTCGAT<br>GTGG  | 60.0                             | 655                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold943_P4_267616 | scaffold943                             | 267616                        | T/TTACC                                                             | CAAACTCAAATGGG<br>CAAA     | GCTTCCACAAACCGT<br>GATT   | 59.6                             | 151                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold943_P4_38379  | scaffold943                             | 38379                         | AGGTG/AG                                                            | TGATAACTCGAGTCGT<br>TGCG   | ATTGCAATTTGACCT<br>TGC    | 60.0                             | 778                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold943_P4_94409  | scaffold943                             | 94409                         | TTATATATATATATATATATATATA<br>TAT/TTATATATATATATATATATA<br>TATATATAT | TTTGACTGACTTGACC<br>ACGC   | TGCCCCAATTTTGTTA<br>TCC   | 59.9                             | 543                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold944_P4_2389   | scaffold944                             | 2389                          | CAAAAAA/CAAAAA                                                | GAACGGGAAATTTCA<br>CGTCAT | TCGGACCACACTCCTA<br>ATCC  | 60.1                             | 495                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold944_P4_2557   | scaffold944                             | 2557                          | TG/T                                                          | GGATTAGGAGTGTGGT<br>CCGA  | CAACTGGGTACCACTA<br>AGCCA | 59.9                             | 450                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold944_P4_3122   | scaffold944                             | 3122                          | GAAAAAAAA/GAAAAAAAA                                           | TGGCTTAGTGGTACCC<br>AGTTG | TGGCGCTTATATTCAAA<br>GCA  | 60.0                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold944_P4_3226   | scaffold944                             | 3226                          | GTTTTTTT/GTTTTTTT                                             | TGGCTTAGTGGTACCC<br>AGTTG | TGGCGCTTATATTCAAA<br>GCA  | 60.0                             | 643                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold944_P4_672    | scaffold944                             | 672                           | ATTTT/ATTT                                                    | TTGTAAGTTGAGTTGC<br>GACGA | TGTGGTCGCAGGTTTT<br>ATGA  | 59.5                             | 308                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold9444_P4_3467  | scaffold9444                            | 3467                          | AG/A                                                          | TCCACAACGCAACCAA<br>ATTA  | AGCAGGTCTGTCCAAT<br>CAGG  | 60.0                             | 228                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold948_P4_131354 | scaffold948                             | 131354                        | AATATATATA/AATATATA                                           | TGACGACCGAGTCATT<br>TTCA  | TTTCAAGCCTAGACGC<br>CTGT  | 60.2                             | 841                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold948_P4_162996 | scaffold948                             | 162996                        | CAA/CA                                                        | AGGCATCAAAGCATC<br>ATCC   | TGGATTTGACATTGGC<br>TTTG  | 60.0                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold948_P4_179874 | scaffold948                             | 179874                        | T/TA                                                          | TCATATCACGGGTCT<br>GCAC   | CTGGGTGTTATGTTGC<br>GTTG  | 59.7                             | 574                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold9484_P4_1239  | scaffold9484                            | 1239                          | A/ATAC                                                        | CATCACAACGCCTCAA<br>GCTA  | ATGACGGTCCAAACCA<br>ACTC  | 60.0                             | 344                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold949_P4_12574  | scaffold949                             | 12574                         | GTTTTTTTTT/GTTTTTTTTTTT                                       | TTGGGCCATTGGATAA<br>ATGT | ATGCACACGATTGGTT<br>GAAA | 60.0                             | 589                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold949_P4_21151  | scaffold949                             | 21151                         | T/TG                                                          | TCATTTTCGTCCTCCCA<br>AAG | TTGCATGCACAAGATT<br>GGTT | 60.0                             | 465                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold949_P4_26559  | scaffold949                             | 26559                         | GTT/GT                                                        | AGGTCATTTTCGTCCT<br>CCCT | TCCAATGACACCAACA<br>CACC | 59.9                             | 692                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold950_P4_3787   | scaffold950                             | 3787                          | TG/T                                                          | AGGGAGGACGAAAATG<br>ACCT | TCCTCTCGAAGCCTAT<br>CCAA | 59.9                             | 707                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold953_P4_117005 | scaffold953                             | 117005                        | C/CT                                                          | CTACTCCAGAGCGGAT<br>TTGC | AAGTTACGTCAGTTT<br>GGCG  | 60.0                             | 752                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold953_P4_118840 | scaffold953                             | 118840                        | CT/C                                                          | TCCGAAGTACCGTTGG<br>GTAG | GGTGACGGTGGAAC<br>AAGA   | 60.0                             | 538                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold953_P4_123729 | scaffold953                             | 123729                        | TA/TAAATTGAGGAACCAA                                           | GAGCCACCGACTTGAA<br>GAAG | TTGTGTAGGTGGGCTT<br>TTCC | 60.0                             | 542                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold953_P4_141896 | scaffold953                             | 141896                        | ATTTTTTTTTT/ATTTTTTTTT                                        | TCGTTTTGCCATGTGT<br>GTTT | GCGTGGGAAAAGGGAA<br>CTTA | 60.0                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold953_P4_141960 | scaffold953                             | 141960                        | GATATATATAT/GATATATATATAT<br>AT                               | TCGTTTTGCCATGTGT<br>GTTT | GCGTGGGAAAAGGGAA<br>CTTA | 60.0                             | 594                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold953_P4_40733  | scaffold953                             | 40733                         | CAAAAAA/CAAAAA                                                | CACGACGACAAGTTTC<br>CTTA | TTAGTGAGCGTTTGATT<br>GGC | 60.1                             | 306                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold953_P4_44213 | scaffold953                             | 44213                         | TTTTGTT/TTT                                                   | GCATGCATGTTGAGGT<br>CATT  | TGGATGGGGTAGATG<br>GTGTT | 59.5                             | 494                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold953_P4_46110 | scaffold953                             | 46110                         | ATTTTTTTTTTTT/ATTTTTTTTTTT                                    | GGAGCACAAATTGAGAG<br>CACA | TCCTACGTATCCCCAA<br>GTGC | 60.0                             | 682                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold953_P4_62969 | scaffold953                             | 62969                         | GTTTTTTTTTT/GTTTTTTTTTTT                                      | TACCTGTGGATGGGA<br>ATGT   | TTATCCCTTCCTATGC<br>TGG  | 60.1                             | 413                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold953_P4_7421  | scaffold953                             | 7421                          | A/AG                                                          | TTCTCGGTTTAATTT<br>GGG    | GCTGAAACCAGATGCA<br>AACA | 58.9                             | 955                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold953_P4_75360 | scaffold953                             | 75360                         | GAAAAAAAAA/GAAAAAAAAA                                         | TCAATGGGATTCCTC<br>TATGC  | CACCCTCGCTTAGAAA<br>AACG | 59.0                             | 762                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold953_P4_79145 | scaffold953                             | 79145                         | TGTN/T                                                        | CAGCACGATTACCA<br>AGCA    | GAATTTAATGCGTTGC<br>GGAT | 59.9                             | 531                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold954_P4_39112 | scaffold954                             | 39112                         | CA/CAA                                                        | ATCCTTGGGAGGACGA<br>AAAT  | TTCGTAATCGATTGCA<br>GGTG | 59.8                             | 790                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold956_P4_19709 | scaffold956                             | 19709                         | G/GCTTCTT                                                     | TCCAGATGAAATCGAG<br>GACC  | GGATTAGCCTTTGAG<br>TCCC  | 60.0                             | 381                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold958_P4_3567  | scaffold958                             | 3567                          | AATATATATATATATATAT/AA<br>TATATATATATATATAT                   | GATGATGATGATGCG<br>TGCC   | GAATGAAATCACAGAC<br>CGGC | 59.9                             | 328                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold959_P4_11831 | scaffold959                             | 11831                         | TG/T                                                          | CAAGCGTTTCCATCTC<br>CATT  | GTGGTAATCGCGTTGA<br>AGGT | 60.1                             | 817                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                        | Forward primers (5'-3')      | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------------|------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                                                                      |                              |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold96_P4_316614  | scaffold96                              | 316614                        | A/AT                                                                                                                                 | TCGACTATGAGTGATT<br>ACGTGGTT | CAATCAAGGTACAATG<br>AGTCAAACA | 60.0                             | 426                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold962_P4_183800 | scaffold962                             | 183800                        | GATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAA/GATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA | GATAATTGTCGCGTTC<br>GGTT     | TCGTTGACTCGTGAAT<br>CTGC      | 60.0                             | 653                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold962_P4_196124 | scaffold962                             | 196124                        | GTATATATATATATATATATAT/GTAT<br>ATATATATATAT                                                                                          | GATATTGCTCAACGGG<br>TCGT     | TCATGCGATGCCAAA<br>ATAA       | 60.0                             | 534                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold962_P4_231201 | scaffold962                             | 231201                        | AATATATATATATATATATATATAT<br>ATATATATATATATATATATATAT<br>T                                                                           | ATGCGTTATGGGTGAA<br>ATGG     | GTTGGTTCCCTAGCAC<br>CGTA      | 60.6                             | 477                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold963_P4_101485 | scaffold963                             | 101485                        | GAAAA/GAAAAA                                                                                                                         | TATTTTGGATTTTGGCT<br>CGG     | AAATTGGTCCACTAGC<br>ACCG      | 59.9                             | 631                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold963_P4_17319  | scaffold963                             | 17319                         | AATATATATATATATATATATATAT<br>ATATATATATATAT/ATATATATATA<br>TATATATATATATAT                                                           | CCGGGGATAATGGCTT<br>AAAT     | GGGGTATGCATTGTGTT<br>GGAC     | 60.0                             | 429                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold963_P4_6111   | scaffold963                             | 6111                          | TAAA/TAA                                                                                                                             | GCGGGGAAGAACATTC<br>ATAA     | GCAATTTTGTCAACGC<br>ACTG      | 59.9                             | 400                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold964_P4_74245  | scaffold964                             | 74245                         | TTATATATATATATATATATATATA<br>TATATATAT/TTATATATATATATA<br>TATATATATATATATATATATAT                                                    | GATGATGCAAGGTGGC<br>TTTT     | GGTGTGTCTGTGTGTT<br>TGCC      | 60.1                             | 389                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold964_P4_79837  | scaffold964                             | 79837                         | TATTAATAA/TATTAATAATAAATTAA<br>TAA                                                                                                   | TTGAAGGTGCAATGCC<br>TTTA     | GCATGAACAGCAACGT<br>CAAC      | 59.3                             | 469                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold972_P4_18681  | scaffold972                             | 18681                         | GTTTTT/GTTTTTT                                                                                                                       | CCTGAAGCCTGCACAC<br>ATAA     | ACCCGGGTTACGTCTA<br>GTCC      | 59.9                             | 695                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                               | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                                                                                                             |                          |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold974_P4_3959  | scaffold974                             | 3959                          | GTTTTTTT/GTTTTTTT                                                                                                                           | TGCGTCCAATCTGTGT<br>GTTT | AAGCCTAGGGAGGACG<br>AAAA   | 60.2                             | 498                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold9740_P4_598  | scaffold9740                            | 598                           | TTATGATCTATGATCT/TTATGATCT                                                                                                                  | GGAGACACCTGTGGAG<br>GGTA | TTTCCCAGTCGTTTGG<br>TTTC   | 60.0                             | 704                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold9757_P4_838  | scaffold9757                            | 838                           | TAAAA/TAAAAA                                                                                                                                | TGTTAATCCAACGGCA<br>CAAA | TCCCTGGCTTATTGTT<br>GTC    | 60.0                             | 279                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold977_P4_6872  | scaffold977                             | 6872                          | GTGATGATG/GTGATGATGATGATG                                                                                                                   | CGTATTTCCCAACGAT<br>CCAT | ACGAGGTCGTACCAAC<br>CAAC   | 59.6                             | 637                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold9784_P4_548  | scaffold9784                            | 548                           | A/AATTAG                                                                                                                                    | CCGGTGCATCCAATTA<br>GTTC | CACCCGTTGACACAAA<br>TGAA   | 60.3                             | 632                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold98_P4_135448 | scaffold98                              | 135448                        | AA/AATAATAATA                                                                                                                               | CGTCCCCATTATGGTT<br>TTTG | GGGCATGCTGATTTTG<br>ACTT   | 60.0                             | 623                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold98_P4_138017 | scaffold98                              | 138017                        | TAAAAAAAAA/TAAAAAAAAA                                                                                                                       | AATGTGCCTCAGGTGG<br>ATCT | GCCACTATCGGGCTGA<br>GTTA   | 59.5                             | 613                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold98_P4_151426 | scaffold98                              | 151426                        | TAAA/TAAAA                                                                                                                                  | CACTAGGGACCCTTTG<br>GTGA | GTCGTGTGTGTGGGA<br>TGTA    | 60.0                             | 845                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold98_P4_185642 | scaffold98                              | 185642                        | TTAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA<br>TAATAA/TTAATAATAATAATAATA<br>AATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATAA<br>A | TTGGTTCGGATTTTCG<br>ATAA | GGCAAGGTATCAAAAC<br>ACAAA  | 60.3                             | 824                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold98_P4_241916 | scaffold98                              | 241916                        | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATAT<br>TATATATATAT                                                                      | ATTGGGGTTTAAGGG<br>TTGG  | AACAAACAAAGAAAAG<br>CAAGGC | 59.9                             | 663                                           | INTERGENIC                                        | --                                  | --                    | --  |



| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                               | Forward primers (5'-3')  | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                                                                                                                             |                          |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold98_P4_336266 | scaffold98                              | 336266                        | TAAAAA/TAAAAA                                                                                                                                               | CGCGTTAACAGAGGAA<br>GAGG | GCAAACTTGGACCATT<br>TGCT      | 60.0                             | 514                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold98_P4_361226 | scaffold98                              | 361226                        | T/TCACACTCTTTCAGG                                                                                                                                           | TGGGGTTGCATACTCT<br>CCAT | TATTGCGAAAAGGGGT<br>CAAG      | 60.3                             | 573                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold98_P4_362243 | scaffold98                              | 362243                        | AATATATATATATATATATATATAT<br>AT/AATATATATATATATATATATAT                                                                                                     | CCCACCCTTAATCCTC<br>AACA | TTGAGTACAAGACCATT<br>GACCTTC  | 59.8                             | 572                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold98_P4_432437 | scaffold98                              | 432437                        | AATATATATATATATATATAT/AA<br>TATATATATATATATATAT                                                                                                             | AAATGACGATGAACCG<br>GAAG | TTGATAACATGAAAATG<br>AAATGAAA | 59.9                             | 488                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold98_P4_449349 | scaffold98                              | 449349                        | CTTTTTTTTT/CTTTTTTTTTTT                                                                                                                                     | GAAATTGCGCATGCAG<br>TAGA | TCACCCTTGTGAGTCC<br>ATCA      | 60.0                             | 224                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold98_P4_584017 | scaffold98                              | 584017                        | AG/A                                                                                                                                                        | AAATGGGGAGCAATT<br>GACA  | TGAAGTTCATCCGACG<br>ACAG      | 60.3                             | 558                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold98_P4_584690 | scaffold98                              | 584690                        | GTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>AGTATTATTATTATTAT/GTTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTAGT<br>ATTATTATTATTATT | AGCTGTCGTCGGATGA<br>ACTT | CCCATGTGCAATAGGG<br>AAAT      | 59.9                             | 475                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold98_P4_657346 | scaffold98                              | 657346                        | AATATATATATATATATAT/AA<br>TATATATATATATATATAT                                                                                                               | TTGCACCTTCATAAGA<br>CCCA | CACCACTCCTATCCCTT<br>GGT      | 59.1                             | 680                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold981_P4_10911 | scaffold981                             | 10911                         | CGAAACCTGAAACCTGAAACCTGAA<br>ACCT/CGAAACCTGAAACCTGAAAC<br>CT                                                                                                | AACCCGAGAACCAAAA<br>TCCT | GTTTCGGGTTTACGGT<br>TTCA      | 59.8                             | 326                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold981_P4_6691  | scaffold981                             | 6691                          | ATAAACCTAAACCTAAACCTAA<br>ACCCTAAACC/ATAAACCTAAACCC<br>TAAACCTAAACC                                                                                         | CCCGAAACGATTAAC<br>TGAA  | TTTAGGGTGTCGGGAT<br>TCAA      | 59.9                             | 567                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                               |                            |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold9813_P4_1199  | scaffold9813                            | 1199                          | GAAA/GAAAA                                                    | AAAATCGCGCGAAAAA<br>TCTA   | TCCTGGTCCTCGATT<br>CATC       | 60.0                             | 772                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold982_P4_1547   | scaffold982                             | 1547                          | GAAAAAAAAA/GAAAAAAAAA                                         | TTGGAGAGGAAGATGA<br>AAAACC | GGCTAATATATCCGTG<br>GTCCC     | 59.6                             | 461                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold982_P4_1609   | scaffold982                             | 1609                          | A/AAT                                                         | TAAAGACCAAGTCGG<br>GAAA    | TTCACCTTTGAGAGTGT<br>ATCTTTGG | 59.5                             | 108                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold982_P4_5778   | scaffold982                             | 5778                          | AT/A                                                          | GCAAAGCATTCAAATG<br>CAGA   | TTCATCTTCTCCAATT<br>CAAAAA    | 60.0                             | 755                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold982_P4_729    | scaffold982                             | 729                           | ATTTTTTTTT/ATTTTTTTTT                                         | TCCTTGTCATTTTCCTG<br>CAA   | TATTGTGGCACTCCAT<br>CCAA      | 59.2                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold982_P4_766    | scaffold982                             | 766                           | GTTTTTT/GTTTTTTT                                              | TCCTTGTCATTTTCCTG<br>CAA   | TATTGTGGCACTCCAT<br>CCAA      | 59.2                             | 416                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold982_P4_874    | scaffold982                             | 874                           | ATT/ATTT                                                      | TTGGATGGAGTGCCAC<br>AATA   | AACTTGGGGTTGAAGA<br>TGAAGA    | 59.9                             | 164                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold9821_P4_582   | scaffold9821                            | 582                           | GTTTTTTTTTT/GTTTCTTTTTTTT<br>TT                               | GCACTCCTGAACCACG<br>TTAAA  | TCCTATCACGAAACATT<br>CAACAA   | 60.2                             | 336                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold983_P4_141844 | scaffold983                             | 141844                        | TAAAAAAA/TAAAAAAA                                             | GCTCACGAGGCAGTAA<br>TGAA   | CGTGACAATTACATGG<br>GGACT     | 59.0                             | 938                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold983_P4_141925 | scaffold983                             | 141925                        | T/TCATAAAGG                                                   | AGGTGTGACAACAAGA<br>TGCCT  | CGTGACAATTACATGG<br>GGACT     | 59.6                             | 851                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                       | Forward primers (5'-3')       | Reverse primers (5'-3')         | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------|-------------------------------|---------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                     |                               |                                 |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold983_P4_255175 | scaffold983                             | 255175                        | GTTTT/GTTT                                                                          | TTACCGGATTTACTCAC<br>GGC      | ACCCGTCAAATACGAC<br>GAAC        | 60.0                             | 319                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold983_P4_276897 | scaffold983                             | 276897                        | GTTATTATTATTATTATTATTATT<br>ATTATTATTA/GTTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA | ACAAAGCTCTAAGCCC<br>CACA      | GGAATGTTGGATAGGA<br>TTTTGG      | 59.9                             | 641                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold983_P4_287478 | scaffold983                             | 287478                        | A/ACTAAAC                                                                           | GAAGCTCAGATGGCAC<br>ACAA      | CGCAATGAAATCAGA<br>GCAA         | 60.0                             | 472                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold983_P4_287686 | scaffold983                             | 287686                        | A/ATT                                                                               | TTGCTCTGATTTTCATT<br>GCG      | AATTGTGCCAGTCGAT<br>TGCT        | 60.0                             | 642                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold983_P4_88220  | scaffold983                             | 88220                         | T/TG                                                                                | CACCCACAAGGAGGAA<br>GAAC      | CATGGATCAAACAGGC<br>TTCA        | 59.5                             | 517                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold983_P4_88456  | scaffold983                             | 88456                         | AGTG/AG                                                                             | TTTATTCGCATGTTGTT<br>GCC      | CATGGATCAAACAGGC<br>TTCA        | 59.6                             | 274                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold984_P4_11529  | scaffold984                             | 11529                         | CATATATATAT/CATATATATATAT                                                           | AGGTTTGACTGCATAA<br>CGAAGA    | GAACAAAATTGAGTTGT<br>CAAATAAACA | 58.9                             | 457                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold984_P4_143777 | scaffold984                             | 143777                        | CTTAATAATGTAATTAATAATGTAAT/<br>CTTAATAATGTAATTAATAATGTAAT<br>TAATAATGTAAT           | AGCGATTTTTGAACCA<br>CCTG      | AACAATCTCCCCCTTTT<br>TGG        | 60.1                             | 539                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold984_P4_36248  | scaffold984                             | 36248                         | TA/TAA                                                                              | CATTTTTATTGACGAC<br>TCAATTTTC | TGCAGTCAAACTTTAAA<br>AGGAAG     | 59.4                             | 363                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold986_P4_26134  | scaffold986                             | 26134                         | GA/GAA                                                                              | CGGGAACTCGATTTGA<br>ACAT      | AGCCTGGGTTTGTTTC<br>ACAC        | 59.9                             | 323                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs     | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                         | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|----------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                      |                                         |                               |                                                                                                       |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold986_P4_9646  | scaffold986                             | 9646                          | TTGGTTAAAAA/T                                                                                         | GAGGACGAAGATGACC<br>CAAA | ATTTTCGTCCCATAG<br>GCTT  | 60.1                             | 411                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold99_P4_215336 | scaffold99                              | 215336                        | TAA/TA                                                                                                | AGATTTCTGCACGAATT<br>GGG | TCTCCGTAAAGGATTG<br>ACCG | 60.1                             | 507                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold99_P4_69243  | scaffold99                              | 69243                         | CAAAGGAAAG/CAAAG                                                                                      | TGGATTACGGGTGAAA<br>TGGT | AAATTGGTCCACTAGC<br>ACCG | 60.1                             | 491                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold99_P4_81654  | scaffold99                              | 81654                         | ATTTT/ATTT                                                                                            | CAGGGGCTGAGATATG<br>CTGT | CTCTCATCTGAGGGCA<br>AAGC | 60.2                             | 395                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold992_P4_33182 | scaffold992                             | 33182                         | CATA/CATATA                                                                                           | TGCGCCTCTTCTAAAT<br>CGT  | AACTTTTCCGCTGCTT<br>GAA  | 60.0                             | 670                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold992_P4_37824 | scaffold992                             | 37824                         | ACTCTCTCTCTCTCTCTC/ACTCT<br>CTCTCTCTCTCTCTCTCTC                                                       | GCACCTCATAAAACGA<br>CGGT | AAAGAGCCAAGAGGCA<br>TCAA | 60.0                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold992_P4_37883 | scaffold992                             | 37883                         | ATCTCTCTCTCTCTCTTTCTCTCT<br>CTCTCTATCTCTCTCTCTCT/ATC<br>TCTCTCTCTCTTTCTCTCTCTCTC<br>TATCTCTCTCTCTCTCT | GCACCTCATAAAACGA<br>CGGT | AAAGAGCCAAGAGGCA<br>TCAA | 60.0                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold992_P4_37946 | scaffold992                             | 37946                         | TC/T                                                                                                  | GCACCTCATAAAACGA<br>CGGT | AAAGAGCCAAGAGGCA<br>TCAA | 60.0                             | 349                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold992_P4_40175 | scaffold992                             | 40175                         | CATACATAGATTAAACATA/CATACAT<br>AGATTAAACATAATACATAGATTAACA<br>TA                                      | TCAGTTCGCAAGAAA<br>ACCT  | ATTGCATGTTTTGGCAT<br>TGA | 59.9                             | 201                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold992_P4_40484 | scaffold992                             | 40484                         | CA/CACCGAAA                                                                                           | TCAATGCCAAAACATG<br>CAAT | TTCGGATGTCCCCTTA<br>AACA | 59.9                             | 513                                           | INTERGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                      | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|-----------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                       |                                         |                               |                                                                                    |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold992_P4_42011  | scaffold992                             | 42011                         | CT/C                                                                               | CAACCTTAACGCACCG<br>TACC    | TTTGTTC AATTCATGC<br>TCCC | 60.4                             | 563                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold992_P4_42274  | scaffold992                             | 42274                         | A/AATCT                                                                            | GGGAGCATGAAATTGA<br>ACAAA   | ACCAAAATTCAGCACT<br>GCAC  | 59.9                             | 561                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold992_P4_42301  | scaffold992                             | 42301                         | CTCT/CTTTCT                                                                        | GGGAGCATGAAATTGA<br>ACAAA   | TCTTTTGC GTCTGAATT<br>TGG | 59.9                             | 708                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold996_P4_139646 | scaffold996                             | 139646                        | AATATATATATATATATATATATAT<br>/AATATATATATATATATATATATAT<br>TATATATAT               | TCCGAATTCGAATCCA<br>AGAC    | CCCAATTTGCTGTCCAT<br>TTC  | 60.0                             | 520                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold996_P4_201342 | scaffold996                             | 201342                        | CATATATATATATATATATATATAT<br>TATATATAT/CATATATATATATATAT<br>ATATATATATATATATATATAT | GGAGGGACCTGAAGTC<br>ACAA    | TAGAGCCTGGTTTGG<br>TTGG   | 60.1                             | 740                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold999_P4_123863 | scaffold999                             | 123863                        | ATCTCTCT/ATCTCT                                                                    | CCAAATGTTATGATCA<br>GTATGCC | TGCGAAGAAGCTCACT<br>TGAA  | 58.4                             | 734                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold999_P4_130386 | scaffold999                             | 130386                        | TG/TGG                                                                             | TGTAAACCTGCTTGCA<br>CACC    | CTGCACAACAATCCCA<br>CAAC  | 59.8                             | 160                                           | INTERGENIC                                        | --                                  | --                    | --  |
| scaffold999_P4_132777 | scaffold999                             | 132777                        | TGGG/TGGG                                                                          | CCGACTCATCACGAGA<br>CTCA    | GGCAATCCAAGTTATT<br>GCGT  | 60.0                             | 635                                           | INTERGENIC                                        | --                                  | --                    | --  |
| Ca5_P4_18683897       | Ca5                                     | 18683897                      | AGCG/AGCGCGAGTCATCAGCTCG<br>CG                                                     | ATGGCCGTTCTTAGTT<br>GGTG    | GTACAAAGGCGAGGGA<br>CGTA  | 60.0                             | 395                                           | INTRAGENIC                                        | --                                  | --                    | --  |
| scaffold158_P4_131634 | scaffold158                             | 131634                        | T/TAAC                                                                             | GTGACTGGTGACTGGG<br>GACT    | TTATGCCTGCTGTTCT<br>GCAC  | 60.0                             | 227                                           | INTRAGENIC                                        | --                                  | --                    | --  |

| INDEL marker IDs  | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|-------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                   |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| C11177592_P4_7683 | C11177592                               | 7683                          | CAAA/CAA                                                      | CAGGCACACTGCACAA<br>AGTT   | TCCCTCGGATTATGTG<br>AAGC   | 59.9                             | 533                                           | INTRON                                            | Ca_27746                            | O                     | bHLH        |
| Ca1_P4_10040103   | Ca1                                     | 10040103                      | ATTT/ATT                                                      | ATGCATCGAAAACCA<br>CACA    | TGCAATCCGGGCTTAC<br>TATC   | 60.0                             | 378                                           | INTRON                                            | Ca_02784                            | LK                    | --          |
| Ca1_P4_10419588   | Ca1                                     | 10419588                      | GAATAATAATAATAATAATA/GA<br>ATAATAATAATAATAATA                 | TGATTCCGAGACCCAA<br>AAAG   | CTTCTTACC GTTGTCT<br>CCC   | 60.0                             | 258                                           | INTRON                                            | Ca_02735                            | R                     | ERF         |
| Ca1_P4_1063427    | Ca1                                     | 1063427                       | CATTATTATTATTATTATTATTAT<br>TATTA/CATTATTATTATTATTAT<br>TATTA | CCAACTCGCCTTCTTA<br>GTCG   | TTCCGTTTTTGAATTCC<br>TGC   | 60.0                             | 692                                           | INTRON                                            | Ca_00130                            | J                     | --          |
| Ca1_P4_11766496   | Ca1                                     | 11766496                      | TA/TATAAA                                                     | TCGTCGACCTTTCTTA<br>GAATTT | AGAATTTTGATTGCGG<br>GTTG   | 57.2                             | 891                                           | INTRON                                            | Ca_02576                            | --                    | YABBY       |
| Ca1_P4_13342022   | Ca1                                     | 13342022                      | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATATA<br>T   | GTCCCATTTGTGGAAC<br>CAGT   | TCGGATCGGATCAAAT<br>TTCT   | 59.7                             | 633                                           | INTRON                                            | Ca_14096                            | --                    | --          |
| Ca1_P4_13685328   | Ca1                                     | 13685328                      | CTATA/CTA                                                     | CACCCATTGCTTGGTC<br>TTTT   | TGGTGAACCTTACTCG<br>GTCC   | 60.0                             | 650                                           | INTRON                                            | Ca_14134                            | --                    | MYB_related |
| Ca1_P4_13686356   | Ca1                                     | 13686356                      | T/TCTC                                                        | TTGTACGGGTGGTGTC<br>AAAA   | GAGGGTGACTCTGCTG<br>GAAC   | 59.9                             | 655                                           | INTRON                                            | Ca_14134                            | --                    | MYB_related |
| Ca1_P4_13686733   | Ca1                                     | 13686733                      | CAAAAAAAAA/CAAAAAAAAA                                         | AGCATTTGCTACCGTG<br>ATCC   | TTTACCTTGCCAAAAT<br>GCC    | 60.1                             | 698                                           | INTRON                                            | Ca_14134                            | --                    | MYB_related |
| Ca1_P4_13699506   | Ca1                                     | 13699506                      | GAAAAAAAA/GAAAAAAAA                                           | GGCAAGACCATTGAGC<br>TCTC   | CGGTTATGGGATGATT<br>TAGGAA | 60.0                             | 921                                           | INTRON                                            | Ca_14135                            | --                    | bHLH        |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                                     | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                                                                                                   |                           |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca1_P4_13701840  | Ca1                                     | 13701840                      | AGAATGTATAT/A                                                                                                                                                     | TGCAAAACCAAGTCTG<br>TCCA  | ACCTTGCCCCTGAAGT<br>AGGT      | 60.3                             | 632                                           | INTRON                                            | Ca_14135                            | --                    | bHLH     |
| Ca1_P4_13704708  | Ca1                                     | 13704708                      | A/AAT                                                                                                                                                             | CAAACCGACACAAATTT<br>TCAA | GGATATGCAATTGGGA<br>TGCT      | 58.6                             | 725                                           | INTRON                                            | Ca_14135                            | --                    | bHLH     |
| Ca1_P4_13767969  | Ca1                                     | 13767969                      | TA/TACA                                                                                                                                                           | TGTTCTTTTCACGTGC<br>TTTG  | CTCAACAAACGAGCCC<br>TCTC      | 59.9                             | 655                                           | INTRON                                            | Ca_14138                            | BK                    | bHLH     |
| Ca1_P4_13814189  | Ca1                                     | 13814189                      | ATTTTTTTTT/ATTTTTTTTT                                                                                                                                             | AATGGCTTTTGGTGGA<br>AGTG  | AATTCCTGAAATCAGCA<br>AAACA    | 60.0                             | 753                                           | INTRON                                            | Ca_14146                            | G                     | Trihelix |
| Ca1_P4_15579150  | Ca1                                     | 15579150                      | CATATATATATATATATA/CATATA<br>TATATATATATATATA                                                                                                                     | CCAATTGCGTTCGTAA<br>CAGA  | AAATCTTTCAAAAGAAT<br>CACAAAAA | 59.7                             | 587                                           | INTRON                                            | Ca_06985                            | S                     | --       |
| Ca1_P4_15865372  | Ca1                                     | 15865372                      | TTATATATATATATATATA/TTATA<br>TATATATATATATATA                                                                                                                     | AAAATGGGTTGGTGTC<br>AAGC  | ACAATAATGAAGGGGG<br>AGCC      | 59.8                             | 654                                           | INTRON                                            | Ca_06964                            | QR                    | B3       |
| Ca1_P4_15871801  | Ca1                                     | 15871801                      | G/GA                                                                                                                                                              | GAAAATTTCAACGAGG<br>GGGT  | CGCTTGTTTTCGGATG<br>AGAT      | 60.2                             | 566                                           | INTRON                                            | Ca_06964                            | QR                    | B3       |
| Ca1_P4_15971212  | Ca1                                     | 15971212                      | CATATATATATATATAT/CATATATAT<br>ATATATATATAT                                                                                                                       | TGTCCACATGAGTTCC<br>TCCA  | TGTGATCAACACTGAAA<br>TTGACA   | 60.1                             | 212                                           | INTRON                                            | Ca_06955                            | O                     | bHLH     |
| Ca1_P4_16185243  | Ca1                                     | 16185243                      | TTCATTA/TTCAATCAATCA                                                                                                                                              | AGGAAAATTGTGGTGC<br>CTTG  | AGGTAACGCATAAAGA<br>AAACAAA   | 60.0                             | 404                                           | INTRON                                            | Ca_06937                            | --                    | --       |
| Ca1_P4_16475601  | Ca1                                     | 16475601                      | TATAATAATAATAATAATAATAAA<br>TAATAATAATAATAATAATAATA<br>AAAAATAATAAAAAATAATAAT/<br>TATAATAATAATAATAATAATAAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAATA | TGAAAAAACCAAAAC<br>CCAA   | TTCTCCGGTATTGGAG<br>GATG      | 60.2                             | 753                                           | INTRON                                            | Ca_06916                            | Z                     | WRKY     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                                 |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca1_P4_16813585  | Ca1                                     | 16813585                      | GATTAATTAATTAATTAATTAATTA<br>TTAATTAA/GATTAAATTAATTAATTA<br>TTAATTAATTAATTAATTA | ATCCATCAGCTGCAAT<br>ACCC | GTTTGTCTGTGGCT<br>TGAT   | 59.9                             | 399                                           | INTRON                                            | Ca_06890                            | --                    | --   |
| Ca1_P4_1744820   | Ca1                                     | 1744820                       | GAAGAAA/GAA                                                                     | ACCCTGTGGCACAATA<br>CCAT | CCATGCAATGCAATCA<br>CAAT | 60.1                             | 486                                           | INTRON                                            | Ca_00219                            | --                    | TALE |
| Ca1_P4_1744972   | Ca1                                     | 1744972                       | CA/CACAGTTCACCTTTA                                                              | ACCCTGTGGCACAATA<br>CCAT | AGCACCGATCAAATCA<br>CACA | 60.1                             | 820                                           | INTRON                                            | Ca_00219                            | --                    | TALE |
| Ca1_P4_1745433   | Ca1                                     | 1745433                       | ATGAATTGAATT/ATGAATTGAATTG<br>AATT                                              | TGTGTGATTTGATCGG<br>TGCT | GAGTAGGTGCCTTCCC<br>ACAA | 60.1                             | 214                                           | INTRON                                            | Ca_00219                            | --                    | TALE |
| Ca1_P4_1746242   | Ca1                                     | 1746242                       | ACAAAT/A                                                                        | AATGCAAAAAGCCGAC<br>ATCT | GTGGGAGTCGTGAAC<br>TCGT  | 59.7                             | 281                                           | INTRON                                            | Ca_00219                            | --                    | TALE |
| Ca1_P4_17705846  | Ca1                                     | 17705846                      | TAAAAAAA/TAAAAAAA                                                               | ACCACCATCATGAGCA<br>TCAA | CATTTTTCGAGCTTTGC<br>CTC | 59.9                             | 971                                           | INTRON                                            | Ca_14764                            | R                     | B3   |
| Ca1_P4_1789018   | Ca1                                     | 1789018                       | GTTTTTTTTT/GTTTTTTTT                                                            | TCATAGACAGTTTGC<br>AGCG  | CACAATCGTCCACCA<br>ACTG  | 60.0                             | 324                                           | INTRON                                            | Ca_00225                            | --                    | --   |
| Ca1_P4_1824386   | Ca1                                     | 1824386                       | ATGTGT/ATGTGTGTGT                                                               | ACGTGAAGCTTTGCGA<br>GATT | TGAACCAAACACAGGG<br>ATGA | 60.0                             | 859                                           | INTRON                                            | Ca_00230                            | K                     | --   |
| Ca1_P4_1860532   | Ca1                                     | 1860532                       | ACC/ACCC                                                                        | GAATCAAGTGAAAAAG<br>GCCA | TGAGGCAATTGATAGA<br>GGGG | 60.1                             | 573                                           | INTRON                                            | Ca_00233                            | FP                    | bHLH |
| Ca1_P4_186468    | Ca1                                     | 186468                        | AATC/AATCATC                                                                    | CAGCAGAATCTTGGA<br>ACCA  | TGATGAAGATCCCCCA<br>AGAG | 58.8                             | 502                                           | INTRON                                            | Ca_00014                            | --                    | --   |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca1_P4_1988980   | Ca1                                     | 1988980                       | TC/TCCC                                                       | ACCTGCCAAAAGCAGA<br>AGAA | CACTGAGTTTTCGGG<br>AGAA  | 60.0                             | 776                                           | INTRON                                            | Ca_00248                            | T                     | --          |
| Ca1_P4_1998212   | Ca1                                     | 1998212                       | GAAAAAA/GAAAAA                                                | CAACAGGCCCTATT<br>CTCA   | CCAGGTGGACCTGAAG<br>TGTT | 60.1                             | 449                                           | INTRON                                            | Ca_00250                            | CR                    | HB-other    |
| Ca1_P4_2004325   | Ca1                                     | 2004325                       | AC/ACCATC                                                     | TACCTGGTGTCATTGC<br>TTGG | CATATCCTCATGGCAG<br>TCCC | 59.6                             | 625                                           | INTRON                                            | Ca_00252                            | --                    | TCP         |
| Ca1_P4_2004592   | Ca1                                     | 2004592                       | T/TA                                                          | TCAGCAGTTGCTACCT<br>CCCT | CGCCAAGAACAATAAT<br>GCCT | 60.0                             | 447                                           | INTRON                                            | Ca_00252                            | --                    | TCP         |
| Ca1_P4_2018284   | Ca1                                     | 2018284                       | GCT/GCTCT                                                     | GGAAACAAGGAGCACG<br>ACAT | GCCGCAATGATGTGT<br>TATG  | 60.1                             | 344                                           | INTRON                                            | Ca_00254                            | FP                    | bHLH        |
| Ca1_P4_2018598   | Ca1                                     | 2018598                       | GGCGGC/GGCGGCCGGCGGC                                          | CATAAACACATCATTGC<br>GGC | TTCGGTTCTAGACAAT<br>CGG  | 60.0                             | 594                                           | INTRON                                            | Ca_00254                            | FP                    | bHLH        |
| Ca1_P4_2028913   | Ca1                                     | 2028913                       | CT/CTT                                                        | ACCTGTTCCCGTCTTC<br>TCAA | CCCCTTCTCTGTAAGT<br>CCCC | 59.7                             | 597                                           | INTRON                                            | Ca_00256                            | U                     | M-type      |
| Ca1_P4_2069251   | Ca1                                     | 2069251                       | C/CTT                                                         | CGTCAGGGATTTTCCT<br>TTGA | CGAATTTGTCACGTTTG<br>GTG | 60.0                             | 498                                           | INTRON                                            | Ca_00262                            | U                     | M-type      |
| Ca1_P4_2097669   | Ca1                                     | 2097669                       | CTTTTTTTTT/CTTTTTTTTTT                                        | GTGCTCTCGGTTTTG<br>CTCC  | TTCGGCTTTATGGCAA<br>ATTC | 60.0                             | 339                                           | INTRON                                            | Ca_00266                            | --                    | MYB_related |
| Ca1_P4_2108793   | Ca1                                     | 2108793                       | GTT/GTTTT                                                     | GTTTTATCTGCCGAAC<br>CTGC | CAATGGCAGTGATCTG<br>CTCT | 59.7                             | 678                                           | INTRON                                            | Ca_00267                            | D                     | NAC         |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                       |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca1_P4_21746056  | Ca1                                     | 21746056                      | AC/ACACATATCAGCTTTC                                                   | CTATTGCCCTCCTC<br>CTAC   | TACCGATACCTCCAAG<br>TGCC | 59.9                             | 585                                           | INTRON                                            | Ca_22116                            | S                     | --          |
| Ca1_P4_21923721  | Ca1                                     | 21923721                      | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATA<br>TATATATATAT | TCCTTGGTGGTGTCAC<br>TGGA | CACTGCCATCTGCAAC<br>CTTA | 60.1                             | 723                                           | INTRON                                            | Ca_22107                            | P                     | GRAS        |
| Ca1_P4_21938049  | Ca1                                     | 21938049                      | CACTGAGTCCAGA/CACTGAGTCCA<br>GACTGAGTCCAGA                            | TGTCAAAGGCCAAGAT<br>TCCT | CCTCACATCAAGAGCA<br>GCAA | 59.7                             | 526                                           | INTRON                                            | Ca_22106                            | --                    | MIKC        |
| Ca1_P4_2233184   | Ca1                                     | 2233184                       | GAAA/GAAAA                                                            | AATGGTTAATGAGTTG<br>CGGC | ATTCTTGACCATTCGG<br>CTTG | 60.0                             | 621                                           | INTRON                                            | Ca_00279                            | F                     | --          |
| Ca1_P4_2250886   | Ca1                                     | 2250886                       | TAAA/TAA                                                              | TGAATATCCAGAGATC<br>GCCC | CATTGCCCTTTCACCCT<br>TTA | 60.0                             | 858                                           | INTRON                                            | Ca_00281                            | O                     | --          |
| Ca1_P4_2250936   | Ca1                                     | 2250936                       | GA/GAA                                                                | TGAATATCCAGAGATC<br>GCCC | CATTGCCCTTTCACCCT<br>TTA | 60.0                             | 858                                           | INTRON                                            | Ca_00281                            | O                     | --          |
| Ca1_P4_2252313   | Ca1                                     | 2252313                       | GAA/GAAA                                                              | TGCAGTCAGGCAAGAC<br>AATC | TTCTTTTCTCTCCAG<br>CCA   | 60.0                             | 880                                           | INTRON                                            | Ca_00281                            | O                     | --          |
| Ca1_P4_22536709  | Ca1                                     | 22536709                      | GAAAAAAAAA/GAAAAAAAAA                                                 | TGAGGGAATAAGCGAG<br>ATCC | ATGAACTTGCCCTTGT<br>TGG  | 59.2                             | 568                                           | INTRON                                            | Ca_20619                            | C                     | bHLH        |
| Ca1_P4_2263034   | Ca1                                     | 2263034                       | AAAAA/AAAAAAAAAGAAAA                                                  | TTCCACCTCTTCTCATT<br>GGG | TGCTCCCTGTCTCAG<br>TTCT  | 60.0                             | 436                                           | INTRON                                            | Ca_00282                            | --                    | --          |
| Ca1_P4_2277770   | Ca1                                     | 2277770                       | AACAT/A                                                               | TTCTGTGCCTTGCTC<br>TTTT  | GCACGCCTTACGGTTA<br>ATGT | 60.0                             | 454                                           | INTRON                                            | Ca_00285                            | A                     | MYB_related |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca1_P4_2278321   | Ca1                                     | 2278321                       | ACT/ACTCT                                                     | ACATTAAACGTAAGGC<br>GTGC | ATGCGATTAGGGTTGT<br>CTGG | 60.0                             | 348                                           | INTRON                                            | Ca_00285                            | A                     | MYB_related |
| Ca1_P4_2279478   | Ca1                                     | 2279478                       | TA/TAA                                                        | GGGATGAATGCTGCAA<br>GTTT | TTTGGGCGAGGAATAA<br>CAAC | 60.1                             | 489                                           | INTRON                                            | Ca_00285                            | A                     | MYB_related |
| Ca1_P4_2291663   | Ca1                                     | 2291663                       | GAT/GATAAT                                                    | AGTGAATGGAAATCCG<br>CATC | AGAGTGCTGCTGAGGA<br>TGGT | 59.9                             | 552                                           | INTRON                                            | Ca_00287                            | --                    | --          |
| Ca1_P4_2298244   | Ca1                                     | 2298244                       | ACA/ACACATAACCA                                               | CTGAACATTTGAGCA<br>TGGA  | TCAGTGCTGTTTCTTG<br>GTGC | 59.6                             | 290                                           | INTRON                                            | Ca_00287                            | --                    | --          |
| Ca1_P4_2298416   | Ca1                                     | 2298416                       | GA/G                                                          | GCACCAAGAAACAGCA<br>CTGA | GAGGATTTTGATGGCG<br>AAGA | 60.0                             | 375                                           | INTRON                                            | Ca_00287                            | --                    | --          |
| Ca1_P4_2301600   | Ca1                                     | 2301600                       | ACCCCC/ACCCCCC                                                | AGATTTTGCGGGATAC<br>ATGG | TTGCATCTTGGTCTGA<br>GCAC | 59.8                             | 291                                           | INTRON                                            | Ca_00288                            | R                     | --          |
| Ca1_P4_2313379   | Ca1                                     | 2313379                       | GTTTT/GTT                                                     | GCCAAAGGCATTCATT<br>GTTT | TGTCATAAAAGGGTT<br>CCCG  | 59.9                             | 528                                           | INTRON                                            | Ca_00290                            | --                    | --          |
| Ca1_P4_2337136   | Ca1                                     | 2337136                       | TG/T                                                          | AGATGGGTTTGCTGGT<br>TTTG | GCATGGGCAGTACCTC<br>AAAT | 60.0                             | 581                                           | INTRON                                            | Ca_00294                            | A                     | --          |
| Ca1_P4_2370923   | Ca1                                     | 2370923                       | CA/CAA                                                        | CTATGGAAAATGCTCC<br>CGAA | CCGAAACTCACAATGA<br>ACCA | 60.0                             | 507                                           | INTRON                                            | Ca_00301                            | DR                    | --          |
| Ca1_P4_2371308   | Ca1                                     | 2371308                       | AGT/A                                                         | TGGTTCATTGTGAGTT<br>TCGG | GGTTTGCCATCTTGAT<br>GCTT | 59.5                             | 719                                           | INTRON                                            | Ca_00301                            | DR                    | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca1_P4_24030910  | Ca1                                     | 24030910                      | CAAAAAAAAA/CAAAAAAAAAA<br>A                                   | TGTTGGGAAAGGAGGA<br>TCTG  | CCTTCACGTGGGAGTT<br>TGAT  | 60.0                             | 240                                           | INTRON                                            | Ca_19291                            | OK                    | --   |
| Ca1_P4_24501689  | Ca1                                     | 24501689                      | ACATTCA/ACA                                                   | TACAGCCCCGATTTGT<br>CTTC  | ACTGCCTGCACTAAAG<br>CCAT  | 60.1                             | 520                                           | INTRON                                            | Ca_18342                            | --                    | --   |
| Ca1_P4_26358637  | Ca1                                     | 26358637                      | TTTTAGT/TTTTAGTTTAGT                                          | TGTGTTTCATCCTTCCA<br>CCA  | GGGTTCAACTTCAAAA<br>GCCA  | 59.9                             | 754                                           | INTRON                                            | Ca_18604                            | U                     | LSD  |
| Ca1_P4_27665473  | Ca1                                     | 27665473                      | C/CCCTAA                                                      | GCGTTTGAATGATTGT<br>TGGA  | TTGAGAGACTTGTGCC<br>CTAGC | 59.5                             | 819                                           | INTRON                                            | Ca_25073                            | --                    | --   |
| Ca1_P4_28345653  | Ca1                                     | 28345653                      | TGAGAGAGAGAGAGAGAGAGAG<br>A/TGAGAGAGAGAGAGAGAGAG<br>AGAGA     | GGTTGCATTAACCTGCA<br>GGGT | GCGCCAACCTACAAA<br>CATT   | 60.0                             | 548                                           | INTRON                                            | Ca_18516                            | --                    | --   |
| Ca1_P4_2898163   | Ca1                                     | 2898163                       | CAAAAAAAAA/CAAAAAAAAA                                         | TGGTGTTTACCACTCC<br>GTCA  | TTAAATCACAGTGGCG<br>GTCA  | 60.0                             | 368                                           | INTRON                                            | Ca_00354                            | --                    | bHLH |
| Ca1_P4_2899871   | Ca1                                     | 2899871                       | AT/ATTTCAAAATT                                                | AGGCCCAGCATTTGTA<br>TGTC  | AAGGCACTCTCCCGCT<br>TAAT  | 60.0                             | 629                                           | INTRON                                            | Ca_00354                            | --                    | bHLH |
| Ca1_P4_2900278   | Ca1                                     | 2900278                       | ATTT/ATTTTT                                                   | AATGCAGGCGTTTTGA<br>TAGG  | GGCAGAGAGCCATTCA<br>GTTC  | 60.1                             | 213                                           | INTRON                                            | Ca_00354                            | --                    | bHLH |
| Ca1_P4_2900742   | Ca1                                     | 2900742                       | AAC/A                                                         | CTGCAGGATCTGAGT<br>GACA   | GGAATGGTTTGGGGAA<br>TTTT  | 60.0                             | 637                                           | INTRON                                            | Ca_00354                            | --                    | bHLH |
| Ca1_P4_2901135   | Ca1                                     | 2901135                       | TTCTGAGAAAGTTATCT/TTCTGAGA<br>AAGTTATCTGAGAAAGTTATCT          | AGCTTCCACGAAAAT<br>CAGC   | GCACATTACAGTTGG<br>GGCT   | 59.5                             | 565                                           | INTRON                                            | Ca_00354                            | --                    | bHLH |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)              | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                            |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca1_P4_2935316   | Ca1                                     | 2935316                       | GAAATAAAAAATAAAAAA/GAAAT<br>AAAAAA                                         | ACTGATTCCCCACAC<br>CATA  | AACTGGGAGAGTTGAA<br>GGCA | 60.1                             | 776                                           | INTRON                                            | Ca_00358                            | E                     | --   |
| Ca1_P4_29636835  | Ca1                                     | 29636835                      | AA/AAGA                                                                    | TCACAAATCTCAACCCT<br>CCC | ATCAGTTGGAGCCTGG<br>TTGT | 59.9                             | 497                                           | INTRON                                            | Ca_24382                            | AR                    | --   |
| Ca1_P4_29637072  | Ca1                                     | 29637072                      | GAAAAAAAA/GAAAAAAAAA                                                       | ACAACCAGGCTCCAAC<br>TGAT | ATGCTGCCAGCCTACA<br>AAAT | 59.6                             | 503                                           | INTRON                                            | Ca_24382                            | AR                    | --   |
| Ca1_P4_2975302   | Ca1                                     | 2975302                       | ATT/AT                                                                     | TCCTGCAACCAATTTT<br>ACA  | AGCCAAGTGGAATGAG<br>TTGG | 60.1                             | 662                                           | INTRON                                            | Ca_00361                            | --                    | --   |
| Ca1_P4_29847994  | Ca1                                     | 29847994                      | TAAAAA/TAAAAA                                                              | TCTTTTCATCAGGCC<br>AATC  | GGAAAGTGAGGGAACC<br>AATG | 60.0                             | 228                                           | INTRON                                            | Ca_24388                            | --                    | --   |
| Ca1_P4_29848026  | Ca1                                     | 29848026                      | ATGT/AT                                                                    | TCTTTTCATCAGGCC<br>AATC  | GGAAAGTGAGGGAACC<br>AATG | 60.0                             | 228                                           | INTRON                                            | Ca_24388                            | --                    | --   |
| Ca1_P4_2991508   | Ca1                                     | 2991508                       | GTTTTTTTTTTTT/GTTTTTTTTTT                                                  | AACAACCATGCTGACC<br>CTTC | TTTACCCACAAGTGG<br>CATA  | 60.0                             | 394                                           | INTRON                                            | Ca_00363                            | PET                   | NAC  |
| Ca1_P4_2994933   | Ca1                                     | 2994933                       | CCAAATTCAAATTCAAATTC<br>AAATTCAAATTCAAATTC<br>AAATTCAAATTCAAATTC<br>AAATTC | GAGAGGAGAGAACAA<br>GGCG  | AAGCAATGAGTCTTCC<br>ACCG | 60.0                             | 425                                           | INTRON                                            | Ca_00364                            | A                     | bHLH |
| Ca1_P4_3037452   | Ca1                                     | 3037452                       | AT/ATTTAAAGTATTTGTT                                                        | ACACCAGCCGTTGAAT<br>AAGG | ATAACGGTGGAGCCTG<br>TTTG | 60.0                             | 916                                           | INTRON                                            | Ca_00370                            | --                    | ARF  |
| Ca1_P4_3068457   | Ca1                                     | 3068457                       | TTA/TTAAGTA                                                                | TCATTGGGTTGGGTTT<br>TCAT | TTATCAGTTGCAGCCT<br>GTGC | 60.0                             | 626                                           | INTRON                                            | Ca_00374                            | EH                    | bHLH |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                              |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca1_P4_3074494   | Ca1                                     | 3074494                       | AATA/AA                                                       | TTTGTGGGTCTTAATC<br>ATTTTACA | ATAATTGTGCAAGTGC<br>GGTG     | 58.9                             | 475                                           | INTRON                                            | Ca_00375                            | --                    | bHLH |
| Ca1_P4_3074826   | Ca1                                     | 3074826                       | A/AT                                                          | CACGAGGTTTGACCTC<br>TTCC     | CGTGTGAACATTTCATA<br>CACCTCA | 59.7                             | 578                                           | INTRON                                            | Ca_00375                            | --                    | bHLH |
| Ca1_P4_3075028   | Ca1                                     | 3075028                       | A/AT                                                          | CACGAGGTTTGACCTC<br>TTCC     | CGATCGTCGCATTTTTC<br>ATA     | 59.7                             | 841                                           | INTRON                                            | Ca_00375                            | --                    | bHLH |
| Ca1_P4_3075271   | Ca1                                     | 3075271                       | TAA/TAAA                                                      | GAGGTGTATGAATGTT<br>CACACGTA | TCATGGCAGTCTGCAA<br>AAAG     | 59.0                             | 542                                           | INTRON                                            | Ca_00375                            | --                    | bHLH |
| Ca1_P4_3075564   | Ca1                                     | 3075564                       | ATTTTT/ATTTTT                                                 | TGCGACGATCGACAAA<br>ATTA     | TCATGGCAGTCTGCAA<br>AAAG     | 60.2                             | 268                                           | INTRON                                            | Ca_00375                            | --                    | bHLH |
| Ca1_P4_3080532   | Ca1                                     | 3080532                       | CCTTTTCTTTTCTTTTCTTT/CCT<br>TTTTCTTTTCTTT                     | ATCATCCTAATGGACG<br>CTGC     | CAATCGCAAAATTCAC<br>TCCA     | 60.1                             | 260                                           | INTRON                                            | Ca_00376                            | --                    | bHLH |
| Ca1_P4_3081375   | Ca1                                     | 3081375                       | TG/T                                                          | AGATGGTGACCAGATT<br>GACG     | TGCCTCCTATCTCTCC<br>CACA     | 58.5                             | 683                                           | INTRON                                            | Ca_00376                            | --                    | bHLH |
| Ca1_P4_3088550   | Ca1                                     | 3088550                       | A/AG                                                          | CAAGTCGTTTGAGCTT<br>GTGC     | TTCCCGATAAGACGTTT<br>TGC     | 59.6                             | 349                                           | INTRON                                            | Ca_00377                            | J                     | --   |
| Ca1_P4_31089670  | Ca1                                     | 31089670                      | AATA/AA                                                       | TTGGAGCAGTTGCATT<br>TGAG     | ACCATTGCTGCAAACG<br>TACA     | 60.0                             | 750                                           | INTRON                                            | Ca_25826                            | S                     | --   |
| Ca1_P4_3124071   | Ca1                                     | 3124071                       | T/TC                                                          | ATAAACCAACGCGACA<br>AAGG     | AAAGTGCAGCTGGGAC<br>TACA     | 60.0                             | 946                                           | INTRON                                            | Ca_00382                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_3124658   | Ca1                                     | 3124658                       | CATATATATA/CATATATATATATA                                     | TTTACGGTGCATCAATT<br>TGC | CATTCTGTTGGTTTGTG<br>CATC | 59.6                             | 133                                           | INTRON                                            | Ca_00382                            | --                    | --  |
| Ca1_P4_3125906   | Ca1                                     | 3125906                       | GAAAAA/GAAAAAA                                                | GAAATCCACACCATCG<br>AACC | TGATTCATGTGCCTTAC<br>CCA  | 60.2                             | 595                                           | INTRON                                            | Ca_00382                            | --                    | --  |
| Ca1_P4_3125978   | Ca1                                     | 3125978                       | CAA/CAAA                                                      | GAAATCCACACCATCG<br>AACC | TGATTCATGTGCCTTAC<br>CCA  | 60.2                             | 595                                           | INTRON                                            | Ca_00382                            | --                    | --  |
| Ca1_P4_31457092  | Ca1                                     | 31457092                      | TC/T                                                          | CCCAAATTGTTACCA<br>ATCC  | GCAAATCCCATGAAGG<br>AAGA  | 60.0                             | 609                                           | INTRON                                            | Ca_21861                            | --                    | --  |
| Ca1_P4_3148374   | Ca1                                     | 3148374                       | TAAAAA/TAAAAAA                                                | AATACCCCATGACCC<br>ATCT  | GTGGACACCAGATACG<br>CCTT  | 60.3                             | 579                                           | INTRON                                            | Ca_00385                            | --                    | --  |
| Ca1_P4_3148999   | Ca1                                     | 3148999                       | CAATTAATTAATTAATTAAT/CA<br>ATTAATTAATTAATTAAT                 | GATTTGGAACAGCAAG<br>AGCC | ATTCCCGAATATGGTG<br>GACA  | 60.0                             | 512                                           | INTRON                                            | Ca_00385                            | --                    | --  |
| Ca1_P4_31590373  | Ca1                                     | 31590373                      | GTT/GT                                                        | TCGCTGCAACTCTCAA<br>ACAC | TGCTGTCAAATTGTC<br>GAGG   | 60.2                             | 315                                           | INTRON                                            | Ca_21868                            | F                     | --  |
| Ca1_P4_31592114  | Ca1                                     | 31592114                      | CT/CTTT                                                       | TCAGCTGCAGTTCCAA<br>CATC | GCACAAGTCCTTGAGG<br>AAGC  | 60.0                             | 375                                           | INTRON                                            | Ca_21868                            | F                     | --  |
| Ca1_P4_31592347  | Ca1                                     | 31592347                      | GAA/GAAAA                                                     | CCTGTGTAGCCAGCTT<br>CCTC | TAGCCTCATTCACTCTC<br>GCA  | 60.0                             | 618                                           | INTRON                                            | Ca_21868                            | F                     | --  |
| Ca1_P4_32078246  | Ca1                                     | 32078246                      | TA/TAAAAA                                                     | CTCGGTTCGAACAGGA<br>GAAG | TATGTCAACAACCCCT<br>GGT   | 60.0                             | 702                                           | INTRON                                            | Ca_26405                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca1_P4_32080106  | Ca1                                     | 32080106                      | T/TC                                                          | TTCCCATGTCGATCT<br>AAGC   | AACCCTGAACAGATTG<br>TCGG  | 60.0                             | 612                                           | INTRON                                            | Ca_26405                            | --                    | --       |
| Ca1_P4_32222272  | Ca1                                     | 32222272                      | ATTTT/ATTTT                                                   | ACAACCTCTCATGCTC<br>GCAA  | GGTGGCATACCTCAAC<br>GAGT  | 59.6                             | 620                                           | INTRON                                            | Ca_26127                            | --                    | Trihelix |
| Ca1_P4_32281608  | Ca1                                     | 32281608                      | GTTT/GTTT                                                     | GCATTTCCCCTGACTT<br>CTGA  | TTCAAAGTGTGTTGCC<br>CAAAA | 60.2                             | 819                                           | INTRON                                            | Ca_26129                            | --                    | --       |
| Ca1_P4_3285628   | Ca1                                     | 3285628                       | ATTTTTTTTT/ATTTTTTTTT                                         | AGGTGCAACGAGGAAA<br>ACAG  | AGCAACACTGATGCCA<br>TTGA  | 60.3                             | 805                                           | INTRON                                            | Ca_00398                            | --                    | LBD      |
| Ca1_P4_3287281   | Ca1                                     | 3287281                       | TAAAAAA/TAAAAAA                                               | TGCTGAAAGAGTTGTC<br>GGTG  | AGAGGGACCACAAAGT<br>CAAA  | 60.0                             | 516                                           | INTRON                                            | Ca_00398                            | --                    | LBD      |
| Ca1_P4_33116756  | Ca1                                     | 33116756                      | TAAAAAAAA/TAAAAAAAAA                                          | CGCAATCTTTTCCACC<br>TTC   | TTGACGAACCTTGTGC<br>TTTG  | 59.7                             | 117                                           | INTRON                                            | Ca_19439                            | --                    | --       |
| Ca1_P4_33187249  | Ca1                                     | 33187249                      | GTAT/GTATAT                                                   | TAAAGGTTCCCTCGCA<br>TCTG  | CACCACAGAAGAACTT<br>GGCA  | 60.2                             | 530                                           | INTRON                                            | Ca_19440                            | A                     | --       |
| Ca1_P4_33330670  | Ca1                                     | 33330670                      | CTTTTTTTTT/CTTTTTTTTT                                         | TTTGCTCATTCTACGT<br>TGC   | GAGTCACAAGAAAGCG<br>AGGG  | 58.9                             | 174                                           | INTRON                                            | Ca_19441                            | --                    | MIKC     |
| Ca1_P4_33331863  | Ca1                                     | 33331863                      | ATTTTT/ATTTTT                                                 | TGAAGAACTGAATCC<br>GAACAA | CTCGAAACCTTCTTCC<br>CAA   | 59.7                             | 606                                           | INTRON                                            | Ca_19441                            | --                    | MIKC     |
| Ca1_P4_33336930  | Ca1                                     | 33336930                      | GAAAA/GAAAA                                                   | CAATGGCAACAAGGTC<br>AATG  | TCACATCTGTTGGTAAC<br>GGG  | 60.0                             | 856                                           | INTRON                                            | Ca_19441                            | --                    | MIKC     |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                            |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca1_P4_33354017  | Ca1                                     | 33354017                      | ATTCA/ATTCAACCCCTTTTCA                                        | GGAGGGTCAGGTGCTT<br>TGTA   | CAGCCTCCATCCTTCTT<br>CTG     | 60.1                             | 516                                           | INTRON                                            | Ca_19441                            | --                    | MIKC        |
| Ca1_P4_33356994  | Ca1                                     | 33356994                      | TCC/TC                                                        | CGAGTGGTTTTGTGTG<br>TCGT   | ATCATTATCCTCGTGTG<br>GGC     | 59.6                             | 345                                           | INTRON                                            | Ca_19441                            | --                    | MIKC        |
| Ca1_P4_33365935  | Ca1                                     | 33365935                      | CTTTTTTTTT/CTTTTTTTTTTTT                                      | CCACGTGTGGTCCCTT<br>AACT   | TTTTTCTCCGATTTGG<br>TCA      | 59.9                             | 485                                           | INTRON                                            | Ca_19441                            | --                    | MIKC        |
| Ca1_P4_33757154  | Ca1                                     | 33757154                      | TAAAAAAAAA/TAAAAAAAAA                                         | ATTCCCATCCCTATGT<br>GCAA   | CCTTATTTCACTGTGTC<br>CGTTCA  | 60.2                             | 772                                           | INTRON                                            | Ca_19458                            | --                    | --          |
| Ca1_P4_34263760  | Ca1                                     | 34263760                      | T/TTGCAC                                                      | ATCCAAATGGGATGG<br>ATGA    | GTTCCGAACATGCTGT<br>CCTT     | 60.0                             | 703                                           | INTRON                                            | Ca_25475                            | M                     | MYB_related |
| Ca1_P4_345766    | Ca1                                     | 345766                        | GAA/GA                                                        | TCAACTTTGAGGTCTC<br>CGGT   | TCACTCCGTTTCTGCC<br>TCT      | 59.7                             | 182                                           | INTRON                                            | Ca_00035                            | O                     | --          |
| Ca1_P4_346903    | Ca1                                     | 346903                        | AG/AGG                                                        | AATGAAATGGGCATT<br>GAGC    | CTTTTAGCCATGTTTG<br>GGA      | 59.9                             | 577                                           | INTRON                                            | Ca_00035                            | O                     | --          |
| Ca1_P4_34907461  | Ca1                                     | 34907461                      | TT/TTCT                                                       | TAGCGTTGTGTCGGAA<br>AGTG   | TATAAGGTTGGCTTGG<br>TGCC     | 59.9                             | 372                                           | INTRON                                            | Ca_21409                            | --                    | --          |
| Ca1_P4_35112845  | Ca1                                     | 35112845                      | ATTATTTATTTATTT/ATTATTTATTT<br>ATTTATTT                       | TCCTGCATCAACACAT<br>AACACA | TGAGCTTATACCGTTT<br>TCTGAG   | 60.0                             | 495                                           | INTRON                                            | Ca_21404                            | K                     | HD-ZIP      |
| Ca1_P4_35281444  | Ca1                                     | 35281444                      | ATTTTTTTT/ATTTTTTTT                                           | ACAAAGGCCTGCCTAG<br>ATCA   | TTTTTGATGTCTCTCTG<br>TTCAAAT | 59.8                             | 591                                           | INTRON                                            | Ca_26099                            | QI                    | bHLH        |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                                |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca1_P4_35281490  | Ca1                                     | 35281490                      | ATTTTTTT/ATTTTTT                                              | CTAAGGCACCCCTCTC<br>CACA       | TTTTTGATGTCTCTCTG<br>TTCAAAT | 60.2                             | 543                                           | INTRON                                            | Ca_26099                            | QI                    | bHLH |
| Ca1_P4_35281570  | Ca1                                     | 35281570                      | TC/T                                                          | ATGACACGTCATTCGT<br>TTCG       | GGTTCGAGACATCCAT<br>AATTCA   | 59.6                             | 733                                           | INTRON                                            | Ca_26099                            | QI                    | bHLH |
| Ca1_P4_35281940  | Ca1                                     | 35281940                      | TA/TAA                                                        | AAACGTGATCTATACA<br>GTTTCCAAAA | TTACATCTGGAACAA<br>CGC       | 59.4                             | 529                                           | INTRON                                            | Ca_26099                            | QI                    | bHLH |
| Ca1_P4_373618    | Ca1                                     | 373618                        | AGGGGG/AGGGGGG                                                | ACCCTTAGTCTCTCCC<br>ACCC       | GGGCTTCGAACCTTCC<br>TTCT     | 60.4                             | 318                                           | INTRON                                            | Ca_00038                            | S                     | --   |
| Ca1_P4_374767    | Ca1                                     | 374767                        | TCA/TCACA                                                     | AACACGGCAGTGGTAT<br>CTCC       | CATCATCAAGGCCATC<br>CTCT     | 60.0                             | 722                                           | INTRON                                            | Ca_00038                            | S                     | --   |
| Ca1_P4_37724987  | Ca1                                     | 37724987                      | A/ATT                                                         | ACCCTGTTGCTGCCAA<br>ATAC       | GCTCCAATCCCTCAG<br>ATCA      | 60.0                             | 664                                           | INTRON                                            | Ca_23534                            | --                    | --   |
| Ca1_P4_37797311  | Ca1                                     | 37797311                      | AT/ATT                                                        | TGCTATGACCCACCA<br>ATTT        | TTGATTATCCCTCCGT<br>GCT      | 60.2                             | 500                                           | INTRON                                            | Ca_23537                            | --                    | NAC  |
| Ca1_P4_37797366  | Ca1                                     | 37797366                      | T/TA                                                          | TGCTATGACCCACCA<br>ATTT        | AGAAGGAACAAGGGCA<br>AGGT     | 60.2                             | 913                                           | INTRON                                            | Ca_23537                            | --                    | NAC  |
| Ca1_P4_37798489  | Ca1                                     | 37798489                      | ATTTTTTTTT/ATTTTTT                                            | GGCATGTGCATCCTTG<br>TAGA       | GGAATCACATCCTGGT<br>GCTT     | 59.7                             | 644                                           | INTRON                                            | Ca_23537                            | --                    | NAC  |
| Ca1_P4_37798793  | Ca1                                     | 37798793                      | TATTA/TATTATTAATATCTGATTA                                     | TGTGGAACCTTGATTT<br>GGTGA      | TATCGCCTCATGGAAT<br>CACA     | 59.0                             | 583                                           | INTRON                                            | Ca_23537                            | --                    | NAC  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca1_P4_37799193  | Ca1                                     | 37799193                      | TAAAA/TAAAA                                                   | TGTGATTCCATGAGGC<br>GATA | TTGATTGCAACAGTGG<br>CCTA | 60.0                             | 785                                           | INTRON                                            | Ca_23537                            | --                    | NAC    |
| Ca1_P4_37799228  | Ca1                                     | 37799228                      | CACTAATTTA/CA                                                 | TGTGATTCCATGAGGC<br>GATA | TTGATTGCAACAGTGG<br>CCTA | 60.0                             | 785                                           | INTRON                                            | Ca_23537                            | --                    | NAC    |
| Ca1_P4_37851381  | Ca1                                     | 37851381                      | GGTTAATA/GGTTAATAGTTAATA                                      | GGGGGTGACAAATTTA<br>GGTG | ACCTGGCCTCTTCAAC<br>CTTT | 59.1                             | 630                                           | INTRON                                            | Ca_23538                            | T                     | E2F/DP |
| Ca1_P4_37851702  | Ca1                                     | 37851702                      | AAATAA/AAA                                                    | AAAGGTTGAAGAGGCC<br>AGGT | AACATGCTATGGGCAA<br>CCTC | 60.1                             | 568                                           | INTRON                                            | Ca_23538                            | T                     | E2F/DP |
| Ca1_P4_37872084  | Ca1                                     | 37872084                      | CCAGAGTATTTCTGCAGAG/CCAG<br>AG                                | AAGGTACCATCAGCAA<br>TCCG | CGGCATAAATCTTGCC<br>AACT | 60.0                             | 401                                           | INTRON                                            | Ca_23539                            | KT                    | --     |
| Ca1_P4_37875883  | Ca1                                     | 37875883                      | TTAT/TT                                                       | GCTGGGACTTATTTC<br>GTGA  | TGCCAGGTGACAAAAT<br>CTCA | 60.1                             | 201                                           | INTRON                                            | Ca_23539                            | KT                    | --     |
| Ca1_P4_37876112  | Ca1                                     | 37876112                      | ACCCCC/ACCCC                                                  | GCTGGGACTTATTTC<br>GTGA  | CAACACCCCCTTTTCA<br>AGA  | 60.1                             | 601                                           | INTRON                                            | Ca_23539                            | KT                    | --     |
| Ca1_P4_37887479  | Ca1                                     | 37887479                      | GTTTTTTTTT/GTTTTTTTTTTTT                                      | GATTGCAAAATCCGGA<br>AAAA | TGGGCACTATTGTTG<br>GACA  | 59.9                             | 530                                           | INTRON                                            | Ca_23539                            | KT                    | --     |
| Ca1_P4_38195545  | Ca1                                     | 38195545                      | CATA/CATATA                                                   | CAGACCAACTGCAAGT<br>CCAA | TCACGAATCCCATGTT<br>TGA  | 59.9                             | 539                                           | INTRON                                            | Ca_13974                            | L                     | C2H2   |
| Ca1_P4_38196253  | Ca1                                     | 38196253                      | CTA/C                                                         | CGTTCAAGAGGTGGAA<br>AAGC | TGCAGTGCCCTGTTG<br>ACAT  | 59.9                             | 435                                           | INTRON                                            | Ca_13974                            | L                     | C2H2   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_38740282  | Ca1                                     | 38740282                      | GAATTAA/GAA                                                   | AAACCGTTACCTGCAT<br>TTCG   | TGAGAGCTATTTTTCG<br>GACACA  | 60.0                             | 548                                           | INTRON                                            | Ca_13954                            | --                    | --  |
| Ca1_P4_39027902  | Ca1                                     | 39027902                      | CA/C                                                          | CACCAATCTCATGGTG<br>TTCG   | GCATTTTCAGGAAAAG<br>AAAAAGG | 60.0                             | 618                                           | INTRON                                            | Ca_13946                            | --                    | --  |
| Ca1_P4_39028142  | Ca1                                     | 39028142                      | AATATATATATAT/AATATATATAT                                     | TCATGGAAGGAGCAAT<br>CACA   | TAAGGTTTAGGATGCC<br>CCAA    | 60.2                             | 764                                           | INTRON                                            | Ca_13946                            | --                    | --  |
| Ca1_P4_39041564  | Ca1                                     | 39041564                      | TAAA/TAA                                                      | GAAAAAGCGCTGTTGT<br>AGGG   | TGGCCGCACAATATGT<br>AGAG    | 59.9                             | 435                                           | INTRON                                            | Ca_13946                            | --                    | --  |
| Ca1_P4_39055997  | Ca1                                     | 39055997                      | GAAAAAAAA/GAAAAAAAAA                                          | AGCATGCTGTAAGGGA<br>TCTGA  | CAAATAAGCGCGGTAA<br>AAGG    | 59.9                             | 426                                           | INTRON                                            | Ca_13946                            | --                    | --  |
| Ca1_P4_39060053  | Ca1                                     | 39060053                      | ACACGTTTTTC/AC                                                | TGATTCTTGCCGAAAA<br>AGTACC | TACTGCGCAAGAAAAAC<br>TCCC   | 60.5                             | 496                                           | INTRON                                            | Ca_13946                            | --                    | --  |
| Ca1_P4_39063031  | Ca1                                     | 39063031                      | CATAT/CAT                                                     | AAGGGTGTTTCGTGTCC<br>CATA  | TGAATTTGTGAGCTTCT<br>TGTGAA | 60.2                             | 277                                           | INTRON                                            | Ca_13946                            | --                    | --  |
| Ca1_P4_39070957  | Ca1                                     | 39070957                      | ATTTTTTTT/ATTTTTTT                                            | TGAAAAATGCAATCCT<br>CAGA   | AATTGATAACCCACCG<br>CAAG    | 59.2                             | 609                                           | INTRON                                            | Ca_13946                            | --                    | --  |
| Ca1_P4_39144961  | Ca1                                     | 39144961                      | CACGTAC/CAC                                                   | CATCCTTTGCAGGATT<br>GGTT   | TTGTGCTTTGGAAAAATG<br>CAG   | 59.9                             | 494                                           | INTRON                                            | Ca_13942                            | --                    | ARF |
| Ca1_P4_39433392  | Ca1                                     | 39433392                      | CTTTTTTT/CTTTTTT                                              | TATCCATACCACCTG<br>CCAT    | CTCAGGATCCTCAACC<br>CAAA    | 60.0                             | 378                                           | INTRON                                            | Ca_13931                            | Z                     | NAC |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca1_P4_39440225  | Ca1                                     | 39440225                      | CA/CAA                                                        | GCCACCAATCTTTG<br>CCTA   | CCTGCGAAGTTTCAGG<br>TTTC | 60.1                             | 380                                           | INTRON                                            | Ca_13931                            | Z                     | NAC   |
| Ca1_P4_39440990  | Ca1                                     | 39440990                      | TTCT/TTCTCT                                                   | TTGAAGAAGCTAAGGG<br>GCAA | CTGCTGTTTGCATGGA<br>TTGT | 60.0                             | 445                                           | INTRON                                            | Ca_13931                            | Z                     | NAC   |
| Ca1_P4_39441175  | Ca1                                     | 39441175                      | T/TG                                                          | TTGAAGAAGCTAAGGG<br>GCAA | CTGCTGTTTGCATGGA<br>TTGT | 60.0                             | 445                                           | INTRON                                            | Ca_13931                            | Z                     | NAC   |
| Ca1_P4_39442423  | Ca1                                     | 39442423                      | TAAAAAA/TAAAAA                                                | GCCTCAAGGATCGGAT<br>AACA | CTGCTGCCTTTCTGTG<br>AGTG | 60.0                             | 842                                           | INTRON                                            | Ca_13931                            | Z                     | NAC   |
| Ca1_P4_39442566  | Ca1                                     | 39442566                      | A/AT                                                          | GCCTCAAGGATCGGAT<br>AACA | GCCAGTGTTCGTGCTT<br>CATA | 60.0                             | 917                                           | INTRON                                            | Ca_13931                            | Z                     | NAC   |
| Ca1_P4_39442792  | Ca1                                     | 39442792                      | A/ACT                                                         | TGAATGGCATGCAAGA<br>AAAG | GCCAGTGTTCGTGCTT<br>CATA | 59.8                             | 631                                           | INTRON                                            | Ca_13931                            | Z                     | NAC   |
| Ca1_P4_39445206  | Ca1                                     | 39445206                      | ATTTT/ATTT                                                    | TTTACAGGGGTCATCT<br>TGGG | TCAAATTGAAGGCGTG<br>TCAG | 59.8                             | 448                                           | INTRON                                            | Ca_13931                            | Z                     | NAC   |
| Ca1_P4_39613155  | Ca1                                     | 39613155                      | AATTATTATTATTA/AATTATTATTAT<br>TATTA                          | GGATTGACAACCATCC<br>CTTG | AACAAATGGCTAATG<br>GCGT  | 60.2                             | 525                                           | INTRON                                            | Ca_13924                            | F                     | YABBY |
| Ca1_P4_39614109  | Ca1                                     | 39614109                      | TA/T                                                          | TGTCATTGAGTTGGGT<br>GGAA | ACCAAAACAAAGTGC<br>CAGG  | 59.9                             | 325                                           | INTRON                                            | Ca_13924                            | F                     | YABBY |
| Ca1_P4_39615125  | Ca1                                     | 39615125                      | ATTTTTTTT/ATTTTTTTTT                                          | TGTCGCTGTTCAAAGG<br>TACG | TTGTCCTAACGGTCCA<br>CTCC | 59.9                             | 740                                           | INTRON                                            | Ca_13924                            | F                     | YABBY |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca1_P4_39726359  | Ca1                                     | 39726359                      | CATGAA/CA                                                     | TGTGGAAAGGTTTACA<br>GAACCC | TAAAAGCCCAACAAT<br>GGG   | 60.3                             | 537                                           | INTRON                                            | Ca_13917                            | C                     | --  |
| Ca1_P4_39844169  | Ca1                                     | 39844169                      | AT/ATCACTT                                                    | AATTAATATTCGCGCAA<br>CGC   | AATGGATGCATCAAAT<br>GGGT | 60.1                             | 879                                           | INTRON                                            | Ca_13909                            | --                    | --  |
| Ca1_P4_40355282  | Ca1                                     | 40355282                      | ATTGTCC/ATTGTCCATTTGTCC                                       | GCACAGGTTAGGGTTT<br>TGGA   | TTCATGTTGCTTTAAG<br>GGG  | 60.0                             | 739                                           | INTRON                                            | Ca_13893                            | S                     | --  |
| Ca1_P4_40355583  | Ca1                                     | 40355583                      | TAAAA/TAAAAA                                                  | GGAATTCTCAGGTTTT<br>CGCA   | TTCATGTTGCTTTAAG<br>GGG  | 60.2                             | 616                                           | INTRON                                            | Ca_13893                            | S                     | --  |
| Ca1_P4_40358428  | Ca1                                     | 40358428                      | CT/CTTT                                                       | AACCACAATCGGCGAA<br>TAAG   | TCGGTAAGGCAAGAAC<br>CATC | 60.0                             | 357                                           | INTRON                                            | Ca_13893                            | S                     | --  |
| Ca1_P4_406876    | Ca1                                     | 406876                        | C/CCCTCTT                                                     | TGACACAAAATCAGGC<br>CAAA   | ACACATGGCAAAATTC<br>ACG  | 60.1                             | 629                                           | INTRON                                            | Ca_00043                            | --                    | --  |
| Ca1_P4_4258559   | Ca1                                     | 4258559                       | ATTT/ATTTT                                                    | GGTATGGGATGGTTGG<br>TGTC   | CGTAACGGGACTGGAA<br>AGAA | 59.9                             | 154                                           | INTRON                                            | Ca_00507                            | --                    | --  |
| Ca1_P4_430134    | Ca1                                     | 430134                        | AT/ATT                                                        | GTGGGGTGTAGCTTGC<br>TCTC   | AGAAGCTCGCATAAGC<br>CAAA | 59.9                             | 746                                           | INTRON                                            | Ca_00048                            | U                     | --  |
| Ca1_P4_432009    | Ca1                                     | 432009                        | CAATAATAAAT/CAATAATAAAT<br>AATAAT                             | AAACCCACCCCTCTTG<br>AAAT   | ATGCACGCGTATGATT<br>GTGT | 59.7                             | 458                                           | INTRON                                            | Ca_00048                            | U                     | --  |
| Ca1_P4_46271     | Ca1                                     | 46271                         | CAAAAAAAAA/CAAAAAAAAAAA<br>AA                                 | TCCATCCTTTTTCATCT<br>GCC   | AAGGGGTCAGTGAAC<br>GGTG  | 60.0                             | 926                                           | INTRON                                            | Ca_00004                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca1_P4_46831943  | Ca1                                     | 46831943                      | CTTTT/CTTT                                                    | GTGGTTGGTTGCAAG<br>AGGT   | AACTGGGTGAGAGCCT<br>GAGA | 60.0                             | 725                                           | INTRON                                            | Ca_25116                            | U                     | --          |
| Ca1_P4_4718653   | Ca1                                     | 4718653                       | CATAT/CAT                                                     | TTTGACACGACCAACC<br>AAAA  | TGGACACAGCAAGTTA<br>AGCG | 60.0                             | 781                                           | INTRON                                            | Ca_00555                            | T                     | MYB_related |
| Ca1_P4_4720237   | Ca1                                     | 4720237                       | CTTA/CTTAATTA                                                 | TCAGAGTTCATTGCAA<br>ACGG  | GGGATTCCCATTTTCC<br>ATCT | 59.8                             | 691                                           | INTRON                                            | Ca_00555                            | T                     | MYB_related |
| Ca1_P4_4720443   | Ca1                                     | 4720443                       | AT/A                                                          | TCAGAGTTCATTGCAA<br>ACGG  | GGGATTCCCATTTTCC<br>ATCT | 59.8                             | 691                                           | INTRON                                            | Ca_00555                            | T                     | MYB_related |
| Ca1_P4_4720541   | Ca1                                     | 4720541                       | ATTTTTTTTT/ATTTTTTTT                                          | GCTTTACAATGCACCT<br>GTTGA | GGGATTCCCATTTTCC<br>ATCT | 58.8                             | 359                                           | INTRON                                            | Ca_00555                            | T                     | MYB_related |
| Ca1_P4_4721444   | Ca1                                     | 4721444                       | TA/T                                                          | TCCCTGTCGCTCAAAA<br>ACTT  | TCGAAATCGAGGTATG<br>GAGG | 59.9                             | 519                                           | INTRON                                            | Ca_00555                            | T                     | MYB_related |
| Ca1_P4_4808961   | Ca1                                     | 4808961                       | GTTTTT/GTTT                                                   | AACTGCCAATAAGGCC<br>CCTT  | TCGGAAAATCCCTCTC<br>CTTT | 60.0                             | 377                                           | INTRON                                            | Ca_00566                            | UD                    | --          |
| Ca1_P4_5290057   | Ca1                                     | 5290057                       | ACC/AC                                                        | AGAAACGGTCACCTTC<br>CCTT  | CTCATTGCTTCCCAAAC<br>CAT | 60.0                             | 811                                           | INTRON                                            | Ca_00616                            | P                     | --          |
| Ca1_P4_5464246   | Ca1                                     | 5464246                       | T/TC                                                          | TGGTAAATGGCCATGA<br>GGAT  | CCCTCAACACACTCAT<br>GTGG | 60.2                             | 468                                           | INTRON                                            | Ca_00631                            | --                    | --          |
| Ca1_P4_5803481   | Ca1                                     | 5803481                       | TTAAGATAAGAT/TTAAGAT                                          | GCTCATGAGTTCCCTA<br>CCCA  | GTCAGGGGCTCGTGTA<br>TGAT | 60.1                             | 560                                           | INTRON                                            | Ca_00671                            | O                     | FAR1        |





| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca1_P4_7885437   | Ca1                                     | 7885437                       | TAAAA/TAA                                                     | AAGCATAACATAACCGGCG     | GATCGTGAAGGACACCCTGT    | 60.0                             | 520                                           | INTRON                                            | Ca_08037                            | I                     | bHLH        |
| Ca1_P4_7950391   | Ca1                                     | 7950391                       | AGAAAAAATATGAAAAA/AGAAAA<br>AA                                | CGACAATTAAGGAACGAGG     | CAGAAAGGAGCATAAGGCAGG   | 60.0                             | 600                                           | INTRON                                            | Ca_08045                            | QI                    | B3          |
| Ca1_P4_7950727   | Ca1                                     | 7950727                       | CAAATTCATAA/CA                                                | AAATGGAAGGAATTCCCTTG    | TCCAAAAGGATGGAAAGTGC    | 60.1                             | 222                                           | INTRON                                            | Ca_08045                            | QI                    | B3          |
| Ca1_P4_7951829   | Ca1                                     | 7951829                       | CAACT/CACTAACT                                                | TGAAGTAGCACCTTGGCCTT    | CCTGTTATGGAGGCTTTGGA    | 59.9                             | 688                                           | INTRON                                            | Ca_08045                            | QI                    | B3          |
| Ca1_P4_7952780   | Ca1                                     | 7952780                       | AC/A                                                          | GCCAACCAGGTGTGAATCTT    | AAATCCATCAACGAGCCACT    | 60.0                             | 577                                           | INTRON                                            | Ca_08045                            | QI                    | B3          |
| Ca1_P4_7952996   | Ca1                                     | 7952996                       | CT/CTT                                                        | AGTGGCTCGTTGATGGATT     | GCCTTGTGTTGATTTGTCACC   | 59.6                             | 120                                           | INTRON                                            | Ca_08045                            | QI                    | B3          |
| Ca1_P4_7953353   | Ca1                                     | 7953353                       | TATA/TATAGAATA                                                | AGTGGCTCGTTGATGGATT     | TGGTGTCACGTGCCATGTC     | 59.6                             | 786                                           | INTRON                                            | Ca_08045                            | QI                    | B3          |
| Ca1_P4_7991091   | Ca1                                     | 7991091                       | T/TTGAATGGTGAAAA                                              | TAGATGCAACTGATGCGACC    | TGGTTTGATTCTGCAACCA     | 59.8                             | 624                                           | INTRON                                            | Ca_08049                            | --                    | WRKY        |
| Ca1_P4_8063349   | Ca1                                     | 8063349                       | CTGGTTGGT/CTGGT                                               | GCAGTATGGCAAGAGCAACA    | TCATCACATTAAGGCCAGCA    | 60.0                             | 486                                           | INTRON                                            | Ca_08053                            | O                     | MYB_related |
| Ca1_P4_8102400   | Ca1                                     | 8102400                       | CAA/CA                                                        | CCCACCATCCATCTTCTTA     | CCTGCTGTTACACCCCTCAT    | 59.7                             | 403                                           | INTRON                                            | Ca_08056                            | C                     | --          |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                            | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                                                          |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca2_P4_1412343   | Ca2                                     | 1412343                       | TTTATTATTATTATTATTATTATT<br>ATTATTATTA/TTTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA                                      | TAAATTTGGAGGACC<br>GTGG    | TAGCACGACACTTCGG<br>ATTG  | 59.8                             | 523                                           | INTRON                                            | Ca_20697                            | R                     | --       |
| Ca2_P4_1842322   | Ca2                                     | 1842322                       | AG/AGGCAGG                                                                                                               | CGGCTTCTGACACACA<br>AAGA   | CTAAATGCAGAAAAAG<br>CCGC  | 60.0                             | 395                                           | INTRON                                            | Ca_12600                            | --                    | SBP      |
| Ca2_P4_1857596   | Ca2                                     | 1857596                       | CTTTTTTTTT/CTTTTTTTTT                                                                                                    | CCGGCACATGTACTAA<br>TTTGAG | GACGGGCATAAATCCT<br>TCAA  | 59.5                             | 926                                           | INTRON                                            | Ca_12598                            | YU                    | --       |
| Ca2_P4_19008979  | Ca2                                     | 19008979                      | TAAAAA/TAAAAAAA                                                                                                          | GGCTATATCTCCCATG<br>CCAA   | GCAAGAAACGAGGAAA<br>GAAGG | 59.9                             | 663                                           | INTRON                                            | Ca_15954                            | --                    | bHLH     |
| Ca2_P4_19015976  | Ca2                                     | 19015976                      | T/TA                                                                                                                     | AAACACTTATGGGCGA<br>GGTG   | ATTGAATTGGTGGTCG<br>AAGC  | 60.0                             | 256                                           | INTRON                                            | Ca_15954                            | --                    | bHLH     |
| Ca2_P4_1990862   | Ca2                                     | 1990862                       | GATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATT/GATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATT             | GAGGATTAAGCCAATG<br>CCAA   | ACTTGTGTTTGGTCCC<br>ATGA  | 60.0                             | 635                                           | INTRON                                            | Ca_12580                            | GE                    | HB-other |
| Ca2_P4_20439742  | Ca2                                     | 20439742                      | TTT/TTTATATATTCTT                                                                                                        | CAGCGTTTTGGCATT<br>ACAA    | TGCTGTCTTCTCCGA<br>GTTT   | 59.7                             | 761                                           | INTRON                                            | Ca_25923                            | LT                    | --       |
| Ca2_P4_21652629  | Ca2                                     | 21652629                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATT/TTTATTATTATTATT<br>TATTATTATTATTATTATTATTAT<br>TATTATT | GCCATGTCAAAGTATC<br>GCCT   | TGCCATGCAAAAATATC<br>AGG  | 60.1                             | 548                                           | INTRON                                            | Ca_23050                            | --                    | Trihelix |
| Ca2_P4_22517081  | Ca2                                     | 22517081                      | ATTTTTTT/ATTTTTTT                                                                                                        | TGTGCAATTTCTCCAC<br>CAAA   | CAGTTAACAGCCACCT<br>TCCA  | 60.1                             | 149                                           | INTRON                                            | Ca_14997                            | G                     | --       |
| Ca2_P4_25768325  | Ca2                                     | 25768325                      | CT/C                                                                                                                     | CATCACGATCTTTGTC<br>CACG   | AAGGGAGACGCAAGAA<br>ATGA  | 60.1                             | 551                                           | INTRON                                            | Ca_14294                            | G                     | NAC      |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca2_P4_3046091   | Ca2                                     | 3046091                       | C/CAT                                                         | TCCTACCCAAGATCCG<br>TCAG  | AACCAATGGAAGGTAA<br>GGGG  | 60.1                             | 494                                           | INTRON                                            | Ca_10543                            | --                    | --   |
| Ca2_P4_30569240  | Ca2                                     | 30569240                      | AT/ATT                                                        | AGTTTTGCAGCTTTTG<br>CCTC  | CCGTCCAATTTTCTCTT<br>GGA  | 59.6                             | 609                                           | INTRON                                            | Ca_12495                            | E                     | --   |
| Ca2_P4_30569699  | Ca2                                     | 30569699                      | CTTTT/CTTTTT                                                  | TCCAAGAGAAAATTGG<br>ACGG  | GCCATCCATTACGAGG<br>AAGA  | 60.0                             | 570                                           | INTRON                                            | Ca_12495                            | E                     | --   |
| Ca2_P4_30615697  | Ca2                                     | 30615697                      | CATCATAA/CATCATAATCATAA                                       | TACTAAAACGGCAAAA<br>CCCG  | TCCTGTGCGTAAGACT<br>GGTG  | 60.0                             | 533                                           | INTRON                                            | Ca_12491                            | --                    | --   |
| Ca2_P4_30621875  | Ca2                                     | 30621875                      | TT/TTCT                                                       | TAAGCTTTCCCGTGTC<br>TGCT  | TTGGGGTCAAATGGTT<br>GATT  | 60.0                             | 813                                           | INTRON                                            | Ca_12490                            | R                     | --   |
| Ca2_P4_30622722  | Ca2                                     | 30622722                      | A/ACCGTAATCC                                                  | CTTGGTCAGAATCACG<br>GAGC  | CACGTTGACCCTTTTTG<br>TCA  | 60.8                             | 380                                           | INTRON                                            | Ca_12490                            | R                     | --   |
| Ca2_P4_30664778  | Ca2                                     | 30664778                      | CTTTTTTTTT/CTTTTTTTTT                                         | TTGACCGTCTTATTCG<br>CCTT  | CTAAACCCCGAACCAT<br>GAGA  | 59.7                             | 437                                           | INTRON                                            | Ca_12489                            | QI                    | bHLH |
| Ca2_P4_30665443  | Ca2                                     | 30665443                      | ATTTTTTTTT/ATTTTTTTTT                                         | TCATGGTGGACCGTAA<br>TCTG  | CTACTGCCTTGGATTC<br>CTTTT | 59.4                             | 403                                           | INTRON                                            | Ca_12489                            | QI                    | bHLH |
| Ca2_P4_30665911  | Ca2                                     | 30665911                      | ATTTTTTTTT/ATTTTTTTTT                                         | AAAAGGAATCCAAGGC<br>AGTAG | TCCATTACCATCATACG<br>CCA  | 57.5                             | 788                                           | INTRON                                            | Ca_12489                            | QI                    | bHLH |
| Ca2_P4_30665994  | Ca2                                     | 30665994                      | CTTTTTTTTT/CTTTTTTTTT                                         | AAAAGGAATCCAAGGC<br>AGTAG | ACGAACGCAGATCCAT<br>TACC  | 57.5                             | 799                                           | INTRON                                            | Ca_12489                            | QI                    | bHLH |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca2_P4_30667302  | Ca2                                     | 30667302                      | AT/ATGT                                                       | TTTCTTGTTTCTCCAC<br>CGC  | TGAAGCAGACTGCAGA<br>ATCG | 60.2                             | 461                                           | INTRON                                            | Ca_12489                            | QI                    | bHLH  |
| Ca2_P4_30668518  | Ca2                                     | 30668518                      | ATAATTAATTAATTAATT/ATAATTAA<br>TTAATT                         | GGTGGCTGAGGCATTA<br>ACAT | TATTTCAAATTTCCGCC<br>GAC | 60.0                             | 780                                           | INTRON                                            | Ca_12489                            | QI                    | bHLH  |
| Ca2_P4_30668742  | Ca2                                     | 30668742                      | TAAAAAAA/TAAAAAA                                              | TGTGGTGTGGTCTCCT<br>TTCA | TATTTCAAATTTCCGCC<br>GAC | 60.1                             | 197                                           | INTRON                                            | Ca_12489                            | QI                    | bHLH  |
| Ca2_P4_30669952  | Ca2                                     | 30669952                      | AATATAT/AATATATAT                                             | AGACCCAATCATGCAA<br>ATCC | AAAACGGTGAAGAAAC<br>ACGG | 59.8                             | 776                                           | INTRON                                            | Ca_12489                            | QI                    | bHLH  |
| Ca2_P4_30670148  | Ca2                                     | 30670148                      | TGAAGAA/TGAA                                                  | CCATGGAGATGGCAGG<br>TAGT | AAAACGGTGAAGAAAC<br>ACGG | 60.0                             | 220                                           | INTRON                                            | Ca_12489                            | QI                    | bHLH  |
| Ca2_P4_30698523  | Ca2                                     | 30698523                      | CAACTAACT/CAACT                                               | CTGGTTGGGCATCTCC<br>TAAA | TCTGTTCTCGAAGGT<br>TGCT  | 60.1                             | 735                                           | INTRON                                            | Ca_12487                            | KLB                   | YABBY |
| Ca2_P4_30713265  | Ca2                                     | 30713265                      | A/AG                                                          | TTCTGCTGGTCTGGCT<br>TTTT | TGAAAGGGAATTGGGT<br>GAAG | 60.0                             | 233                                           | INTRON                                            | Ca_12485                            | T                     | RAV   |
| Ca2_P4_30732861  | Ca2                                     | 30732861                      | A/AG                                                          | TCACAGAAGGGGTTTT<br>GGTC | AAAATTGTGAACGGAG<br>ACCG | 59.9                             | 394                                           | INTRON                                            | Ca_12484                            | T                     | RAV   |
| Ca2_P4_30732922  | Ca2                                     | 30732922                      | AATCATCAT/AATCAT                                              | TCACAGAAGGGGTTTT<br>GGTC | AAAATTGTGAACGGAG<br>ACCG | 59.9                             | 394                                           | INTRON                                            | Ca_12484                            | T                     | RAV   |
| Ca2_P4_30733374  | Ca2                                     | 30733374                      | GTTGTGTCTGGTACTTGTGTC/GTT<br>GTGTC                            | CTAAATGCGGTCTCC<br>GTTC  | AACGATTGGAATATCG<br>CTGC | 59.7                             | 668                                           | INTRON                                            | Ca_12484                            | T                     | RAV   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_30768995  | Ca2                                     | 30768995                      | GTTCCTTTT/GTTCCTTTT                                           | TTGAAGTGGACGCAAG<br>AGTG | TTTGCTGATAGCTGTT<br>GGA  | 60.0                             | 783                                           | INTRON                                            | Ca_12479                            | K                     | ERF |
| Ca2_P4_30771512  | Ca2                                     | 30771512                      | TAAAA/TAAAA                                                   | GACCACCTTTGTGGAC<br>CAGT | AATTGTATGGTTATGG<br>GCGA | 59.9                             | 713                                           | INTRON                                            | Ca_12479                            | K                     | ERF |
| Ca2_P4_30872420  | Ca2                                     | 30872420                      | AAGA/AA                                                       | CAAAAGCACACAAGC<br>CAGA  | GGTCAATGGGAATGAA<br>GCTG | 60.0                             | 484                                           | INTRON                                            | Ca_12473                            | U                     | --  |
| Ca2_P4_30873239  | Ca2                                     | 30873239                      | TAAAA/TAAAA                                                   | AGAAAAGTGGGAAGG<br>GAAA  | TGTTAAAGTCCCAGGC<br>TTGC | 59.9                             | 200                                           | INTRON                                            | Ca_12473                            | U                     | --  |
| Ca2_P4_30892524  | Ca2                                     | 30892524                      | GTTT/GTT                                                      | AGTGGCTTGGTTTGTG<br>GAAA | TAAACAAAATGACGCCA<br>CCA | 60.5                             | 342                                           | INTRON                                            | Ca_12472                            | --                    | --  |
| Ca2_P4_30892831  | Ca2                                     | 30892831                      | ATGATGATTGATGAT/ATGATGAT                                      | TGGTGGCGTCATTTTG<br>TTTA | ATTTGTGGGCTCAAAC<br>AACC | 60.0                             | 174                                           | INTRON                                            | Ca_12472                            | --                    | --  |
| Ca2_P4_30893852  | Ca2                                     | 30893852                      | T/TC                                                          | CTCGAGGCTTGTTTT<br>GCTC  | CTTTAGCTTGCCATTGC<br>TCC | 60.1                             | 491                                           | INTRON                                            | Ca_12472                            | --                    | --  |
| Ca2_P4_30893869  | Ca2                                     | 30893869                      | ATTTTTTTTT/ATTTTTTTTT                                         | CTCGAGGCTTGTTTT<br>GCTC  | CTTTAGCTTGCCATTGC<br>TCC | 60.1                             | 491                                           | INTRON                                            | Ca_12472                            | --                    | --  |
| Ca2_P4_30899063  | Ca2                                     | 30899063                      | GTTCCTTTT/GTTCCTTTT                                           | GAATTGGAAATGGCAG<br>CCTA | TTGCACAAGCTGGATA<br>CTCG | 60.0                             | 459                                           | INTRON                                            | Ca_12471                            | --                    | --  |
| Ca2_P4_30899363  | Ca2                                     | 30899363                      | ATTTT/ATTT                                                    | GAATTGGAAATGGCAG<br>CCTA | TTGCACAAGCTGGATA<br>CTCG | 60.0                             | 459                                           | INTRON                                            | Ca_12471                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca2_P4_30904965  | Ca2                                     | 30904965                      | CTATAT/CTAT                                                   | TTGGACCCACCTATA<br>TTGC   | GCCTGATTGAGCACTT<br>TCCT  | 59.6                             | 419                                           | INTRON                                            | Ca_12470                            | DO                    | --   |
| Ca2_P4_30905223  | Ca2                                     | 30905223                      | ATTTTTTTTT/ATTTTTTT                                           | AGGAAAGTGCTCAATC<br>AGGC  | GCCAGAGAGTGATGAC<br>CGAT  | 59.4                             | 599                                           | INTRON                                            | Ca_12470                            | DO                    | --   |
| Ca2_P4_30907113  | Ca2                                     | 30907113                      | TAAA/TAA                                                      | ACTGGCACCCAATAGG<br>ATCA  | AGTTCCATTGCTGCTTT<br>GCT  | 60.3                             | 812                                           | INTRON                                            | Ca_12470                            | DO                    | --   |
| Ca2_P4_30911658  | Ca2                                     | 30911658                      | A/AG                                                          | TTGTTTGTTGGGTGAGC<br>TGAG | TTTTTGAGGGTAGGGC<br>AATG  | 59.9                             | 639                                           | INTRON                                            | Ca_12470                            | DO                    | --   |
| Ca2_P4_30915268  | Ca2                                     | 30915268                      | A/ACAATCACTAAG                                                | GAAGTGAAGTGGTTCT<br>TTGCG | CAAGACCTTGTTGGCTC<br>ATCA | 59.9                             | 783                                           | INTRON                                            | Ca_12470                            | DO                    | --   |
| Ca2_P4_30916172  | Ca2                                     | 30916172                      | TCC/TCCC                                                      | TGAATTGCCACAGGTC<br>TTGA  | TAAAGAGTGGCACCCC<br>TCAC  | 60.2                             | 411                                           | INTRON                                            | Ca_12470                            | DO                    | --   |
| Ca2_P4_30928001  | Ca2                                     | 30928001                      | ATTCTTCT/ATTCT                                                | CAATCCGCAATCAACA<br>ACAC  | GCCAGATGAGCACACA<br>AGAA  | 60.0                             | 232                                           | INTRON                                            | Ca_12470                            | DO                    | --   |
| Ca2_P4_30946157  | Ca2                                     | 30946157                      | TG/T                                                          | CCCAACTCCAAGGGAC<br>TACA  | ATATACCTCGGGGGAA<br>CCAG  | 60.0                             | 548                                           | INTRON                                            | Ca_12469                            | U                     | bHLH |
| Ca2_P4_30949260  | Ca2                                     | 30949260                      | TA/TAAAAA                                                     | CCATCAATAGGAGAGG<br>CCAA  | CCACAACCTGCAATGA<br>CAAC  | 60.0                             | 817                                           | INTRON                                            | Ca_12469                            | U                     | bHLH |
| Ca2_P4_30956624  | Ca2                                     | 30956624                      | ATTT/ATT                                                      | GCATGGGATATCCAAG<br>CAAT  | CAAGAGGCAACAATTG<br>AGCA  | 59.8                             | 677                                           | INTRON                                            | Ca_12469                            | U                     | bHLH |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca2_P4_30956905  | Ca2                                     | 30956905                      | TAAAAAAAA/TAAAAAAAA                                           | TCCGTGAGTACACTGG<br>CAAA | CAAGAGGCAACAATTG<br>AGCA  | 60.3                             | 545                                           | INTRON                                            | Ca_12469                            | U                     | bHLH |
| Ca2_P4_31602924  | Ca2                                     | 31602924                      | TATAATAATAATAAT/TATAATAATAA<br>T                              | GGAAGTCAGCAGCGGA<br>ATAG | TCCACACGCGTATGTG<br>TTTT  | 60.0                             | 404                                           | INTRON                                            | Ca_17854                            | --                    | SAP  |
| Ca2_P4_31871335  | Ca2                                     | 31871335                      | CTATATATATATA/CTATATATATA                                     | ATGGGTCAAAATGGGT<br>GTGT | AGGCTGATTCAAACCC<br>TG TG | 60.0                             | 290                                           | INTRON                                            | Ca_17832                            | --                    | FAR1 |
| Ca2_P4_31881002  | Ca2                                     | 31881002                      | ATT/ATTTT                                                     | GACAGAGACTGCTCCC<br>AAGG | GCTCCCATCCAATA<br>CTCA    | 60.0                             | 357                                           | INTRON                                            | Ca_17830                            | D                     | LBD  |
| Ca2_P4_31882952  | Ca2                                     | 31882952                      | CTTTATTTATTTAT/CTTTATTTATTT<br>ATTTAT                         | TTTCTGGTGGGATCAG<br>CTCT | GACATCCTGCGCCAGT<br>TATT  | 59.8                             | 591                                           | INTRON                                            | Ca_17830                            | D                     | LBD  |
| Ca2_P4_31883010  | Ca2                                     | 31883010                      | AAGAG/AAG                                                     | TTTCTGGTGGGATCAG<br>CTCT | GACATCCTGCGCCAGT<br>TATT  | 59.8                             | 591                                           | INTRON                                            | Ca_17830                            | D                     | LBD  |
| Ca2_P4_31883642  | Ca2                                     | 31883642                      | TAA/TAAA                                                      | AATAACTGGCGCAGGA<br>TGTC | TAAAGATGGCACCAGG<br>AAGG  | 60.1                             | 632                                           | INTRON                                            | Ca_17830                            | D                     | LBD  |
| Ca2_P4_31896775  | Ca2                                     | 31896775                      | CAAAAAAAAA/CAAAAAAAAA                                         | ATCTTTGGAAAAAGCA<br>GCCA | CTTAGAAGAGTGCATC<br>CGCC  | 59.8                             | 347                                           | INTRON                                            | Ca_17828                            | I                     | C3H  |
| Ca2_P4_31918707  | Ca2                                     | 31918707                      | T/TG                                                          | TGATCCAGTGTTGGT<br>TGAA  | TGGGCATGTTGTGAGT<br>TCAT  | 59.9                             | 637                                           | INTRON                                            | Ca_17825                            | O                     | --   |
| Ca2_P4_32034817  | Ca2                                     | 32034817                      | TAAAAAAAAAAAAAAAA/TAAAAAAAA<br>AAAA                           | TATTCTTCACGCTGCAA<br>TCC | GCACCTTTGAAGGCTG<br>AAGG  | 58.9                             | 552                                           | INTRON                                            | Ca_17818                            | R                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca2_P4_32060197  | Ca2                                     | 32060197                      | AA/ATAAATTA                                                   | TTACCATTGGTTCCCC<br>AAAA   | AATTTGGTGGCAAAAT<br>CCA     | 60.0                             | 478                                           | INTRON                                            | Ca_17816                            | R                     | --      |
| Ca2_P4_32060578  | Ca2                                     | 32060578                      | CATATATAT/CATATAT                                             | TTGACGCTGAAAATCC<br>ATCA   | CCATCTCGTTTCCATTG<br>AGG    | 60.2                             | 498                                           | INTRON                                            | Ca_17816                            | R                     | --      |
| Ca2_P4_32127033  | Ca2                                     | 32127033                      | TGC/TGCGC                                                     | TGCAAGTTGTGATGGG<br>TTGT   | TGTCTGTTCTGCACGG<br>AGTC    | 60.0                             | 650                                           | INTRON                                            | Ca_17812                            | O                     | --      |
| Ca2_P4_32130215  | Ca2                                     | 32130215                      | ATTGAA/ATTGAATTGAATTGAA                                       | CCGGGTCAGTTTCCTT<br>CTTT   | ACTCCACCAACTTCCAA<br>TGC    | 60.5                             | 388                                           | INTRON                                            | Ca_17811                            | J                     | --      |
| Ca2_P4_32130589  | Ca2                                     | 32130589                      | CT/C                                                          | GCATTGGAAGTTGGTG<br>GAGT   | CCCGCCACTTGTACGA<br>TAAT    | 60.0                             | 610                                           | INTRON                                            | Ca_17811                            | J                     | --      |
| Ca2_P4_32145004  | Ca2                                     | 32145004                      | TA/TACA                                                       | GGCCTTCAAAATTC AAT<br>GAGA | TGGATACCTAGCACCT<br>TAGCAA  | 59.1                             | 598                                           | INTRON                                            | Ca_17808                            | --                    | G2-like |
| Ca2_P4_32146563  | Ca2                                     | 32146563                      | A/AC                                                          | ATTCCCACGCCACTTA<br>GATG   | CACTGTACAGAGATA<br>AGATGCAA | 60.0                             | 807                                           | INTRON                                            | Ca_17808                            | --                    | G2-like |
| Ca2_P4_32157704  | Ca2                                     | 32157704                      | ATAA/ATAATTATATTAGATTAA                                       | TGCAGGCACTTATGGC<br>TATG   | CTTGTTCCATTGTTGG<br>CCTT    | 59.9                             | 478                                           | INTRON                                            | Ca_17807                            | --                    | B3      |
| Ca2_P4_32203826  | Ca2                                     | 32203826                      | GATATATATATATATATATATA/GA<br>TATATATATATATATATATA             | GGGCAATTCCTGCAAT<br>TTTA   | GATGCACCGAATAAGG<br>AAGC    | 59.9                             | 390                                           | INTRON                                            | Ca_10295                            | --                    | G2-like |
| Ca2_P4_32204202  | Ca2                                     | 32204202                      | AATATATAT/AATAT                                               | AGCCTGCTTCCTTATT<br>CGGT   | TGGAGGAAAAATAACT<br>GCCG    | 60.2                             | 523                                           | INTRON                                            | Ca_10295                            | --                    | G2-like |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca2_P4_32247082  | Ca2                                     | 32247082                      | ATTTTT/ATTTTTT                                                | AATTCCAAACATGGG<br>GACA  | AAGAAGGCCAAGCAAG<br>TTGA | 60.0                             | 680                                           | INTRON                                            | Ca_10291                            | E                     | C3H         |
| Ca2_P4_32347455  | Ca2                                     | 32347455                      | ATTTTT/ATTTT                                                  | ACAAGCTGTTCCCTCC<br>AGAA | TGAGGTTCTTGCACAA<br>CTGC | 59.8                             | 678                                           | INTRON                                            | Ca_10283                            | --                    | --          |
| Ca2_P4_32348888  | Ca2                                     | 32348888                      | GATTGCATAAAATTGCAT/GATTGCA<br>T                               | TATCTCGCTCGGTGGA<br>GTCT | ACAAACACCATCAGGC<br>TTCC | 60.0                             | 669                                           | INTRON                                            | Ca_10283                            | --                    | --          |
| Ca2_P4_32352213  | Ca2                                     | 32352213                      | TTGTGT/TTGTGTGT                                               | GGATCCAGTGCTACGA<br>CCAT | GGAACACCAACCTGGA<br>ACAC | 60.0                             | 498                                           | INTRON                                            | Ca_10283                            | --                    | --          |
| Ca2_P4_32409946  | Ca2                                     | 32409946                      | ATTTTT/ATTTT                                                  | TGGAGAGTTGAGAAGC<br>CAGG | TACTCGAGGCCTCTCG<br>CTAC | 60.5                             | 850                                           | INTRON                                            | Ca_10279                            | --                    | bHLH        |
| Ca2_P4_32482955  | Ca2                                     | 32482955                      | ATTTTTTT/ATTTTTTTTT                                           | TCCTTGCAGCGACTTT<br>CTTT | TGCTTGAAGAAGGAGC<br>ATGA | 60.1                             | 739                                           | INTRON                                            | Ca_10272                            | R                     | --          |
| Ca2_P4_32510389  | Ca2                                     | 32510389                      | TGGGGGGGGG/TGGGGGGGGG                                         | TACTGGCTGATTTGCG<br>ACAG | CATATTTGACAAGGAC<br>CGGG | 60.0                             | 880                                           | INTRON                                            | Ca_10271                            | O                     | GATA        |
| Ca2_P4_32573339  | Ca2                                     | 32573339                      | G/GGCT                                                        | TCTGGGGCATGTTGAC<br>ATTA | GCGTCCACCTTTTGT<br>GAT   | 59.9                             | 502                                           | INTRON                                            | Ca_10266                            | D                     | --          |
| Ca2_P4_32934778  | Ca2                                     | 32934778                      | TTAAATAAATAAATAAATAA/TTAAA<br>TAAATAAATAAATAAATAA             | ACAGCGACACGAAGGA<br>CTCT | GGAACAAGTTTCCGTG<br>AAGG | 60.1                             | 396                                           | INTRON                                            | Ca_10230                            | OJ                    | MYB_related |
| Ca2_P4_33346809  | Ca2                                     | 33346809                      | C/CA                                                          | ATGCACATGAACCGAT<br>TGAA | AAACAAGGTTGAATCA<br>CGCC | 59.9                             | 718                                           | INTRON                                            | Ca_10191                            | T                     | FAR1        |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca2_P4_34347196  | Ca2                                     | 34347196                      | TAC/T                                                         | TCGCAGCCCAACTAAC<br>TTTT  | ACGAAACATGCACATG<br>GAAA | 59.9                             | 502                                           | INTRON                                            | Ca_15263                            | --                    | --  |
| Ca2_P4_34416432  | Ca2                                     | 34416432                      | AGT/AGTGT                                                     | GGCCCAGATGAGTCCT<br>GATA  | TTCTGTTGTGCAACTCA<br>GGC | 60.0                             | 624                                           | INTRON                                            | Ca_15269                            | J                     | --  |
| Ca2_P4_35834317  | Ca2                                     | 35834317                      | TTATATATATATATATATATATAT/<br>TTATATATATATATATATATATAT         | CAAACCGTATTAGCCT<br>CACCA | GGTTGAAGATGTTCGT<br>CGGT | 60.0                             | 675                                           | INTRON                                            | Ca_09758                            | O                     | MYB |
| Ca2_P4_35864202  | Ca2                                     | 35864202                      | GGA/G                                                         | GCAAATTCTGCCACGC<br>TATT  | AATCCTCCACCGTCTTT<br>CCT | 60.2                             | 675                                           | INTRON                                            | Ca_09762                            | R                     | --  |
| Ca2_P4_35895623  | Ca2                                     | 35895623                      | T/TC                                                          | ATTGGGTCCAACCTT<br>TTCC   | GCCTGGACAATGCTTT<br>TTC  | 60.0                             | 267                                           | INTRON                                            | Ca_09764                            | T                     | --  |
| Ca2_P4_35935962  | Ca2                                     | 35935962                      | AATATATATATATA/AATATATATATA                                   | CATGTTCCACAACACA<br>ACCC  | CTTGCCCCATTCTTTT<br>GTA  | 59.7                             | 747                                           | INTRON                                            | Ca_09768                            | --                    | SAP |
| Ca2_P4_35938206  | Ca2                                     | 35938206                      | AAGA/AA                                                       | TGCATATATTGCTGCA<br>GGTTG | ATCAATGAAGTTTGGC<br>CTGC | 59.7                             | 453                                           | INTRON                                            | Ca_09768                            | --                    | SAP |
| Ca2_P4_35945134  | Ca2                                     | 35945134                      | TAAAAA/TAAAAA                                                 | AACATCATACTTTTGC<br>GGC   | GCCTGAAATATGCCGA<br>GGTA | 60.0                             | 417                                           | INTRON                                            | Ca_09769                            | --                    | --  |
| Ca2_P4_35945318  | Ca2                                     | 35945318                      | CCAA/C                                                        | AACATCATACTTTTGC<br>GGC   | GCCTGAAATATGCCGA<br>GGTA | 60.0                             | 417                                           | INTRON                                            | Ca_09769                            | --                    | --  |
| Ca2_P4_35967362  | Ca2                                     | 35967362                      | GACAC/GACACAC                                                 | TTGAGGGGAGGTAAGC<br>CTTT  | TGATAGGAGGAAGCGT<br>GACC | 60.1                             | 583                                           | INTRON                                            | Ca_09771                            | J                     | NAC |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)          | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                        |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca2_P4_35967799  | Ca2                                     | 35967799                      | TACAACAACAACAACAA/TACAACAA<br>CAACAACAACAA                             | TAAATTACCCTGCGCC<br>TGAC | TGCTCAAAGTGCAGTA<br>AATG | 60.1                             | 514                                           | INTRON                                            | Ca_09771                            | J                     | NAC      |
| Ca2_P4_35967841  | Ca2                                     | 35967841                      | AATATATATATA/AATATATATATATA                                            | TAAATTACCCTGCGCC<br>TGAC | TGAAACCCTATCGCGA<br>AATC | 60.1                             | 698                                           | INTRON                                            | Ca_09771                            | J                     | NAC      |
| Ca2_P4_35999918  | Ca2                                     | 35999918                      | CAAAAA/CAAAAAA                                                         | GGAATCAAAGCGGAAT<br>TCAA | AAGGAGCATGGTCCAA<br>TCAC | 60.0                             | 221                                           | INTRON                                            | Ca_09774                            | --                    | FAR1     |
| Ca2_P4_36032844  | Ca2                                     | 36032844                      | C/A/C                                                                  | CCTGAGCGGAAATTGG<br>TTTA | GTGGGATTGACCGAGT<br>TTGT | 60.1                             | 358                                           | INTRON                                            | Ca_09778                            | P                     | --       |
| Ca2_P4_36032894  | Ca2                                     | 36032894                      | CA/CATAA                                                               | CCTGAGCGGAAATTGG<br>TTTA | GTGGGATTGACCGAGT<br>TTGT | 60.1                             | 358                                           | INTRON                                            | Ca_09778                            | P                     | --       |
| Ca2_P4_36137407  | Ca2                                     | 36137407                      | GAAAAAAAAA/GAAAAAAAAA                                                  | ACCATCGCTTTATCTG<br>GTGA | GTTATCTCAGCTCGCG<br>AAGG | 58.2                             | 824                                           | INTRON                                            | Ca_09792                            | J                     | B3       |
| Ca2_P4_4204531   | Ca2                                     | 4204531                       | GTATATATATATATATATATATAT<br>A/GTATATATATATATATATATATA                  | GGGTTTGAACCGTCCC<br>TACT | CTTCTCCATCTCCTTC<br>CCC  | 60.2                             | 633                                           | INTRON                                            | Ca_21114                            | --                    | --       |
| Ca2_P4_5003705   | Ca2                                     | 5003705                       | G/GATT                                                                 | TGTAGCATGCAGGTTG<br>AAGG | GAAAGGACTTTGTCCA<br>GCCA | 59.9                             | 605                                           | INTRON                                            | Ca_14709                            | I                     | --       |
| Ca2_P4_5268950   | Ca2                                     | 5268950                       | GAAAAAA/GAAAAAA                                                        | TTTCAATCTCCCTCG<br>GATG  | GACTTCCGTCCCTCAC<br>AAAA | 60.0                             | 558                                           | INTRON                                            | Ca_14681                            | G                     | Trihelix |
| Ca2_P4_5286155   | Ca2                                     | 5286155                       | AATATATATATATATATATATATAT<br>ATATAAATATATATATATATATAT<br>ATATATATATATA | TTCATGCCTCCCATTTT<br>TTC | CGCTCTGTCAACATGT<br>CAGC | 60.0                             | 752                                           | INTRON                                            | Ca_14679                            | T                     | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                  | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                                                                                |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca2_P4_6047361   | Ca2                                     | 6047361                       | AATTATTATTATTATTATTATTAT<br>TATTATTAT/AATTATTATTATTATTA<br>TTATTATTATTATTATTATTATTA<br>TTAT                                    | ACCTTCCACACAAGCC<br>AAAC   | AGGCCTTTATGTGGCC<br>TTTT | 60.0                             | 456                                           | INTRON                                            | Ca_19707                            | K                     | MYB         |
| Ca2_P4_6056245   | Ca2                                     | 6056245                       | TATAAATAAATAAATAAATAAATAA<br>TAAATAAATAAATAAATAAATAAATA<br>AA/TATAAATAAATAAATAAATAAATA<br>AATAAATAAATAAATAAATAAATAA<br>TAAATAA | ATCCCAAGTTTGGTTG<br>TTGG   | TCGTGGTCCAGAAAAC<br>ATGA | 59.7                             | 489                                           | INTRON                                            | Ca_19707                            | K                     | MYB         |
| Ca2_P4_7681954   | Ca2                                     | 7681954                       | TAAAA/TAAA                                                                                                                     | GAAAAAGAGCCACGGT<br>GGTA   | TTCCAGCTCCAAGCT<br>CATT  | 60.1                             | 643                                           | INTRON                                            | Ca_18121                            | R                     | ERF         |
| Ca2_P4_7753009   | Ca2                                     | 7753009                       | A/AC                                                                                                                           | AAGTGGCGAAGCTTGT<br>TGAT   | AGCTTGCCATTGCAGC<br>TACT | 59.9                             | 797                                           | INTRON                                            | Ca_18125                            | --                    | MYB_related |
| Ca2_P4_7891193   | Ca2                                     | 7891193                       | CAAAAAAAAA/CAAAAAAAAA                                                                                                          | TATCTGCATCACAGCC<br>TTGC   | AGGCGTGATGGTTATC<br>CAAG | 60.0                             | 202                                           | INTRON                                            | Ca_18137                            | E                     | --          |
| Ca2_P4_7926426   | Ca2                                     | 7926426                       | CTTT/CTT                                                                                                                       | CTTGGCGAAGTGAAGG<br>GATA   | GAGGCTTGGTTCCTA<br>ATCC  | 60.2                             | 471                                           | INTRON                                            | Ca_18142                            | U                     | --          |
| Ca2_P4_7938788   | Ca2                                     | 7938788                       | AA/AACA                                                                                                                        | TGATCAATAATTGAAA<br>CAAGCG | GCCGTATTGGGAGAAG<br>ATGA | 59.2                             | 589                                           | INTRON                                            | Ca_18144                            | --                    | --          |
| Ca2_P4_7939192   | Ca2                                     | 7939192                       | GTTACAT/GT                                                                                                                     | TCATCTTCTCCAATAC<br>GGC    | TCGAACCGCATTGAAT<br>CATA | 60.0                             | 266                                           | INTRON                                            | Ca_18144                            | --                    | --          |
| Ca2_P4_7939489   | Ca2                                     | 7939489                       | TAAAAAAAAA/TAAAAAAAA                                                                                                           | TCATCTTCTCCAATAC<br>GGC    | CTCTCATCCGATTCCG<br>TTGT | 60.0                             | 506                                           | INTRON                                            | Ca_18144                            | --                    | --          |
| Ca2_P4_8105865   | Ca2                                     | 8105865                       | TTGAT/TT                                                                                                                       | GGGACAAAGCATCCAA<br>GAGA   | CTGCATCATACGACGG<br>ATTC | 60.2                             | 381                                           | INTRON                                            | Ca_18152                            | K                     | TALE        |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                      | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                                                                                    |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca2_P4_8328118   | Ca2                                     | 8328118                       | TATTTATTTATGCATTT/TATTTATTT<br>ATGCATTTATTTATGCATTT                                                                                | AGGTTCAATTTGGTGG<br>CAAG    | TTGAATTGTTATGCCCG<br>TGA  | 60.0                             | 570                                           | INTRON                                            | Ca_21469                            | --                    | C2H2        |
| Ca2_P4_9481914   | Ca2                                     | 9481914                       | CTATATATATATATAT/CTATATATAT<br>ATATATAT                                                                                            | GGTCGTGTTTTGATCA<br>TGGA    | TTGATTGTCCGACTTG<br>TGG   | 59.3                             | 681                                           | INTRON                                            | Ca_20024                            | T                     | M-type      |
| Ca3_P4_10860554  | Ca3                                     | 10860554                      | TG/T                                                                                                                               | GCACACTGGTGTGGA<br>TTTG     | TCAATGGTAACTTCCC<br>CAGC  | 60.0                             | 851                                           | INTRON                                            | Ca_19358                            | G                     | --          |
| Ca3_P4_1288242   | Ca3                                     | 1288242                       | GTTTTTTTTTTT/GTTTTTTTTTTT                                                                                                          | TGGTGAGATCAACGAT<br>ACGC    | TGGTAACAAATCTCCG<br>AAGGA | 59.7                             | 371                                           | INTRON                                            | Ca_19421                            | R                     | --          |
| Ca3_P4_14653349  | Ca3                                     | 14653349                      | A/AG                                                                                                                               | AGGAGCTTCTGCCATT<br>GAAA    | TAAAAGGAGCAAAGGC<br>CAGA  | 60.0                             | 408                                           | INTRON                                            | Ca_22505                            | O                     | --          |
| Ca3_P4_16730062  | Ca3                                     | 16730062                      | TTTATTATTATTATTATTATTATTATT<br>ATTATTATTACTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>TTATTATTATTATTATTATTACTA<br>TTATTATTATTATTA | TTGCAACATTTGTAGG<br>CATTTTC | TAGGTTTTTGCTCCTTC<br>CGA  | 60.0                             | 706                                           | INTRON                                            | Ca_18280                            | F                     | MYB_related |
| Ca3_P4_17187813  | Ca3                                     | 17187813                      | CT/CTTT                                                                                                                            | AAACAAATAAGCCTGG<br>CGTG    | GGAGAGACCAAGCTCT<br>CGAA  | 60.1                             | 462                                           | INTRON                                            | Ca_24618                            | S                     | B3          |
| Ca3_P4_21487649  | Ca3                                     | 21487649                      | GAAAAAAA/GAAAAAAA                                                                                                                  | CGTGAAAGGGAGGCAA<br>ATAA    | GCCGTTGTGCAACTGG<br>TATT  | 60.1                             | 413                                           | INTRON                                            | Ca_09505                            | O                     | MYB_related |
| Ca3_P4_21635589  | Ca3                                     | 21635589                      | GCATCATCA/GCATCA                                                                                                                   | AAGCATGCCAAACCA<br>AAAC     | TGAACATCAAAGATCTG<br>CGG  | 60.0                             | 521                                           | INTRON                                            | Ca_09516                            | --                    | --          |
| Ca3_P4_21870840  | Ca3                                     | 21870840                      | TTTATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTAT/TTT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTAT        | ATGTTAGACCGTCCGT<br>CAGG    | GGTCTAAATCTGGCTT<br>ACGGC | 60.0                             | 655                                           | INTRON                                            | Ca_20433                            | I                     | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')      | Reverse primers (5'-3')  | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|------------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                 |                              |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca3_P4_22409468  | Ca3                                     | 22409468                      | TTAATAATAATAATAATAATAATAA/T<br>TAATAATAATAATAATAATAATAATA<br>A  | TCCCCTCCCTGAAAAT<br>AACC     | TCCCTTTGTTTGGGAA<br>CTTG | 60.1                             | 474                                           | INTRON                                            | Ca_06268                            | G                     | C3H         |
| Ca3_P4_22438235  | Ca3                                     | 22438235                      | GAAAAAAAA/GAAAAAAAAAAAA                                         | TTCCAAACAAAGCCTTT<br>TGC     | TAGCAACGGAACAAAC<br>CACA | 60.2                             | 690                                           | INTRON                                            | Ca_06267                            | --                    | HD-ZIP      |
| Ca3_P4_23512633  | Ca3                                     | 23512633                      | AATATATATATATATATATATAT/A<br>ATATATATATATATATATAT               | GTTGTTGGGATTTGT<br>TTGG      | TCCCCTTTCATCTCTTC<br>CCT | 60.1                             | 279                                           | INTRON                                            | Ca_06174                            | --                    | --          |
| Ca3_P4_23903613  | Ca3                                     | 23903613                      | TAGAGAGAGAGA/TAGAGAGAGA                                         | GCCCTAACCTTTCTGG<br>GAAC     | ATGTGCTCACATGATT<br>GGGA | 59.9                             | 303                                           | INTRON                                            | Ca_06133                            | R                     | C3H         |
| Ca3_P4_24820044  | Ca3                                     | 24820044                      | TGAGAGAGAGAGAGAGAGAGAGAG<br>AG/TGAGAGAGAGAGAGAGAGAGA<br>GAGAGAG | ATTCTGTTCTCGCTTTCC<br>CTT    | AGTGCAACCAACATG<br>CAAA  | 60.2                             | 555                                           | INTRON                                            | Ca_06044                            | TU                    | bHLH        |
| Ca3_P4_25233299  | Ca3                                     | 25233299                      | GT/GCATAAATTTCCGCCTT                                            | GCATAAATTTCCGCCT<br>TCA      | AACGAGAAACAGCCAG<br>CCTA | 60.0                             | 377                                           | INTRON                                            | Ca_06005                            | L                     | --          |
| Ca3_P4_26071877  | Ca3                                     | 26071877                      | TAAA/TAAAA                                                      | TGCTCCAATCACGTTG<br>ACAT     | AGACGCTGCAACATCA<br>AAGC | 60.1                             | 397                                           | INTRON                                            | Ca_08292                            | --                    | MYB_related |
| Ca3_P4_26074434  | Ca3                                     | 26074434                      | TTATATATA/TTATATATATA                                           | TTTTCAAAATGCTCAAA<br>TTTTCTT | GCTTTGATGGAATCA<br>GGGA  | 58.5                             | 779                                           | INTRON                                            | Ca_08292                            | --                    | MYB_related |
| Ca3_P4_26103278  | Ca3                                     | 26103278                      | ATTTTT/ATTTTTTT                                                 | TGTGTTTGTTTGTTTC<br>ATCTTG   | CAATGTCCACGTGATT<br>GGAG | 59.9                             | 519                                           | INTRON                                            | Ca_08292                            | --                    | MYB_related |
| Ca3_P4_26114282  | Ca3                                     | 26114282                      | ATTATAGTTTTATT/AT                                               | TTTATCCTGGGGACTT<br>CGTG     | ATACACCGATGGAGGG<br>CTTT | 59.9                             | 838                                           | INTRON                                            | Ca_08292                            | --                    | MYB_related |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca3_P4_26114943  | Ca3                                     | 26114943                      | GTTTT/GTTT                                                    | TGGCATGGTACTCAAC<br>CAGA | TTACATGAATGATTGT<br>TGGGT | 60.1                             | 545                                           | INTRON                                            | Ca_08292                            | --                    | MYB_related |
| Ca3_P4_26115029  | Ca3                                     | 26115029                      | AACG/A                                                        | TGGCATGGTACTCAAC<br>CAGA | TTACATGAATGATTGT<br>TGGGT | 60.1                             | 545                                           | INTRON                                            | Ca_08292                            | --                    | MYB_related |
| Ca3_P4_26411861  | Ca3                                     | 26411861                      | AAAATAAA/AAAA                                                 | TGGGGACGTGTCAAAC<br>TAAA | GAAC TTGGGAGCCTCT<br>TTGA | 59.0                             | 515                                           | INTRON                                            | Ca_08265                            | --                    | --          |
| Ca3_P4_28672365  | Ca3                                     | 28672365                      | ATATTATTATTATTATTATTATTA<br>TTA/ATATTATTATTATTATTATT<br>ATTA  | CGAGAGAGGGGACAAA<br>ACTG | ATCGTCAAATGATGG<br>GACC   | 59.8                             | 255                                           | INTRON                                            | Ca_07175                            | E                     | C3H         |
| Ca3_P4_28994933  | Ca3                                     | 28994933                      | AC/A                                                          | CAAATTAAGCAGAGCC<br>CGTC | TTTTGGACAATGTCAAC<br>CCA  | 59.8                             | 165                                           | INTRON                                            | Ca_07207                            | KTDL                  | --          |
| Ca3_P4_28995118  | Ca3                                     | 28995118                      | CAA/CAAA                                                      | CAAATTAAGCAGAGCC<br>CGTC | CGGAATTTGAACAAA<br>CGCT   | 59.8                             | 769                                           | INTRON                                            | Ca_07207                            | KTDL                  | --          |
| Ca3_P4_28996658  | Ca3                                     | 28996658                      | ATT/ATTT                                                      | AGGGCTTTGGTCGTGT<br>ATTG | AACAATTGCGGGTGTA<br>GAGG  | 60.0                             | 861                                           | INTRON                                            | Ca_07207                            | KTDL                  | --          |
| Ca3_P4_28999636  | Ca3                                     | 28999636                      | CT/CTT                                                        | TCTGAATTTCTGTACC<br>GCCC | GGGATAGGGCATGTGT<br>GAGT  | 60.1                             | 536                                           | INTRON                                            | Ca_07207                            | KTDL                  | --          |
| Ca3_P4_29000078  | Ca3                                     | 29000078                      | TG/T                                                          | GCCCTCTGTTCAGGGT<br>AGGT | GATGAGACCACCCAAG<br>CACT  | 60.5                             | 606                                           | INTRON                                            | Ca_07207                            | KTDL                  | --          |
| Ca3_P4_29046303  | Ca3                                     | 29046303                      | TAAA/TAAAGTAAAAA                                              | TGGAGACCTGTGCCTC<br>TCTT | TCATGAAACCTTTTGGA<br>GGC  | 60.0                             | 667                                           | INTRON                                            | Ca_07210                            | --                    | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca3_P4_29486404  | Ca3                                     | 29486404                      | TAAAAAAAAA/TAAAAAAAAA                                         | TCACCCCAACCAAA<br>GAAG   | GAATTAAGACGTGGC<br>GGTA  | 59.9                             | 592                                           | INTRON                                            | Ca_07254                            | --                    | C2H2 |
| Ca3_P4_29845748  | Ca3                                     | 29845748                      | CATAAAATAAAATAAAATAAA<br>A/CATAAAATAAAATAAAATAAA              | CCAAAAGTGAAACCA<br>AGGA  | CTCTGTCCCCGGAAC<br>TACA  | 59.9                             | 345                                           | INTRON                                            | Ca_07292                            | --                    | bZIP |
| Ca3_P4_30049696  | Ca3                                     | 30049696                      | CATATATATATATATATATAT<br>TAT/CATATATATATATATATAT<br>ATATATAT  | TCCCTTTTCCTCATCC<br>TCT  | TGCACTTTGTCCCTCA<br>ACA  | 60.0                             | 546                                           | INTRON                                            | Ca_07320                            | --                    | --   |
| Ca3_P4_30773948  | Ca3                                     | 30773948                      | ACTTCTTC/ACTTC                                                | AAGTTGACTTGGTG<br>TTGC   | ATGATGGCGATCAAAA<br>GGAG | 60.0                             | 560                                           | INTRON                                            | Ca_07399                            | E                     | --   |
| Ca3_P4_31280539  | Ca3                                     | 31280539                      | TC/TCC                                                        | TCATGCTGACGGAGTT<br>TGAG | ACGTGGGCTATCTAAG<br>CGAA | 60.0                             | 126                                           | INTRON                                            | Ca_12224                            | S                     | --   |
| Ca3_P4_31322765  | Ca3                                     | 31322765                      | TAAAAA/TAAAAA                                                 | ATTGGGTATCTTTCAG<br>GGGG | TCAAGGTACCCACCAC<br>ACTG | 60.0                             | 700                                           | INTRON                                            | Ca_12232                            | U                     | bHLH |
| Ca3_P4_31322986  | Ca3                                     | 31322986                      | CT/CTAT                                                       | TCAAGTGATTCACCCC<br>TTCC | CCGTGCGGTAAGTTT<br>CATT  | 59.9                             | 749                                           | INTRON                                            | Ca_12232                            | U                     | bHLH |
| Ca3_P4_31323281  | Ca3                                     | 31323281                      | CTTTT/CTTTT                                                   | AATGCTTCAACAGCCT<br>TCGT | TGGGATCGGTTACATG<br>GATT | 59.9                             | 415                                           | INTRON                                            | Ca_12232                            | U                     | bHLH |
| Ca3_P4_31324543  | Ca3                                     | 31324543                      | TAG/TAGTAATGTAATAAG                                           | CCTGGGTCCAATCCTT<br>ACCT | TCAGCTTATTAGGGCA<br>TGGG | 60.2                             | 660                                           | INTRON                                            | Ca_12232                            | U                     | bHLH |
| Ca3_P4_31488477  | Ca3                                     | 31488477                      | CCTCT/CCT                                                     | AGGCCCTTATGACGTT<br>GATG | ACACATTCATTCGCCAA<br>ACA | 60.0                             | 496                                           | INTRON                                            | Ca_12247                            | T                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca3_P4_31530898  | Ca3                                     | 31530898                      | A/AGTC                                                        | CTTCTTCATTCGGGGA<br>AACA  | GATTGGGATGATTGGT<br>ACGG  | 60.0                             | 549                                           | INTRON                                            | Ca_12252                            | E                     | TALE |
| Ca3_P4_31538436  | Ca3                                     | 31538436                      | T/TTA                                                         | CTACTTGCCGTTGGGA<br>TCAT  | GCCTGGATTCTCATT<br>GGA    | 60.0                             | 177                                           | INTRON                                            | Ca_12253                            | LK                    | --   |
| Ca3_P4_31624685  | Ca3                                     | 31624685                      | CA/CATAA                                                      | TCTGCCATTTTATTTTC<br>GGG  | AATAATGCACCAAGTGC<br>CACA | 59.9                             | 608                                           | INTRON                                            | Ca_12261                            | A                     | --   |
| Ca3_P4_31624803  | Ca3                                     | 31624803                      | AC/ACC                                                        | TCTGCCATTTTATTTTC<br>GGG  | AATAATGCACCAAGTGC<br>CACA | 59.9                             | 608                                           | INTRON                                            | Ca_12261                            | A                     | --   |
| Ca3_P4_31630976  | Ca3                                     | 31630976                      | T/TTGA                                                        | TGCACAAGAAGCATCT<br>CCAC  | TATGGGTTTGGTTTGG<br>CATT  | 60.0                             | 543                                           | INTRON                                            | Ca_12262                            | T                     | --   |
| Ca3_P4_31631967  | Ca3                                     | 31631967                      | AATAT/AAT                                                     | ATTTCAGCAGTCAACC<br>CCAG  | TCGAATTCACAAATGC<br>GTA   | 60.1                             | 738                                           | INTRON                                            | Ca_12262                            | T                     | --   |
| Ca3_P4_31632927  | Ca3                                     | 31632927                      | GTTATTATTATT/GTTATTATT                                        | GAAAATTGATTGTTGG<br>CCGT  | TGTGATCCATAAACCA<br>GCCA  | 59.8                             | 390                                           | INTRON                                            | Ca_12262                            | T                     | --   |
| Ca3_P4_31632996  | Ca3                                     | 31632996                      | C/CT                                                          | GAAAATTGATTGTTGG<br>CCGT  | TGTGATCCATAAACCA<br>GCCA  | 59.8                             | 390                                           | INTRON                                            | Ca_12262                            | T                     | --   |
| Ca3_P4_31633339  | Ca3                                     | 31633339                      | GTATAT/GTAT                                                   | TGGACCCAAGAACAGT<br>GTCA  | GCAATTGCAGAAATGC<br>AAGA  | 60.1                             | 496                                           | INTRON                                            | Ca_12262                            | T                     | --   |
| Ca3_P4_32379633  | Ca3                                     | 32379633                      | TTAATAATAATAATAA/TTAATAATAA<br>TAATAATAA                      | TGCATTTTGCATTTTGT<br>TGTT | TGCGGATTGTATTTTG<br>GGTT  | 59.1                             | 347                                           | INTRON                                            | Ca_11961                            | --                    | FAR1 |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                   | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                 |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_32458289  | Ca3                                     | 32458289                      | CAAAAA/CAAA                                                                                     | CCTCCTCACGCAATTT<br>TGT  | TCAACAGCGTCTTGTG<br>GAAG | 60.1                             | 692                                           | INTRON                                            | Ca_11969                            | J                     | --  |
| Ca3_P4_32853814  | Ca3                                     | 32853814                      | CTTAATATGA/CTTAATATGATTAAT<br>ATGA                                                              | GAAGGAATCATCATGT<br>GGCA | TTGCTCAAAACCAAGCT<br>TCA | 59.5                             | 891                                           | INTRON                                            | Ca_12021                            | O                     | --  |
| Ca3_P4_33018844  | Ca3                                     | 33018844                      | TAAAAAAAA/TAAAAAAAAA                                                                            | CCAATGCTTCCTCCTC<br>CATA | ATAAAGGCATGAGACA<br>CGGG | 60.0                             | 546                                           | INTRON                                            | Ca_12042                            | --                    | --  |
| Ca3_P4_33487866  | Ca3                                     | 33487866                      | TTCTCTCTCTCTCTCTCTCTCTCTCT<br>CTCTCTCTCTCT/TTCTCTCTCTCTC<br>TCTCTCTCTCTCTCTCTCTCTCTCT<br>CTCTCT | TCCATGGCCTCTTCAA<br>TTTC | GCTAACCCGCAAAACA<br>AAAA | 60.0                             | 455                                           | INTRON                                            | Ca_23669                            | S                     | --  |
| Ca3_P4_33590873  | Ca3                                     | 33590873                      | ATTTTTTTTT/ATTTTTTTTT                                                                           | GTTCCCCGATCCTTAT<br>GTGA | GAACGGTCCATGCAAA<br>AGTT | 59.8                             | 558                                           | INTRON                                            | Ca_23666                            | GC                    | --  |
| Ca3_P4_35044678  | Ca3                                     | 35044678                      | TTGTAT/TT                                                                                       | CTTACCTGAAGCTTCC<br>ACCG | CGCTTCCGATTTAACA<br>CCAT | 59.9                             | 342                                           | INTRON                                            | Ca_00777                            | R                     | --  |
| Ca3_P4_35978832  | Ca3                                     | 35978832                      | GAAAAAAAA/GAAAAAAAAA                                                                            | ACTGTGTGCTGCCTTT<br>ACCC | CTTCTGGAACCTTCTCA<br>CCG | 60.2                             | 608                                           | INTRON                                            | Ca_00892                            | C                     | --  |
| Ca3_P4_35979306  | Ca3                                     | 35979306                      | TAAAAAAAA/TAAAAA                                                                                | CGGTGAGAAGGTTCCA<br>GAAG | GTTCCGTTACCCAGCC<br>ACTA | 59.8                             | 592                                           | INTRON                                            | Ca_00892                            | C                     | --  |
| Ca3_P4_35986133  | Ca3                                     | 35986133                      | TACTATATT/TACTATATTTAATAAC<br>TATATT                                                            | CCTTCATCAGCTCGGA<br>GAAA | TTGGAAGCAAAGAATC<br>CACC | 60.5                             | 379                                           | INTRON                                            | Ca_00893                            | --                    | --  |
| Ca3_P4_35986538  | Ca3                                     | 35986538                      | CT/CTT                                                                                          | GGTGGATTCTTGCTT<br>CCAA  | AGGTGCAAGTGCAAGT<br>TCCT | 60.1                             | 479                                           | INTRON                                            | Ca_00893                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca3_P4_35995449  | Ca3                                     | 35995449                      | ATTTTTTTT/ATTTTTTT                                            | AACTGGTGTTTTGGGT<br>TTGC | AAAGCAAAATGTTTG<br>CCAC   | 59.9                             | 285                                           | INTRON                                            | Ca_00895                            | E                     | --    |
| Ca3_P4_36005517  | Ca3                                     | 36005517                      | TAAAA/TAAAA                                                   | GTTACTGGAATTTGGG<br>GCCT | CATCAACTTCTTTGGCA<br>GCA  | 60.2                             | 459                                           | INTRON                                            | Ca_00896                            | OPR                   | --    |
| Ca3_P4_36018992  | Ca3                                     | 36018992                      | CAGA/CAGAGA                                                   | ATGATTTGAAACCCCA<br>AGCA | ATTGCAATGTGGAGC<br>CTTT   | 60.3                             | 741                                           | INTRON                                            | Ca_00900                            | O                     | CAMTA |
| Ca3_P4_36035545  | Ca3                                     | 36035545                      | GTTTTTTTTT/GTTTTTTTT                                          | GTTCCCAACTTCCATT<br>TCC  | TTACCTGTTTGGCATG<br>GACA  | 60.5                             | 559                                           | INTRON                                            | Ca_00902                            | S                     | bZIP  |
| Ca3_P4_36036772  | Ca3                                     | 36036772                      | AAGAT/A                                                       | ACAGGCACAACAAGAT<br>GCAA | TTTGGGGGAACCTATC<br>ATCA  | 60.3                             | 592                                           | INTRON                                            | Ca_00902                            | S                     | bZIP  |
| Ca3_P4_36039531  | Ca3                                     | 36039531                      | ACAATAGCA/ACAATAGCAATAGCA                                     | CCTCTCTAGCTCAGAG<br>CCCA | TACGCCGATAGTGCAA<br>CAAA  | 59.8                             | 423                                           | INTRON                                            | Ca_00902                            | S                     | bZIP  |
| Ca3_P4_36040095  | Ca3                                     | 36040095                      | TAAAAAAAAA/TAAAAAAAAA                                         | TGTTGCACTATCGGCG<br>TAAA | TTTAAACAGGCAGGG<br>TTGC   | 60.3                             | 782                                           | INTRON                                            | Ca_00902                            | S                     | bZIP  |
| Ca3_P4_36040732  | Ca3                                     | 36040732                      | ATTTT/ATTT                                                    | CCACCACTGCAGAAGT<br>GAGA | TCCGAACCTGGAGAGTG<br>TGAA | 60.0                             | 461                                           | INTRON                                            | Ca_00902                            | S                     | bZIP  |
| Ca3_P4_36067224  | Ca3                                     | 36067224                      | TAAAAAAA/TAAAAAAA                                             | GCAGCGATTGTAGAAT<br>GCAA | GAGGGCAGAATGCAGT<br>AAATG | 60.0                             | 700                                           | INTRON                                            | Ca_00904                            | A                     | --    |
| Ca3_P4_36067352  | Ca3                                     | 36067352                      | TGCTTTTGGCTTT/TGCTTT                                          | GCAGCGATTGTAGAAT<br>GCAA | GCAGAATCAGAAAGCC<br>AAGG  | 60.0                             | 865                                           | INTRON                                            | Ca_00904                            | A                     | --    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                             |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca3_P4_36081624  | Ca3                                     | 36081624                      | CAAAAAAAAA/CAAAAAAAAA                                         | TTTCCCCTGCAATATG<br>CTC     | GCAATCCTCAGCTCAA<br>AAGC  | 60.0                             | 499                                           | INTRON                                            | Ca_00906                            | T                     | FAR1 |
| Ca3_P4_36102329  | Ca3                                     | 36102329                      | TAAAAA/TAAAA                                                  | CCTGCAGGCAAGCAAA<br>TAAT    | GGTATTGTGGTGGGAT<br>GGTC  | 60.2                             | 486                                           | INTRON                                            | Ca_00908                            | K                     | --   |
| Ca3_P4_36157688  | Ca3                                     | 36157688                      | CAAAAAAAAAA/CAAAAAAAAAA                                       | ACAAAGGGATGGGGAA<br>AGAC    | TACCGAAACACATGAC<br>GGAA  | 60.2                             | 644                                           | INTRON                                            | Ca_00916                            | A                     | GeBP |
| Ca3_P4_36157739  | Ca3                                     | 36157739                      | CAATAATAATAATAAT/CAATAAT<br>AATAATAAT                         | ACAAAGGGATGGGGAA<br>AGAC    | TACCGAAACACATGAC<br>GGAA  | 60.2                             | 644                                           | INTRON                                            | Ca_00916                            | A                     | GeBP |
| Ca3_P4_36177767  | Ca3                                     | 36177767                      | CAAAAAAAAAA/CGAAAAAAAAA                                       | TCAATGAAGCAATGAG<br>GGCT    | CCAATGCCCTCCAGGT<br>ACTA  | 60.7                             | 534                                           | INTRON                                            | Ca_00920                            | --                    | --   |
| Ca3_P4_36180854  | Ca3                                     | 36180854                      | ATA/ATACTA                                                    | TGTGAATTTCAAATGAA<br>TTACGG | TGATATGCAGGTGTTT<br>CCGA  | 58.9                             | 194                                           | INTRON                                            | Ca_00921                            | Q                     | B3   |
| Ca3_P4_36197056  | Ca3                                     | 36197056                      | TTGTGT/TTGT                                                   | GTGGCGCAAAAAGAAA<br>AGAG    | TGCAGTAACTTCAACG<br>GGTCT | 60.0                             | 756                                           | INTRON                                            | Ca_00923                            | --                    | bHLH |
| Ca3_P4_36197331  | Ca3                                     | 36197331                      | AACACAC/AACACACAC                                             | TTGGTTAAAGCGTATTT<br>TGCC   | TTTGGATTTAGCCGTT<br>GGAC  | 59.2                             | 922                                           | INTRON                                            | Ca_00923                            | --                    | bHLH |
| Ca3_P4_36197565  | Ca3                                     | 36197565                      | CATA/CA                                                       | TCAACGTTCCATCTTCT<br>CTCA   | TTTGGATTTAGCCGTT<br>GGAC  | 58.4                             | 635                                           | INTRON                                            | Ca_00923                            | --                    | bHLH |
| Ca3_P4_36207320  | Ca3                                     | 36207320                      | TGA/TGAGA                                                     | TACCCCATAGTCATC<br>CCAA     | CAACTCCAGTGTTTC<br>GTCA   | 60.0                             | 532                                           | INTRON                                            | Ca_00925                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca3_P4_36212061  | Ca3                                     | 36212061                      | ATTTTTTTTT/ATTTTTTTTT                                         | TGGAGATGGAAAGTGG<br>GAAG  | CCAGAAATTTTAACGAA<br>CGAGG | 60.0                             | 326                                           | INTRON                                            | Ca_00926                            | --                    | LSD         |
| Ca3_P4_36212196  | Ca3                                     | 36212196                      | CAAAA/CAA                                                     | TGGAGATGGAAAGTGG<br>GAAG  | GAATGTGCTATATTTGC<br>ACGGA | 60.0                             | 624                                           | INTRON                                            | Ca_00926                            | --                    | LSD         |
| Ca3_P4_36212450  | Ca3                                     | 36212450                      | T/TTA                                                         | GGGAATACATGTCTGC<br>TACGG | TTGGCTGAGAACAACA<br>ATGC   | 59.5                             | 953                                           | INTRON                                            | Ca_00926                            | --                    | LSD         |
| Ca3_P4_36216845  | Ca3                                     | 36216845                      | TAAAAA/TAAAAAA                                                | CTCTCTGCCGAACCT<br>TACG   | AATTCCGGTTAAACAC<br>GCTG   | 60.0                             | 550                                           | INTRON                                            | Ca_00927                            | --                    | CO-like     |
| Ca3_P4_36218593  | Ca3                                     | 36218593                      | ATT/A                                                         | ACGCCTCGATCAAATC<br>ATCT  | CACTCTCTCGCCACA<br>TGAA    | 59.7                             | 708                                           | INTRON                                            | Ca_00927                            | --                    | CO-like     |
| Ca3_P4_36218738  | Ca3                                     | 36218738                      | TGAGAGAGAGAGAGAGA/TGAGA<br>GAGAGAGAGAGA                       | ACGCCTCGATCAAATC<br>ATCT  | CACTCTCTCGCCACA<br>TGAA    | 59.7                             | 708                                           | INTRON                                            | Ca_00927                            | --                    | CO-like     |
| Ca3_P4_36262377  | Ca3                                     | 36262377                      | GTTTTTTTT/GTTTTTTTTTTTT                                       | CACCATGGAGTGCCAT<br>ATCA  | CAACCACACACCTG<br>CATT     | 60.4                             | 876                                           | INTRON                                            | Ca_00936                            | --                    | MYB_related |
| Ca3_P4_36262538  | Ca3                                     | 36262538                      | CCTC/CCTCTC                                                   | GGCAGAGCTATCCCTC<br>AAGA  | AAAGTGCAGCAACCAC<br>ACAC   | 59.5                             | 591                                           | INTRON                                            | Ca_00936                            | --                    | MYB_related |
| Ca3_P4_36268678  | Ca3                                     | 36268678                      | ATTTTTTTTT/ATTTTTTTTTTT                                       | ATCGGTATCGGAGCTT<br>GATG  | CATGGTTTTGAAAAATG<br>GGG   | 60.1                             | 967                                           | INTRON                                            | Ca_00937                            | J                     | Dof         |
| Ca3_P4_36269834  | Ca3                                     | 36269834                      | AAT/AATTATTAT                                                 | CAGTGATCCTCTGGAT<br>GCAA  | CAGAGCATGAGATGGC<br>AGAA   | 59.8                             | 901                                           | INTRON                                            | Ca_00937                            | J                     | Dof         |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca3_P4_36280737  | Ca3                                     | 36280737                      | GCC/GCCC                                                      | AAAGCAGATGGGGAAC<br>TGTG | ATCCCTTCAGCTTCAC<br>CCTT | 60.1                             | 587                                           | INTRON                                            | Ca_00938                            | R                     | --       |
| Ca3_P4_36322744  | Ca3                                     | 36322744                      | GAAAAAAAAA/GAAAAAAAAA                                         | CAGCTTTCCTAGCATT<br>GCC  | TTTTGTCGCATCTGACT<br>TGC | 60.0                             | 440                                           | INTRON                                            | Ca_00941                            | D                     | TCP      |
| Ca3_P4_36329137  | Ca3                                     | 36329137                      | CTTTTTT/CTTTTTTT                                              | AACAATGGAGGTCTGG<br>AACG | CGGGCTCTCTCAAACA<br>GTCT | 60.0                             | 469                                           | INTRON                                            | Ca_00942                            | --                    | HB-other |
| Ca3_P4_36333973  | Ca3                                     | 36333973                      | ATTTT/ATTT                                                    | AGCAGCCAGGATCTGT<br>GAGT | CCGTGTTAGTATTCGC<br>CGTT | 60.0                             | 807                                           | INTRON                                            | Ca_00942                            | --                    | HB-other |
| Ca3_P4_36336902  | Ca3                                     | 36336902                      | TAAA/TAA                                                      | CCCATCTCCAACCTCT<br>TCAA | GGTGCTAAGTTTTGCC<br>GTGT | 60.0                             | 818                                           | INTRON                                            | Ca_00942                            | --                    | HB-other |
| Ca3_P4_36387524  | Ca3                                     | 36387524                      | TTAT/TT                                                       | TTCGCTCTCACACTTG<br>ATGG | TTTCATGCTCAGAGAC<br>ACCG | 60.0                             | 546                                           | INTRON                                            | Ca_00947                            | S                     | --       |
| Ca3_P4_36400923  | Ca3                                     | 36400923                      | TAAA/TAAA                                                     | TCCTGAACAAGCTTCC<br>GAGT | CAAGCTTGCCAATGTT<br>CAAA | 60.0                             | 434                                           | INTRON                                            | Ca_00951                            | H                     | --       |
| Ca3_P4_36412760  | Ca3                                     | 36412760                      | TAAA/TAAA                                                     | TGCTTTGCTTTGGGTC<br>TTCT | TCTCACGCGAATTCCC<br>TATT | 60.0                             | 307                                           | INTRON                                            | Ca_00954                            | G                     | --       |
| Ca3_P4_36414069  | Ca3                                     | 36414069                      | TTT/TTTATT                                                    | GATGCGCTATCCAACC<br>TCAC | GCCGCCCACATATCAT<br>TTAT | 60.6                             | 659                                           | INTRON                                            | Ca_00954                            | G                     | --       |
| Ca3_P4_36415214  | Ca3                                     | 36415214                      | AAAGAAG/AAAG                                                  | GAGTCAACCTACCGGA<br>CCAA | TGGGAATGACCTTTGC<br>TTTC | 60.0                             | 466                                           | INTRON                                            | Ca_00954                            | G                     | --       |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca3_P4_36416411  | Ca3                                     | 36416411                      | CAAAAAAAAA/CAAAAAAAAA                                         | AGGAGTTTTCGGTGAC<br>ATGG  | CATCGAGTTTTCTGC<br>CATT  | 60.0                             | 623                                           | INTRON                                            | Ca_00954                            | G                     | --  |
| Ca3_P4_36432148  | Ca3                                     | 36432148                      | TA/TAA                                                        | CTTCTTGCAGGGAACG<br>AAAG  | AGTGCTCCAGCAACGA<br>GAAT | 60.0                             | 378                                           | INTRON                                            | Ca_00957                            | H                     | --  |
| Ca3_P4_36444744  | Ca3                                     | 36444744                      | AAAGTCAGAAACCGAA/AAAGTCAG<br>AAACCGAAGTCAGAAACCGAA            | TATCTCGACCCTATTTG<br>CCG  | TGGGCCACGTATACTG<br>TCAA | 60.1                             | 693                                           | INTRON                                            | Ca_00959                            | R                     | --  |
| Ca3_P4_36448609  | Ca3                                     | 36448609                      | CAAAA/CAAA                                                    | GAGCCAGACATCAACT<br>GCAA  | CAATGTAGGAGTGCGA<br>AGCA | 60.0                             | 710                                           | INTRON                                            | Ca_00960                            | O                     | --  |
| Ca3_P4_36448626  | Ca3                                     | 36448626                      | TAACAACAA/TAACAACAACAA                                        | GAGCCAGACATCAACT<br>GCAA  | CAATGTAGGAGTGCGA<br>AGCA | 60.0                             | 710                                           | INTRON                                            | Ca_00960                            | O                     | --  |
| Ca3_P4_36448772  | Ca3                                     | 36448772                      | CAAAAAA/CAAAAAA                                               | TTCTCTCTAAGCCTCC<br>CATT  | CAATGTAGGAGTGCGA<br>AGCA | 60.0                             | 489                                           | INTRON                                            | Ca_00960                            | O                     | --  |
| Ca3_P4_36504591  | Ca3                                     | 36504591                      | AGGAGGGAGG/AGGAGG                                             | TTGCCTTCATTTCATGA<br>CGA  | AAGTCACAAAGTGCGA<br>ACCC | 60.2                             | 796                                           | INTRON                                            | Ca_00967                            | S                     | --  |
| Ca3_P4_37000758  | Ca3                                     | 37000758                      | TTAACTAACTAACTAACTAAC/TTAA<br>CTAACTAACTAAC                   | TGTGTGCTAACCAAAT<br>GCAAA | TGAATTGGATGCATCAT<br>CGT | 60.2                             | 664                                           | INTRON                                            | Ca_01028                            | --                    | --  |
| Ca3_P4_37078968  | Ca3                                     | 37078968                      | CT/C                                                          | GGAAAGTAGCTGCTGT<br>CGCT  | AATGGAGTGCCAGACA<br>AACC | 59.8                             | 556                                           | INTRON                                            | Ca_01034                            | R                     | --  |
| Ca3_P4_37356302  | Ca3                                     | 37356302                      | TGG/TG                                                        | TGGTTGATCACCCGAA<br>TACA  | AACAAACCCCAACAC<br>ATTA  | 59.8                             | 544                                           | INTRON                                            | Ca_01069                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca3_P4_38145521  | Ca3                                     | 38145521                      | ATTT/ATTTT                                                    | CTGATCTGGAGGTCTC<br>TCGC | AAATTGGCACAGAAGG<br>GTTG | 60.1                             | 545                                           | INTRON                                            | Ca_01158                            | C                     | --          |
| Ca3_P4_38145600  | Ca3                                     | 38145600                      | TTATATATATATATATATATATA<br>/TTATATATATATATATA                 | CCATGGATTAAATGCC<br>CATC | AAATTGGCACAGAAGG<br>GTTG | 60.0                             | 228                                           | INTRON                                            | Ca_01158                            | C                     | --          |
| Ca3_P4_38156627  | Ca3                                     | 38156627                      | ACTCT/ACT                                                     | CTGCAAGAGGGGTAA<br>ACCA  | ATGTTCTGAAAATGAG<br>GCGG | 60.1                             | 560                                           | INTRON                                            | Ca_01160                            | L                     | MYB_related |
| Ca3_P4_38162427  | Ca3                                     | 38162427                      | GTACTACTA/GTACTA                                              | TCCAGGCAGATAGCA<br>AGAT  | GTGGTCCAGGAAAAGC<br>AAGA | 59.9                             | 811                                           | INTRON                                            | Ca_01160                            | L                     | MYB_related |
| Ca3_P4_38170925  | Ca3                                     | 38170925                      | CAAT/CAATCAACGCCATAAT                                         | GAACAAATGCAGTGGC<br>TGAA | TGGCGAGGAAGCTTGT<br>AGAT | 59.8                             | 327                                           | INTRON                                            | Ca_01160                            | L                     | MYB_related |
| Ca3_P4_38187106  | Ca3                                     | 38187106                      | AT/ATT                                                        | GTAAAGGGTTCCTCCT<br>TCGC | GAAGACTCCAGCTTGC<br>CATC | 60.1                             | 400                                           | INTRON                                            | Ca_01162                            | --                    | --          |
| Ca3_P4_38203857  | Ca3                                     | 38203857                      | CT/CTT                                                        | AGGAACTGGGCATGGT<br>GTAG | TATTGGATTCTCCTCAA<br>GCG | 60.0                             | 870                                           | INTRON                                            | Ca_01163                            | E                     | --          |
| Ca3_P4_38204342  | Ca3                                     | 38204342                      | TG/T                                                          | GCCCGGATACCATCCT<br>ACTT | TGCCAGGTTACATAT<br>GGGT  | 60.2                             | 396                                           | INTRON                                            | Ca_01163                            | E                     | --          |
| Ca3_P4_38210151  | Ca3                                     | 38210151                      | ATT/A                                                         | GATCTTTGCATCCCA<br>ACAT  | CTAGAACTCACAGCCT<br>CGGG | 59.9                             | 237                                           | INTRON                                            | Ca_01164                            | T                     | WRKY        |
| Ca3_P4_38237845  | Ca3                                     | 38237845                      | GTATA/GTA                                                     | GAGATTGCTTTCCCAT<br>TCCA | ACATGAGCTCCTGGAC<br>TGCT | 60.0                             | 733                                           | INTRON                                            | Ca_01169                            | G                     | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                   | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                                 |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca3_P4_38238518  | Ca3                                     | 38238518                      | TT/TTCT                                                                         | CCAGACAACAACCAGA<br>AGCA | CCGTTACTGGGGTGAG<br>TTGT | 59.9                             | 421                                           | INTRON                                            | Ca_01169                            | G                     | --   |
| Ca3_P4_38555066  | Ca3                                     | 38555066                      | ATG/ATGATTG                                                                     | CCTGCATAGTCCAGCA<br>GACA | ATCCAAATGGCAGGTT<br>TGAG | 60.0                             | 631                                           | INTRON                                            | Ca_01208                            | S                     | NAC  |
| Ca3_P4_3900290   | Ca3                                     | 3900290                       | TTTTATTTATTTATTTATTTATTT/TTT<br>TATTTATTTATTTATTT                               | CTGCAAGTGGTGTGTT<br>TGCT | AATTACTCACGGCCCA<br>AAAA | 59.9                             | 621                                           | INTRON                                            | Ca_21332                            | E                     | --   |
| Ca3_P4_39027474  | Ca3                                     | 39027474                      | CGGGG/CGGGGG                                                                    | CATATGCCACATACGC<br>AAGG | CAATGTTAATGGCGG<br>TGTG  | 60.0                             | 586                                           | INTRON                                            | Ca_01265                            | YU                    | --   |
| Ca3_P4_39518552  | Ca3                                     | 39518552                      | AAATAATAATAATAATAATAATA<br>ATAATAATA/AAATAATAATAATAATA<br>ATAATAATAATAATAATAATA | ATTCCATGCAAACCAC<br>CATT | ACCACTGTAGCATTTTG<br>GGG | 60.1                             | 423                                           | INTRON                                            | Ca_01323                            | --                    | NAC  |
| Ca3_P4_39763068  | Ca3                                     | 39763068                      | CAGAGAGAGAGAGAGAGAGA/CAG<br>AGAGAGAGAGAGAGA                                     | GGTCGCACATTGTCAT<br>CATC | AAAGGTTTCGACCACG<br>TCAC | 59.9                             | 522                                           | INTRON                                            | Ca_01363                            | R                     | --   |
| Ca3_P4_39866286  | Ca3                                     | 39866286                      | GCATTAAGTTTAAAGAACT/G                                                           | TTGAGTCGGTTGAGCT<br>GTTG | CCCATCGAACCAAAGA<br>CTGT | 60.0                             | 562                                           | INTRON                                            | Ca_01372                            | --                    | WRKY |
| Ca3_P4_39892163  | Ca3                                     | 39892163                      | A/ACGTAGGG                                                                      | ATTATCGAATGCCAAG<br>TCGG | GGTCATTGGCATTGCT<br>TCTT | 59.9                             | 461                                           | INTRON                                            | Ca_01375                            | YUJ                   | --   |
| Ca3_P4_414861    | Ca3                                     | 414861                        | T/TG                                                                            | CTATGCAACCACAGCT<br>TCCA | GCAGATTCCGTTCAA<br>AAGA  | 59.9                             | 438                                           | INTRON                                            | Ca_22928                            | O                     | --   |
| Ca3_P4_415189    | Ca3                                     | 415189                        | AATCAATGTTA/AA                                                                  | TCTTTGAACCGGAAT<br>CTGC  | AAGAATGTATTGGGGC<br>TTGG | 60.2                             | 229                                           | INTRON                                            | Ca_22928                            | O                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)            | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                          |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca3_P4_4626820   | Ca3                                     | 4626820                       | TTGTG/TTG                                                                | GGAACGCTCTTTCTC<br>TCCC    | GCGATCAGAGTTCCCA<br>TGTT   | 60.3                             | 573                                           | INTRON                                            | Ca_22084                            | R                     | --       |
| Ca3_P4_6386934   | Ca3                                     | 6386934                       | TGG/TGGG                                                                 | TGTACGAGAAGGTCGT<br>GTGC   | GCCCAACAGCAAGCTA<br>TTTC   | 59.9                             | 574                                           | INTRON                                            | Ca_24834                            | --                    | Trihelix |
| Ca3_P4_6672422   | Ca3                                     | 6672422                       | TTTTATTTATTTATTTATTTATTTAT<br>TAT/TTTTATTTATTTATTTATTTATTT<br>ATTTATTTAT | GCGCCGCAATAGAATA<br>GAAG   | CAACAAAGGGAGGCAA<br>ATGT   | 60.0                             | 672                                           | INTRON                                            | Ca_25772                            | A                     | --       |
| Ca3_P4_6780454   | Ca3                                     | 6780454                       | AAAA/AAAACAAA                                                            | GGATGCTTCGTTTGGT<br>GTTT   | TTTGAACCAAGATGCA<br>GCAG   | 60.0                             | 832                                           | INTRON                                            | Ca_16557                            | R                     | NAC      |
| Ca3_P4_9577976   | Ca3                                     | 9577976                       | AGG/AGGG                                                                 | TTGCGTTCAAAGACTC<br>GATG   | TGAATTGCAGAATCCC<br>ATGA   | 60.0                             | 575                                           | INTRON                                            | Ca_20977                            | --                    | --       |
| Ca4_P4_11211716  | Ca4                                     | 11211716                      | AC/ACTCCC                                                                | GGAACATGGAATGTTG<br>GAGG   | GCAAAGTGCATGAAAA<br>GCAA   | 60.2                             | 500                                           | INTRON                                            | Ca_04353                            | U                     | M-type   |
| Ca4_P4_11227743  | Ca4                                     | 11227743                      | ATCTCTCT/ATCTCTCTCTCTCT                                                  | CGGGAGGTCCACTATT<br>TTCA   | ATTGCACCAACATCGT<br>TGA    | 59.9                             | 211                                           | INTRON                                            | Ca_04355                            | G                     | --       |
| Ca4_P4_11228737  | Ca4                                     | 11228737                      | TC/T                                                                     | TTTCATTTTATTCAAGA<br>GGGGG | CGATTTCACTCACTTAC<br>ATGGG | 59.3                             | 127                                           | INTRON                                            | Ca_04355                            | G                     | --       |
| Ca4_P4_11228782  | Ca4                                     | 11228782                      | ATTT/ATTTT                                                               | TTTCATTTTATTCAAGA<br>GGGGG | TTCAAGATCCGATTTC<br>CTCA   | 59.3                             | 136                                           | INTRON                                            | Ca_04355                            | G                     | --       |
| Ca4_P4_11229115  | Ca4                                     | 11229115                      | ATATTATTA/ATATTA                                                         | CCATGTAAGTGAGTGA<br>AATCGG | GTGCACTTAGGCTTGC<br>ATGA   | 59.5                             | 702                                           | INTRON                                            | Ca_04355                            | G                     | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_11229558  | Ca4                                     | 11229558                      | AATAT/AAT                                                     | GCCTAAGTGCACGATT<br>CACA  | GCAATTCAAAACCCGA<br>CAAA | 59.9                             | 581                                           | INTRON                                            | Ca_04355                            | G                     | --   |
| Ca4_P4_11240777  | Ca4                                     | 11240777                      | TAAAA/TAAAAA                                                  | ACAAAATATCGGCTGC<br>CAAG  | CCTCTCTCCCTCTCGC<br>TTTT | 60.1                             | 622                                           | INTRON                                            | Ca_04357                            | O                     | NAC  |
| Ca4_P4_11309352  | Ca4                                     | 11309352                      | AATGAT/AATGATGAT                                              | AAGAGCTACCTACGGA<br>GGGC  | ACCCAACAGCAAAACC<br>AAAC | 59.9                             | 354                                           | INTRON                                            | Ca_04363                            | --                    | --   |
| Ca4_P4_11333943  | Ca4                                     | 11333943                      | ATT/AT                                                        | TCATTGCATTCTTTGGT<br>GGA  | GTTACGGACCCCACTT<br>GCTA | 60.0                             | 633                                           | INTRON                                            | Ca_04367                            | U                     | FAR1 |
| Ca4_P4_11397641  | Ca4                                     | 11397641                      | TATATATA/TATATATACAAATATATA                                   | TGGCTCACAGGTCTCC<br>TTCT  | TGTGGGTTTTCCCAAT<br>TGT  | 60.0                             | 431                                           | INTRON                                            | Ca_04373                            | J                     | --   |
| Ca4_P4_11424081  | Ca4                                     | 11424081                      | GTTT/GTTTT                                                    | CGGTACCCCTTAGCTC<br>ACAA  | GAGATGGAGTTGGCAG<br>TGGT | 60.1                             | 896                                           | INTRON                                            | Ca_04376                            | GC                    | bHLH |
| Ca4_P4_11434766  | Ca4                                     | 11434766                      | A/AGAGTAACTTTCCGT                                             | TTTTTCCGTCCACTCCT<br>TTG  | CCGGTCTTCCAATGTC<br>AACT | 60.1                             | 368                                           | INTRON                                            | Ca_04378                            | S                     | --   |
| Ca4_P4_12270457  | Ca4                                     | 12270457                      | TCAGAC/TCAGACCAGAC                                            | GGTCGTCGGTAGGGG<br>TTTAT  | GTGGAGAGTATGGGTG<br>GGAA | 60.1                             | 552                                           | INTRON                                            | Ca_04451                            | --                    | C2H2 |
| Ca4_P4_12351718  | Ca4                                     | 12351718                      | TAAAAAAAA/TAAAAAAAAA                                          | CTGCAACAAGTGGCAT<br>ATGAT | AACGAGATCGCTTCTC<br>CAAA | 58.7                             | 328                                           | INTRON                                            | Ca_04459                            | M                     | --   |
| Ca4_P4_12498624  | Ca4                                     | 12498624                      | TAAAAA/TAAAAAAA                                               | TAAATTGGCCTCAAAT<br>GCC   | CCATGCACACGGATCA<br>AATA | 59.9                             | 389                                           | INTRON                                            | Ca_04473                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_12522756  | Ca4                                     | 12522756                      | ATTTTTTT/ATTTTTTT                                             | TTGTTGAACGCCAGAA<br>CTTG | TAGAGGAGGGGTAGGA<br>GGGA | 59.9                             | 317                                           | INTRON                                            | Ca_04475                            | C                     | bZIP  |
| Ca4_P4_12522870  | Ca4                                     | 12522870                      | A/AAT                                                         | CCCCTCCTCTATTCTC<br>CCAG | GGATCGAACCCATGTC<br>CTTA | 60.0                             | 476                                           | INTRON                                            | Ca_04475                            | C                     | bZIP  |
| Ca4_P4_12523416  | Ca4                                     | 12523416                      | ATTTTTTTTT/ATTTTTTTTTTT                                       | TTCTAAGGACATGGG<br>TTCG  | AAGTGGCAGCAGCCTC<br>ATTA | 59.9                             | 393                                           | INTRON                                            | Ca_04475                            | C                     | bZIP  |
| Ca4_P4_12523831  | Ca4                                     | 12523831                      | TTGCT/TT                                                      | GCTGCTGCCACTTGTA<br>ATCA | GGTACGGAATGGGACA<br>AAAA | 60.0                             | 482                                           | INTRON                                            | Ca_04475                            | C                     | bZIP  |
| Ca4_P4_12577562  | Ca4                                     | 12577562                      | T/TC                                                          | TCTGTCAGCCAATGCA<br>CTTC | CAGGAATGCCAAAACC<br>AAAT | 60.0                             | 409                                           | INTRON                                            | Ca_04480                            | L                     | --    |
| Ca4_P4_12577604  | Ca4                                     | 12577604                      | CTTTTTTTTT/CTTTTTTTTT                                         | TCTGTCAGCCAATGCA<br>CTTC | CTGTACCAGCCAACA<br>AAGA  | 60.0                             | 561                                           | INTRON                                            | Ca_04480                            | L                     | --    |
| Ca4_P4_12580791  | Ca4                                     | 12580791                      | T/TTA                                                         | AAATGCGCTCTGATT<br>GCT   | CTTAACCCAATTGGA<br>GGCA  | 60.0                             | 946                                           | INTRON                                            | Ca_04480                            | L                     | --    |
| Ca4_P4_12582939  | Ca4                                     | 12582939                      | TTAATATAA/TTAA                                                | CAAGCTTGACCTGGG<br>GTGT  | CCGAAAAAGCATCACT<br>GGTT | 60.0                             | 503                                           | INTRON                                            | Ca_04480                            | L                     | --    |
| Ca4_P4_12594768  | Ca4                                     | 12594768                      | T/CTG                                                         | AGGAAGACCTGCCTCC<br>TCTC | GCACAACCAACAGGT<br>CAAA  | 60.0                             | 570                                           | INTRON                                            | Ca_04482                            | R                     | --    |
| Ca4_P4_12748853  | Ca4                                     | 12748853                      | TTATATATATATATA/TTATATATA<br>TATATA                           | GTTTTTGGGTTTCTGC<br>CAAA | TTTGCTCTGGAACGAG<br>GAGT | 60.0                             | 441                                           | INTRON                                            | Ca_04495                            | --                    | NF-YB |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                                     |                             |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_13708395  | Ca4                                     | 13708395                      | CAAA/CAA                                                            | TTGGAGGACCAAACT<br>GGAG     | GGCTTGGACAATTTG<br>TGTG  | 60.1                             | 795                                           | INTRON                                            | Ca_04592                            | R                     | --    |
| Ca4_P4_13749552  | Ca4                                     | 13749552                      | AA/AAGA                                                             | TTGACTTCTCCTTGTT<br>GCC     | TTTTTGTGACATGAGG<br>CCA  | 60.2                             | 758                                           | INTRON                                            | Ca_04599                            | R                     | MIKC  |
| Ca4_P4_13757858  | Ca4                                     | 13757858                      | ATTTTT/ATTTT                                                        | GCTCTCCATTTCATCCA<br>AGC    | AGATGGGGAGAGGGAA<br>AGAA | 59.8                             | 327                                           | INTRON                                            | Ca_04600                            | --                    | NF-YB |
| Ca4_P4_13765741  | Ca4                                     | 13765741                      | C/CTGTAATTT                                                         | TGGTATGGTACCCCTG<br>TCGT    | CATTAGCAACCAGCTG<br>GACA | 60.1                             | 430                                           | INTRON                                            | Ca_04601                            | --                    | HSF   |
| Ca4_P4_13781219  | Ca4                                     | 13781219                      | GTATATATATATATAT/GTATATATAT<br>ATAT                                 | AGACCCTCCATCCCTT<br>TTTG    | GGGATTGAATTGATGG<br>ATGG | 60.3                             | 703                                           | INTRON                                            | Ca_04602                            | I                     | --    |
| Ca4_P4_1378564   | Ca4                                     | 1378564                       | GTATATATATATATATATATATATAT<br>AT/GTATATATATATATATATATATAT<br>ATATAT | TTGCAAGAAACAGATG<br>CCAG    | CGCAATAGAAAAGTCC<br>GAGC | 60.0                             | 769                                           | INTRON                                            | Ca_07768                            | Z                     | NAC   |
| Ca4_P4_13792182  | Ca4                                     | 13792182                      | T/TA                                                                | GGCAACATAGATCCTC<br>TCACC   | GCTCACTCCGTCAGGT<br>TAGG | 58.6                             | 719                                           | INTRON                                            | Ca_04604                            | Q                     | --    |
| Ca4_P4_13798128  | Ca4                                     | 13798128                      | A/AT                                                                | CGGAATCTTCTACGCA<br>CCAT    | TTCCCAACCTAAACAAT<br>CGC | 60.1                             | 611                                           | INTRON                                            | Ca_04605                            | R                     | --    |
| Ca4_P4_13822755  | Ca4                                     | 13822755                      | CTAT/CTATAT                                                         | CTGAAAGCACCCAATC<br>CAGT    | CCCAAAAATGGTTGCC<br>TAAA | 60.1                             | 804                                           | INTRON                                            | Ca_04607                            | R                     | --    |
| Ca4_P4_13865484  | Ca4                                     | 13865484                      | T/TTTC                                                              | TCAGATGTTTATTTGAT<br>CCAGCA | CTTTGAGGATCCGTTT<br>GTCA | 59.6                             | 590                                           | INTRON                                            | Ca_04610                            | R                     | --    |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_13865867  | Ca4                                     | 13865867                      | ACAC/A                                                        | TGACAAACGGATCCTC<br>AAAG | GTCTCCAGCAAGTGTC<br>GTGA | 58.7                             | 548                                           | INTRON                                            | Ca_04610                            | R                     | --   |
| Ca4_P4_15269476  | Ca4                                     | 15269476                      | GGGCCC/GGGCCCGGGCCC                                           | AGCCCCATACACTCGT<br>TTTG | TCGCTTGAAACCTTC<br>TCAT  | 60.0                             | 463                                           | INTRON                                            | Ca_05572                            | A                     | --   |
| Ca4_P4_15590624  | Ca4                                     | 15590624                      | GTATTATTATTATTATTATTATTA<br>TT/GTATTATTATTATTATTATTATTA<br>TT | CGACCTTGCATTAGCA<br>GTGA | ATATGTCAGCCGGCCT<br>AGC  | 60.0                             | 397                                           | INTRON                                            | Ca_05543                            | E                     | --   |
| Ca4_P4_15930937  | Ca4                                     | 15930937                      | CAGA/C                                                        | TAAGCACGGACAAAGC<br>ACAG | TTTTTGACCGGTATTT<br>TCC  | 60.1                             | 344                                           | INTRON                                            | Ca_05513                            | R                     | --   |
| Ca4_P4_15933152  | Ca4                                     | 15933152                      | CTAGATAGA/CTAGA                                               | ACACCAGTCGGGTACT<br>CCTG | CCAATCCCTGTCACGT<br>CTTT | 60.0                             | 451                                           | INTRON                                            | Ca_05513                            | R                     | --   |
| Ca4_P4_16048595  | Ca4                                     | 16048595                      | TG/T                                                          | GACCATTTTGGTGATT<br>GGG  | AGGTACCACCAACCAA<br>GTGC | 60.0                             | 258                                           | INTRON                                            | Ca_05504                            | J                     | bHLH |
| Ca4_P4_16063311  | Ca4                                     | 16063311                      | A/ACATGCGCAAGAAATTC                                           | AAGTTGGCGTGCTTGT<br>TTCT | CATCATGGTGAAGGTC<br>GTTG | 59.9                             | 666                                           | INTRON                                            | Ca_05503                            | K                     | MYB  |
| Ca4_P4_16074532  | Ca4                                     | 16074532                      | CT/CTGTT                                                      | GGCTGCCTAACATGGG<br>TTTA | GACAGGCAACCCTGTG<br>AAAT | 60.0                             | 473                                           | INTRON                                            | Ca_05502                            | T                     | --   |
| Ca4_P4_16077645  | Ca4                                     | 16077645                      | AAAGAAGAAGAAGAAGAA/AAA<br>GAAGAAGAAGAAGAA                     | CCTTGTCGGAGGTAAA<br>ACCA | GGTTCCTTGACCGTGT<br>GATT | 60.0                             | 564                                           | INTRON                                            | Ca_05501                            | --                    | TCP  |
| Ca4_P4_16077692  | Ca4                                     | 16077692                      | TAGCAAGG/T                                                    | CCTTGTCGGAGGTAAA<br>ACCA | CCCTGATGGTCTTTGC<br>AACT | 60.0                             | 783                                           | INTRON                                            | Ca_05501                            | --                    | TCP  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca4_P4_16468176  | Ca4                                     | 16468176                      | TTTATTATTATTATTATTATTATT<br>/TTTATTATTATTATTATTATTAT<br>TATT  | ATTGGAATCCGATGCT<br>GAAC | AAACACTGACAGGGAC<br>AGGG | 59.9                             | 416                                           | INTRON                                            | Ca_05478                            | A                     | MYB     |
| Ca4_P4_16532811  | Ca4                                     | 16532811                      | TAGAGAGAGAGAGA/TAGAGAGAGA<br>GAGAGAGAGAGAGAGAGA               | TTTGCAACAACAGCGA<br>CATT | CTGAACCAGCCTCACC<br>ATTT | 60.3                             | 382                                           | INTRON                                            | Ca_05471                            | --                    | bZIP    |
| Ca4_P4_1677374   | Ca4                                     | 1677374                       | TAAAAAA/TAAAAA                                                | TCCAAACTAGTCCGAC<br>GTGA | AGCTGCTGGAGGAGTT<br>GGTA | 59.3                             | 450                                           | INTRON                                            | Ca_07795                            | --                    | --      |
| Ca4_P4_16846897  | Ca4                                     | 16846897                      | C/CTT                                                         | ACATGTGCCTTGGGAC<br>TAGC | GCGAAAAGTCGAAGAT<br>CCTG | 60.1                             | 571                                           | INTRON                                            | Ca_05437                            | --                    | --      |
| Ca4_P4_16985095  | Ca4                                     | 16985095                      | ATTTTT/ATTTTT                                                 | CATGAGACTCGTCAAG<br>GCAA | GTGTGGAAGTGCCAAA<br>GGTT | 60.0                             | 914                                           | INTRON                                            | Ca_05426                            | U                     | --      |
| Ca4_P4_17003772  | Ca4                                     | 17003772                      | TG/T                                                          | TTCTGGCAACATGACA<br>GGAG | TACCATCCAGCAAAT<br>CTCA  | 59.8                             | 158                                           | INTRON                                            | Ca_05424                            | S                     | --      |
| Ca4_P4_17011803  | Ca4                                     | 17011803                      | CTT/CTTT                                                      | TTTGCCCAAAGAAAAG<br>CACT | TAAAGACCGTGGGACA<br>CCTT | 59.9                             | 321                                           | INTRON                                            | Ca_05422                            | --                    | G2-like |
| Ca4_P4_17014077  | Ca4                                     | 17014077                      | GAAATAAATAA/GAAATAAATAAT<br>AAATAAA                           | CCCAATTCACCTCTCAT<br>GCT | TGATTGGCAATTCCAC<br>AAAA | 60.1                             | 701                                           | INTRON                                            | Ca_05422                            | --                    | G2-like |
| Ca4_P4_17081756  | Ca4                                     | 17081756                      | TTATA/TTATATA                                                 | TACCGGAAGATTCGGA<br>AATG | CTGCAGGTAAGCATCC<br>CAAT | 59.9                             | 694                                           | INTRON                                            | Ca_05415                            | --                    | --      |
| Ca4_P4_17081772  | Ca4                                     | 17081772                      | TAATA/T                                                       | TACCGGAAGATTCGGA<br>AATG | CTGCAGGTAAGCATCC<br>CAAT | 59.9                             | 694                                           | INTRON                                            | Ca_05415                            | --                    | --      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca4_P4_17130938  | Ca4                                     | 17130938                      | GTTTTT/GTTTT                                                  | CGAACATAAAGGACGA<br>ATTGA | GCATGTAATGTTGGAA<br>GCCC | 59.1                             | 346                                           | INTRON                                            | Ca_05411                            | CR                    | Nin-like |
| Ca4_P4_17133672  | Ca4                                     | 17133672                      | AATATTG/A                                                     | TCGGGTATTTTCCTTC<br>ATCA  | TTTGAAAAATCCTTTG<br>CGG  | 59.4                             | 522                                           | INTRON                                            | Ca_05411                            | CR                    | Nin-like |
| Ca4_P4_17143680  | Ca4                                     | 17143680                      | TAAAA/TAAAAA                                                  | TTGACCAAGCATGAT<br>TTTG   | GGTTAGGATTCAAGGA<br>GGCA | 59.7                             | 736                                           | INTRON                                            | Ca_05410                            | CR                    | Nin-like |
| Ca4_P4_17203357  | Ca4                                     | 17203357                      | TAAGA/TAAGAAGA                                                | TGTGCTCCATGTCTCT<br>TTGC  | CTCTGGCTGGTAGCT<br>TTGG  | 60.0                             | 611                                           | INTRON                                            | Ca_05403                            | --                    | --       |
| Ca4_P4_17210187  | Ca4                                     | 17210187                      | ATTTTTTTTTT/ATTTTTTTTT                                        | GTGTCACCTGGACATGC<br>TTGG | TAGCCTTCTGAATTCCC<br>CCT | 60.2                             | 626                                           | INTRON                                            | Ca_05402                            | C                     | --       |
| Ca4_P4_17210535  | Ca4                                     | 17210535                      | CTT/CT                                                        | TTCAGGGAGTTCCATC<br>AACC  | TAGCCTTCTGAATTCCC<br>CCT | 59.9                             | 448                                           | INTRON                                            | Ca_05402                            | C                     | --       |
| Ca4_P4_17219620  | Ca4                                     | 17219620                      | GTTTTTT/GTTTTT                                                | GGAATGAGAGAGAGCG<br>TTGG  | TTATGCGATGCCAATTC<br>AAA | 60.0                             | 563                                           | INTRON                                            | Ca_05401                            | O                     | --       |
| Ca4_P4_17286686  | Ca4                                     | 17286686                      | CATTGGATTGGATTG/CATTGGATT<br>G                                | TGCATTTTCATGCCTTTG<br>CTA | TGATTAGCCCGTATTTT<br>GGG | 60.4                             | 648                                           | INTRON                                            | Ca_05393                            | R                     | --       |
| Ca4_P4_17287338  | Ca4                                     | 17287338                      | AC/A                                                          | CCCAAAATACGGGCTA<br>ATCA  | TCTTCACTTGGCTGGA<br>AAGC | 59.8                             | 508                                           | INTRON                                            | Ca_05393                            | R                     | --       |
| Ca4_P4_17297039  | Ca4                                     | 17297039                      | TAAAAAA/TAAAAAAA                                              | TTTGCTCAGCTGTGT<br>TGAC   | TCATCAGCTGGACAAC<br>TTCG | 60.0                             | 607                                           | INTRON                                            | Ca_05392                            | R                     | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_17300807  | Ca4                                     | 17300807                      | TC/TCC                                                        | CCCTCATATCCAGTGA<br>TGCC   | ACCAGAGCTCGTTCCT<br>TTCA | 60.3                             | 564                                           | INTRON                                            | Ca_05391                            | TBLD                  | --  |
| Ca4_P4_17318086  | Ca4                                     | 17318086                      | A/AG                                                          | CTCAAAAGTGGGATAG<br>GGCA   | ACAGCGTGAAACAAGA<br>TCCC | 60.1                             | 429                                           | INTRON                                            | Ca_05390                            | M                     | --  |
| Ca4_P4_17318109  | Ca4                                     | 17318109                      | AA/AATATTA                                                    | CTCAAAAGTGGGATAG<br>GGCA   | ACAGCGTGAAACAAGA<br>TCCC | 60.1                             | 429                                           | INTRON                                            | Ca_05390                            | M                     | --  |
| Ca4_P4_17361143  | Ca4                                     | 17361143                      | TGAGAGAGAGA/TGAGAGAGAGAGA<br>GAGAGA                           | GTCTTGAAAAGCCAG<br>CAAG    | CCTACCCTGCTCAAAG<br>TTGC | 60.0                             | 469                                           | INTRON                                            | Ca_05388                            | T                     | NAC |
| Ca4_P4_17379518  | Ca4                                     | 17379518                      | TG/T                                                          | AACAATGTTGCATCA<br>CGAA    | TCTTCATTGGTCTCGT<br>GCTT | 60.0                             | 740                                           | INTRON                                            | Ca_05387                            | R                     | --  |
| Ca4_P4_17396020  | Ca4                                     | 17396020                      | ATTTTT/ATTT                                                   | CCAAGCATGGTTTAGT<br>GGCT   | TTTCTCTGGCCACCATT<br>TTC | 60.1                             | 371                                           | INTRON                                            | Ca_05386                            | K                     | --  |
| Ca4_P4_17431572  | Ca4                                     | 17431572                      | GC/G                                                          | TCTGTCAATTCCTGCCA<br>TTTTT | TCGCAATGTAGCTCCC<br>TCTT | 59.6                             | 858                                           | INTRON                                            | Ca_05384                            | K                     | --  |
| Ca4_P4_17431624  | Ca4                                     | 17431624                      | T/TG                                                          | TGTCCCTCATTATAAGC<br>ACCC  | TCGCAATGTAGCTCCC<br>TCTT | 58.9                             | 606                                           | INTRON                                            | Ca_05384                            | K                     | --  |
| Ca4_P4_17431799  | Ca4                                     | 17431799                      | ACT/ACTCT                                                     | TTTGCTGTGCTTTGAT<br>GGC    | TCGCAATGTAGCTCCC<br>TCTT | 59.8                             | 186                                           | INTRON                                            | Ca_05384                            | K                     | --  |
| Ca4_P4_17432501  | Ca4                                     | 17432501                      | AC/A                                                          | ATTCTTCGGATGGTGC<br>TTTG   | CTCATTCTGTCCCCCT<br>CCA  | 60.1                             | 531                                           | INTRON                                            | Ca_05384                            | K                     | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                              | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                                                                                            |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_17432865  | Ca4                                     | 17432865                      | CCAAACA/CCA                                                                                                                                | TGGAGGGGAACAGAA<br>TGAG  | CGAGGTGAAAGGAAAG<br>AACG | 60.0                             | 377                                           | INTRON                                            | Ca_05384                            | K                     | --   |
| Ca4_P4_17434023  | Ca4                                     | 17434023                      | TAAA/TAA                                                                                                                                   | CAATTCACCTTGCTGC<br>CTCA | TGCATTTTCTGCACTC<br>TGG  | 60.0                             | 104                                           | INTRON                                            | Ca_05384                            | K                     | --   |
| Ca4_P4_17439028  | Ca4                                     | 17439028                      | ACTC/ACTCTC                                                                                                                                | GTTTCAGAGCTGGGAG<br>ATGC | GGGTGTGGGGATAGTT<br>GATG | 60.0                             | 575                                           | INTRON                                            | Ca_05384                            | K                     | --   |
| Ca4_P4_17439269  | Ca4                                     | 17439269                      | T/TCTA                                                                                                                                     | TCCTCACCAAGTCCGA<br>AATC | GGGTGTGGGGATAGTT<br>GATG | 60.1                             | 534                                           | INTRON                                            | Ca_05384                            | K                     | --   |
| Ca4_P4_17464214  | Ca4                                     | 17464214                      | CTATATAT/CTATATATATAT                                                                                                                      | ACCACTCACCAACCTT<br>CCAG | AACCCGGAGACCCAAT<br>TTAG | 60.0                             | 635                                           | INTRON                                            | Ca_05381                            | O                     | GRAS |
| Ca4_P4_17464247  | Ca4                                     | 17464247                      | CA/CGAGGA                                                                                                                                  | ACCACTCACCAACCTT<br>CCAG | AACCCGGAGACCCAAT<br>TTAG | 60.0                             | 635                                           | INTRON                                            | Ca_05381                            | O                     | GRAS |
| Ca4_P4_17480298  | Ca4                                     | 17480298                      | ATATTATTATTATTATTAT/ATATTAT<br>TATTAT                                                                                                      | TTGTTGGCCGTCATAT<br>GCTA | GACCAATTACAAGCGA<br>GGGA | 60.1                             | 617                                           | INTRON                                            | Ca_05379                            | O                     | --   |
| Ca4_P4_17482178  | Ca4                                     | 17482178                      | ATTTTTTT/ATTTTTTTT                                                                                                                         | TCCATCTGAACCCTGA<br>CTCC | TGCCCTAAGATGGTTT<br>GGTC | 60.0                             | 445                                           | INTRON                                            | Ca_05379                            | O                     | --   |
| Ca4_P4_17482604  | Ca4                                     | 17482604                      | CATTATTATTATTATTATTATTATT<br>TATTATTATTATTATTATTATTATT<br>TATT/CATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT | TGACCAAACCATCTTA<br>GGGC | AAGTTGGGTGATGAAG<br>TGCC | 59.9                             | 204                                           | INTRON                                            | Ca_05379                            | O                     | --   |
| Ca4_P4_17484481  | Ca4                                     | 17484481                      | ATTTTTTTTT/ATTTTTTTTTT                                                                                                                     | TCGCCTGATGCTTGTA<br>CTTG | AGGAGGCTTTTCCACA<br>GGTT | 60.0                             | 361                                           | INTRON                                            | Ca_05379                            | O                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_17491763  | Ca4                                     | 17491763                      | TAAAA/TAAAAA                                                  | TTTCCCGTAGATTCCA<br>TGC  | GCTGGAGAAAGAGTTG<br>GTGC | 59.9                             | 705                                           | INTRON                                            | Ca_05378                            | --                    | --   |
| Ca4_P4_17527467  | Ca4                                     | 17527467                      | AGT/AGTGT                                                     | CAAAGTTAAGAAGGCA<br>GGCG | CAAATTGGTGGGATT<br>TTGG  | 60.0                             | 578                                           | INTRON                                            | Ca_05374                            | R                     | NAC  |
| Ca4_P4_17614699  | Ca4                                     | 17614699                      | AC/A                                                          | CCTTGGGCTGAAATTG<br>AAAA | GCTAATGCCCCATAG<br>ATGA  | 60.0                             | 759                                           | INTRON                                            | Ca_05369                            | E                     | --   |
| Ca4_P4_17632165  | Ca4                                     | 17632165                      | TTTTTGCTT/TTTTGCTTCAATTTG<br>CTT                              | ACACAGATCCCATCCC<br>ATGT | ATTTACGGCCACCAAA<br>ACTG | 60.1                             | 575                                           | INTRON                                            | Ca_05367                            | Z                     | WRKY |
| Ca4_P4_17636026  | Ca4                                     | 17636026                      | C/CCAAGATATA                                                  | GGCCTCATCTCTAGCC<br>AATG | CCAAGGAAGTTTCACC<br>AGGA | 59.8                             | 297                                           | INTRON                                            | Ca_05367                            | Z                     | WRKY |
| Ca4_P4_17636177  | Ca4                                     | 17636177                      | ATTTTT/ATTTTTTT                                               | TCCTGGTGAAACTTCC<br>TTGG | AATGGGATGTGGCATT<br>TTTC | 60.1                             | 129                                           | INTRON                                            | Ca_05367                            | Z                     | WRKY |
| Ca4_P4_17638808  | Ca4                                     | 17638808                      | CAA/CA                                                        | GTTGCTTCAGGGGTTA<br>CCAA | GACAACTGCAGCATCA<br>ATGG | 60.0                             | 301                                           | INTRON                                            | Ca_05367                            | Z                     | WRKY |
| Ca4_P4_17674751  | Ca4                                     | 17674751                      | A/AC                                                          | TGCTCCCAATCTCAATT<br>TCC | GCCTGATTCTTCAGGC<br>AAGT | 60.0                             | 474                                           | INTRON                                            | Ca_05360                            | --                    | --   |
| Ca4_P4_17701687  | Ca4                                     | 17701687                      | ATTCTCAGT/ATTCTCAGTTCTCAGT                                    | GGCTGTCATGACTGTG<br>GTTG | AAAAATGCCAATGATCC<br>TGC | 60.2                             | 184                                           | INTRON                                            | Ca_05355                            | R                     | SBP  |
| Ca4_P4_17769321  | Ca4                                     | 17769321                      | GAACAAACAAACAAACAA/GAA<br>CAAACAAACAAACAA                     | GAGCCCATTCCAAAAG<br>ATGA | TTCAGCCTCGACCAGT<br>TTTT | 60.0                             | 814                                           | INTRON                                            | Ca_05348                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_1777960   | Ca4                                     | 1777960                       | CATAAAAT/CATAAAATAAAAT                                        | AGGGGACGTCTCCCAT<br>TTAT  | AGATAGGACCCCACC<br>ATTC   | 59.7                             | 705                                           | INTRON                                            | Ca_07800                            | K                     | HSF  |
| Ca4_P4_17848485  | Ca4                                     | 17848485                      | CATTATTATT/CATTATT                                            | AACGAAAAGCAAGGCT<br>CAAA  | TCACCATCTTGCCACAT<br>CAT  | 60.0                             | 569                                           | INTRON                                            | Ca_18621                            | J                     | --   |
| Ca4_P4_17849398  | Ca4                                     | 17849398                      | AGGG/AGGGG                                                    | AGTGTAAGTGCCCAAG<br>GTGG  | CCGTTCGTTAAGTGCG<br>AAAT  | 60.0                             | 156                                           | INTRON                                            | Ca_18621                            | J                     | --   |
| Ca4_P4_17851859  | Ca4                                     | 17851859                      | GTTTTTTTT/GTTTTTTTT                                           | TCAGCTCGGTAAATAT<br>CGCC  | CCCTCACTCCCTCAAAT<br>GAA  | 60.2                             | 882                                           | INTRON                                            | Ca_18621                            | J                     | --   |
| Ca4_P4_17854136  | Ca4                                     | 17854136                      | CCTCTCTCTCTCTCTCTC/CCTCT<br>CTCTCTCTCTCTC                     | GCGAAGGGTTTTAGGG<br>TTTC  | TATAGCGAGAAGTTTCG<br>CCGT | 59.9                             | 521                                           | INTRON                                            | Ca_18622                            | K                     | WRKY |
| Ca4_P4_17854849  | Ca4                                     | 17854849                      | CTTTT/CTTTT                                                   | TGACGCAAACGAACT<br>CAAG   | ACTGTTCAAACCAACC<br>CTGC  | 60.0                             | 715                                           | INTRON                                            | Ca_18622                            | K                     | WRKY |
| Ca4_P4_17862773  | Ca4                                     | 17862773                      | AGT/AGTGT                                                     | TTTTCTTCGGATGGAA<br>ATGC  | ACAAAAATGGCAATGC<br>ACAA  | 60.0                             | 571                                           | INTRON                                            | Ca_18623                            | --                    | WOX  |
| Ca4_P4_1786291   | Ca4                                     | 1786291                       | GTTAGTTAGTT/GTTAGTTAGTTGT<br>TATTAGTTAGTT                     | AAATCGTGTC AACCGC<br>TACC | ATCGTCGTCTCTCACC<br>ATCC  | 60.0                             | 870                                           | INTRON                                            | Ca_07801                            | T                     | --   |
| Ca4_P4_17867503  | Ca4                                     | 17867503                      | GTTTTTTTTT/GTTTTTTTTT                                         | TGGCCCAAATAACAGA<br>AAGG  | GCCATGGTGACTTCGA<br>TTCT  | 59.9                             | 362                                           | INTRON                                            | Ca_18624                            | TU                    | WOX  |
| Ca4_P4_1791824   | Ca4                                     | 1791824                       | GA/G                                                          | CGATATTGTCAAATGG<br>CGTG  | TTTTGGATTCTCCCTC<br>CTT   | 60.0                             | 644                                           | INTRON                                            | Ca_07801                            | T                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_1791916   | Ca4                                     | 1791916                       | AGTTAGTTTGTTA/AGTTAGTTTGT<br>AGTTTGTTA                        | CGATATTGTCAAATGG<br>CGTG | CAATGATCACACCAAG<br>GTCC  | 60.0                             | 741                                           | INTRON                                            | Ca_07801                            | T                     | --   |
| Ca4_P4_1801951   | Ca4                                     | 1801951                       | TAAAAAAAAA/TAAAAAAAAA                                         | CGTAGCAAGTGCCACG<br>TAGA | ATTTTACGACCTCGCA<br>CCAC  | 60.1                             | 813                                           | INTRON                                            | Ca_07801                            | T                     | --   |
| Ca4_P4_1807409   | Ca4                                     | 1807409                       | GAAAAAAAA/GAAAAAAAA                                           | TTGAAGATGACGCTGC<br>ATTC | TTTGTGCTTCACTACCG<br>CTG  | 60.0                             | 261                                           | INTRON                                            | Ca_07801                            | T                     | --   |
| Ca4_P4_18121565  | Ca4                                     | 18121565                      | TAAGAAG/TAAG                                                  | GCTGCACCATGAGATC<br>TTGA | ATGGTGCTGGAAGTTG<br>CTTT  | 60.0                             | 440                                           | INTRON                                            | Ca_18652                            | --                    | --   |
| Ca4_P4_1828978   | Ca4                                     | 1828978                       | AGGGGG/AGGGG                                                  | TTGAATGTGAATTGCA<br>GCGT | CATCGTGAGCAAACCA<br>AATG  | 60.3                             | 914                                           | INTRON                                            | Ca_07803                            | T                     | --   |
| Ca4_P4_1829151   | Ca4                                     | 1829151                       | ATT/AT                                                        | AGGGGGCAGTGTAGAT<br>TGTG | TGCAGCCCAAATGTG<br>TAAA   | 60.0                             | 596                                           | INTRON                                            | Ca_07803                            | T                     | --   |
| Ca4_P4_1847466   | Ca4                                     | 1847466                       | ACATATCCA/ACATATCCATATCCA                                     | TTCACAATAGCCGATG<br>ACGA | TCAAGAAGATCCGACT<br>TGCC  | 60.2                             | 796                                           | INTRON                                            | Ca_07806                            | R                     | WRKY |
| Ca4_P4_2032547   | Ca4                                     | 2032547                       | CTGTGTGTGT/CTGTGTGT                                           | TGCTGAGTTCGAGGAA<br>AGGT | CACATCTCTTGTTGCT<br>CCA   | 60.0                             | 517                                           | INTRON                                            | Ca_07822                            | D                     | --   |
| Ca4_P4_2034424   | Ca4                                     | 2034424                       | CTTTT/CTTTT                                                   | ACCAGATACCGCACCA<br>AAAG | TTCTGCATACCTTGCTCC<br>ACG | 60.0                             | 352                                           | INTRON                                            | Ca_07822                            | D                     | --   |
| Ca4_P4_2034663   | Ca4                                     | 2034663                       | TACA/TACACA                                                   | ACCAGATACCGCACCA<br>AAAG | AGTTGGCAAGTTTGTG<br>AGGC  | 60.0                             | 570                                           | INTRON                                            | Ca_07822                            | D                     | --   |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                                                           |                          |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca4_P4_2035225   | Ca4                                     | 2035225                       | GGTTTAA/G                                                                                 | CGCGCCAGAAGTATGT<br>GATA | TGGGCAGCTTAGACTG<br>GACT   | 59.9                             | 275                                           | INTRON                                            | Ca_07822                            | D                     | --     |
| Ca4_P4_2035282   | Ca4                                     | 2035282                       | GTTTTTT/GTTTTTTT                                                                          | CGCGCCAGAAGTATGT<br>GATA | TGGGCAGCTTAGACTG<br>GACT   | 59.9                             | 275                                           | INTRON                                            | Ca_07822                            | D                     | --     |
| Ca4_P4_20773849  | Ca4                                     | 20773849                      | CTTATTATTATTAT/CTTATTATTATT<br>ATTAT                                                      | TCTCGGCTGAAGGAAC<br>AGAT | AGCGGAACAACGACAA<br>GATT   | 60.0                             | 524                                           | INTRON                                            | Ca_17170                            | --                    | E2F/DP |
| Ca4_P4_2136004   | Ca4                                     | 2136004                       | TTATATATATATATATATATATATATA<br>TATATATA/TTATATATATATATATAT<br>ATATATATATATATATATATATATATA | AAGGTTTTCCAAAAATC<br>CGC | TCTCCGGAATCTGAT<br>GCTT    | 60.3                             | 643                                           | INTRON                                            | Ca_07833                            | V                     | --     |
| Ca4_P4_22733383  | Ca4                                     | 22733383                      | TTATAT/TTATATAT                                                                           | TAAAGCAGACCAACCA<br>ACCC | ACTCACCGCTTGCAAT<br>AACC   | 60.0                             | 483                                           | INTRON                                            | Ca_14475                            | T                     | FAR1   |
| Ca4_P4_22812892  | Ca4                                     | 22812892                      | CTT/CT                                                                                    | ATGTCGTGTCAGGTGT<br>CGAA | GGTCTGGAGGAGACA<br>TTGA    | 60.2                             | 466                                           | INTRON                                            | Ca_14470                            | H                     | --     |
| Ca4_P4_22827669  | Ca4                                     | 22827669                      | GAAAAAA/GAAAAA                                                                            | CATGCAGAAAATGCGA<br>AAGA | AAGGGGAATAACCCAA<br>CACC   | 60.0                             | 881                                           | INTRON                                            | Ca_14469                            | --                    | EIL    |
| Ca4_P4_22932481  | Ca4                                     | 22932481                      | CAAAAAAAAA/CAAAAAAAAAA                                                                    | TTGAATGCACCAATC<br>AGGA  | ACAACGCCGTACACAT<br>TCAG   | 60.0                             | 346                                           | INTRON                                            | Ca_14461                            | --                    | --     |
| Ca4_P4_22943635  | Ca4                                     | 22943635                      | GTT/GTTT                                                                                  | TGCATTAATTGAAGGG<br>GAGC | TTTGCTTCAACAATTC<br>CCC    | 60.0                             | 112                                           | INTRON                                            | Ca_14461                            | --                    | --     |
| Ca4_P4_22945533  | Ca4                                     | 22945533                      | TAAAAAAA/TAAAAAA                                                                          | TGTTTTCACCACCAGG<br>ATCA | TTGGCATTTTTAGTTGA<br>AGTCG | 59.9                             | 758                                           | INTRON                                            | Ca_14461                            | --                    | --     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                     |                         |                         |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_22947061  | Ca4                                     | 22947061                      | TAAAAAAAA/TAAAAAAAA                                                 | AACCACCACGGATCAAGAG     | GGAAGGTAAGTATGGGCGGT    | 60.0                             | 455                                           | INTRON                                            | Ca_14461                            | --                    | --   |
| Ca4_P4_22970347  | Ca4                                     | 22970347                      | CCTT/C                                                              | CAGCCTTTCATGTTTTGACG    | CAACTGAAGCCTTCTTGGC     | 59.3                             | 787                                           | INTRON                                            | Ca_14460                            | --                    | --   |
| Ca4_P4_22970889  | Ca4                                     | 22970889                      | ATTTT/ATTTT                                                         | TATGTTGGACCAGGTGCGTA    | CTGCAATCATGAGTAGGCGA    | 60.0                             | 680                                           | INTRON                                            | Ca_14460                            | --                    | --   |
| Ca4_P4_23106593  | Ca4                                     | 23106593                      | ATTTTTTTT/ATTTTTTTT                                                 | GGGGCCTTATTTTCCACATT    | GGCATTTAGCACACCCATCT    | 60.0                             | 480                                           | INTRON                                            | Ca_14456                            | --                    | --   |
| Ca4_P4_23438647  | Ca4                                     | 23438647                      | CTTATTATTATTATTATTATTATTATT/CTTATTATTATTATTATTATTATTATTATT          | TGTTGCTAATATTCACCCCAA   | ACACAGAAGGGAGCAGGAGA    | 59.4                             | 734                                           | INTRON                                            | Ca_14441                            | --                    | --   |
| Ca4_P4_24535158  | Ca4                                     | 24535158                      | CAAAAA/CAAAAA                                                       | GTCGGCTGCTTTTCTAGTGC    | CGGAGGCCATCCCTATATTT    | 60.2                             | 480                                           | INTRON                                            | Ca_20864                            | L                     | FAR1 |
| Ca4_P4_24581547  | Ca4                                     | 24581547                      | AATTA/AA                                                            | TTCCATTTCTCCACAAAGC     | TCATTCCAGAAGGAGATGGG    | 60.1                             | 548                                           | INTRON                                            | Ca_20859                            | --                    | --   |
| Ca4_P4_24607917  | Ca4                                     | 24607917                      | GATGAATGAATGAATGAATGAATGAATGAATGA/GATGAATGAATGAATGAATGAATGAATGAATGA | CTTCAGGGCCGAAATACACA    | CGAAAACATCCCTCCTTTCA    | 60.1                             | 404                                           | INTRON                                            | Ca_20857                            | --                    | --   |
| Ca4_P4_24983663  | Ca4                                     | 24983663                      | TTATATATATATATATATATAT/TTATATATATATATATATATATATATAT                 | TTTTAGTGGGCAAGTGCAAA    | GCTTTTGCATGCCATTTCTA    | 59.3                             | 635                                           | INTRON                                            | Ca_20841                            | --                    | FAR1 |
| Ca4_P4_25188013  | Ca4                                     | 25188013                      | ATTTTTTTTT/ATTTTTTTTTT                                              | TGAAGGTGATGATGTAGGGGA   | TGGTCATTTCCGTTAATTTCG   | 60.3                             | 336                                           | INTRON                                            | Ca_16562                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)               | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                             |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_25228841  | Ca4                                     | 25228841                      | AATATATATATATAT/AATATATATAT<br>ATATAT                                       | ATGATTACCTCGGCAT<br>GGAG | AGCACGAGATCAAAGC<br>ACAA | 59.9                             | 349                                           | INTRON                                            | Ca_16565                            | --                    | --   |
| Ca4_P4_25662987  | Ca4                                     | 25662987                      | A/AC                                                                        | GTCCCCGATCTCAGAA<br>ACAA | AGATGACCAAGTGGCT<br>TTGG | 60.1                             | 609                                           | INTRON                                            | Ca_16591                            | S                     | --   |
| Ca4_P4_26002044  | Ca4                                     | 26002044                      | ATTTTTTT/ATTTTTT                                                            | TAGGGAGGATGCATTT<br>TTGG | TGCCTGTGATCCAGGA<br>ATTT | 59.9                             | 809                                           | INTRON                                            | Ca_16610                            | C                     | --   |
| Ca4_P4_26012883  | Ca4                                     | 26012883                      | CATCTTATAACAGATC/CATCTTATA<br>ACAGATCTTATAACAGATC                           | TCGCAAAACACCACCA<br>AATA | AAGGGTGGTACTGGGA<br>GCTT | 60.0                             | 752                                           | INTRON                                            | Ca_16611                            | C                     | --   |
| Ca4_P4_2638779   | Ca4                                     | 2638779                       | TTATATATATATATATATATATATA<br>TATATATAT/TTATATATATATATATA<br>TATATATATATATAT | GCCCTGCTTCAATAT<br>GCTC  | GAAGGGTGATGGGTGA<br>GAGA | 59.8                             | 848                                           | INTRON                                            | Ca_12067                            | --                    | --   |
| Ca4_P4_26483173  | Ca4                                     | 26483173                      | TAAAAAAA/TAAAAAA                                                            | TTTTGAAAACCAATGCA<br>CCA | CGCTATATCACAGCTT<br>GGCA | 59.9                             | 413                                           | INTRON                                            | Ca_25006                            | O                     | C2H2 |
| Ca4_P4_26635422  | Ca4                                     | 26635422                      | GAAA/GAAAA                                                                  | AGGGGGAGCAGTAAAG<br>TGGT | ACCAATGCCTGACCAA<br>ACTC | 60.0                             | 652                                           | INTRON                                            | Ca_24999                            | L                     | --   |
| Ca4_P4_26644625  | Ca4                                     | 26644625                      | ATTTTTTTTT/ATTTTTTTTTT                                                      | CTTGCAGTGAAGGGAG<br>AAGG | CCAACAAAGACCGCAT<br>TTCT | 60.0                             | 666                                           | INTRON                                            | Ca_24999                            | L                     | --   |
| Ca4_P4_26648113  | Ca4                                     | 26648113                      | AT/ATCTGAATTATCT                                                            | TCGAACAGAAACCTGA<br>GCCT | GATTCGGGAGTTGGTT<br>GATG | 60.0                             | 440                                           | INTRON                                            | Ca_24999                            | L                     | --   |
| Ca4_P4_27115538  | Ca4                                     | 27115538                      | TTCTCTCTCTCTCTCTCTCTCTCT<br>C/TTCTCTCTCTCTCTCTCTCTCTC                       | TATTAGCGCTCGCTGG<br>TTTT | ACCTCCAATGCTCAAA<br>GCAC | 60.0                             | 477                                           | INTRON                                            | Ca_20456                            | R                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                               | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                             |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_27233281  | Ca4                                     | 27233281                      | ATAATTCACAAGGTAATTAATTCACA<br>AGGTA/ATAATTCACAAGGTAATTAA<br>TTCACAAGGTAATTAATTCACAAGG<br>TA | CCAACGCTATTGGTT<br>TCAG  | GCAGGAGAGAGAAAA<br>GTGG  | 60.5                             | 891                                           | INTRON                                            | Ca_20460                            | --                    | --  |
| Ca4_P4_27236181  | Ca4                                     | 27236181                      | AAGA/AA                                                                                     | AGGTCGCTTGAATCG<br>GTTT  | TAAACATTCTCGTGGG<br>GGAG | 58.6                             | 444                                           | INTRON                                            | Ca_20460                            | --                    | --  |
| Ca4_P4_27242402  | Ca4                                     | 27242402                      | A/AC                                                                                        | CCGACCTGACCTGACA<br>TTTT | GATAGGGGCATTAGGG<br>ATGG | 60.0                             | 623                                           | INTRON                                            | Ca_20460                            | --                    | --  |
| Ca4_P4_27242564  | Ca4                                     | 27242564                      | GTTTTTTTTTTT/GTTTTTTTTT                                                                     | CCGACCTGACCTGACA<br>TTTT | CGGAAATTAGATTGAA<br>CGGC | 60.0                             | 883                                           | INTRON                                            | Ca_20460                            | --                    | --  |
| Ca4_P4_27242609  | Ca4                                     | 27242609                      | GTTTTTTTTTTT/GTTTTTTTTT                                                                     | CGATGTCGAATATGGA<br>ACGA | CGGAAATTAGATTGAA<br>CGGC | 59.5                             | 561                                           | INTRON                                            | Ca_20460                            | --                    | --  |
| Ca4_P4_2726003   | Ca4                                     | 2726003                       | AAACAATAACAATAACAATAACAATA<br>ACAATAACAATAA/AAACAATAACAA<br>TAACAATAACAATAACAATAA           | CCGGGATGCAAAGTCA<br>TAGT | GCTTTTTGTACGCAGA<br>AGGG | 60.0                             | 687                                           | INTRON                                            | Ca_12075                            | Z                     | --  |
| Ca4_P4_27376069  | Ca4                                     | 27376069                      | TAA/TAA                                                                                     | ATCCTCTCCATTCCCTG<br>CCT | TTGCTTTCACAGTCCAA<br>TGC | 60.0                             | 304                                           | INTRON                                            | Ca_21323                            | --                    | --  |
| Ca4_P4_27477986  | Ca4                                     | 27477986                      | CATAT/CAT                                                                                   | TTGAGACCGTCGAAG<br>AGTT  | TTGTCTTCCCTACGC<br>ATT   | 60.0                             | 408                                           | INTRON                                            | Ca_21319                            | J                     | --  |
| Ca4_P4_27478253  | Ca4                                     | 27478253                      | TAAAAAAAAA/TAAAAAAAAA                                                                       | TTGAGACCGTCGAAG<br>AGTT  | TTGTCTTCCCTACGC<br>ATT   | 60.0                             | 408                                           | INTRON                                            | Ca_21319                            | J                     | --  |
| Ca4_P4_27480414  | Ca4                                     | 27480414                      | ATG/A                                                                                       | GGCCACTACCTGGTGG<br>ACTA | GTATCGAGCCTTTGCA<br>CCTC | 60.0                             | 283                                           | INTRON                                            | Ca_21319                            | J                     | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_27483493  | Ca4                                     | 27483493                      | ATTTTT/ATTTT                                                  | AAGCCAACCCTACCGC<br>TATT | GAGGTAAGGGAGTGAG<br>GTTGC | 60.0                             | 597                                           | INTRON                                            | Ca_21318                            | --                    | --    |
| Ca4_P4_27573328  | Ca4                                     | 27573328                      | AG/AGG                                                        | CCATGAGAGCTTTGTG<br>CTTG | GGCTCAAATGGGCTTA<br>AACA  | 59.6                             | 652                                           | INTRON                                            | Ca_21314                            | --                    | --    |
| Ca4_P4_27574074  | Ca4                                     | 27574074                      | AAGAGAG/AAGAG                                                 | CGTGTGGGGATGCTTA<br>ACTT | AACCACTCAAGTGTTC<br>GGGC  | 60.0                             | 453                                           | INTRON                                            | Ca_21314                            | --                    | --    |
| Ca4_P4_27580274  | Ca4                                     | 27580274                      | GAAAAAAAA/GAAAAAAAA                                           | TGGGGTCCATGTACCA<br>CTTT | AAGAAATGTGCCTCAG<br>GTGC  | 60.1                             | 305                                           | INTRON                                            | Ca_21314                            | --                    | --    |
| Ca4_P4_27593574  | Ca4                                     | 27593574                      | GTTATTATTATTAT/GTTATTATTATT<br>ATTAT                          | TGCAACGCTTGATCGT<br>TAAT | ACTCGAATCGTTTTCGA<br>AGG  | 59.3                             | 301                                           | INTRON                                            | Ca_21314                            | --                    | --    |
| Ca4_P4_27624221  | Ca4                                     | 27624221                      | ATTTTTTTTT/ATTTTTTTTT                                         | GGCGAAGGAAGAGAG<br>AAAGG | GCAACATCAATGCTGC<br>AACT  | 60.5                             | 767                                           | INTRON                                            | Ca_21312                            | --                    | --    |
| Ca4_P4_27665489  | Ca4                                     | 27665489                      | TAAAAAAAA/TAAAAAAAA                                           | AACAACCTCCCAAGTG<br>ACCG | GGAACACCGCATCCTA<br>CCTA  | 60.0                             | 417                                           | INTRON                                            | Ca_21309                            | --                    | ZF-HD |
| Ca4_P4_28281450  | Ca4                                     | 28281450                      | ATTTTTTTTTTT/ATTTTTTTTTTTTT                                   | AATCGAACGACTGAGA<br>ACGG | GTTCTTTTGGCCACTT<br>GCAT  | 60.3                             | 261                                           | INTRON                                            | Ca_23166                            | TR                    | FAR1  |
| Ca4_P4_28281644  | Ca4                                     | 28281644                      | CTAT/CTATATAT                                                 | ATGCAAGTGGCCAAAA<br>GAAC | ACCAAGAAATGCCTTCT<br>GGA  | 60.1                             | 405                                           | INTRON                                            | Ca_23166                            | TR                    | FAR1  |
| Ca4_P4_28281945  | Ca4                                     | 28281945                      | CTTTTTTT/CTTTTTT                                              | ATGCAAGTGGCCAAAA<br>GAAC | GCTGCCACATGAATAC<br>AACC  | 60.1                             | 673                                           | INTRON                                            | Ca_23166                            | TR                    | FAR1  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca4_P4_28365619  | Ca4                                     | 28365619                      | CAAAATTAAA/CAAA                                               | GGGGGACAAGAGAGAT<br>GTCA | AAATGCTCTTTGCTGC<br>GAAT   | 60.0                             | 637                                           | INTRON                                            | Ca_23163                            | AYT                   | MYB         |
| Ca4_P4_28378874  | Ca4                                     | 28378874                      | CAAAA/CAAA                                                    | CCACATTAGTCGGTGT<br>CGTG | ATTGAACTGCGTTTCC<br>GACT   | 60.0                             | 565                                           | INTRON                                            | Ca_23162                            | C                     | --          |
| Ca4_P4_28993304  | Ca4                                     | 28993304                      | ACAA/ACAATTTTCAA                                              | GGATGGTTGTAAAAGG<br>CGAA | TTTGATGCACATCATTG<br>GGT   | 59.9                             | 894                                           | INTRON                                            | Ca_23706                            | --                    | NF-YB       |
| Ca4_P4_29093206  | Ca4                                     | 29093206                      | TTTATTATTAT/TTTATTAT                                          | GGAAGCTCGGTGATTC<br>TGAC | CTGTGTTTTGCTCCCC<br>AAAT   | 59.8                             | 593                                           | INTRON                                            | Ca_23708                            | C                     | HD-ZIP      |
| Ca4_P4_29093477  | Ca4                                     | 29093477                      | TAAAAAAAA/TAAAAAAAAA                                          | ATTTGGGAGCAAAAC<br>ACAG  | TTTCCTCAAAGTAAATG<br>GGAGC | 60.0                             | 402                                           | INTRON                                            | Ca_23708                            | C                     | HD-ZIP      |
| Ca4_P4_29682181  | Ca4                                     | 29682181                      | CAAAAAA/CAAAAAA                                               | TGCAAAAACCTCCAGC<br>TTCC | TTCAGCACATTCACCT<br>GCTC   | 60.4                             | 201                                           | INTRON                                            | Ca_14166                            | Z                     | MYB_related |
| Ca4_P4_29696309  | Ca4                                     | 29696309                      | CAAAA/CAAAA                                                   | CCAGTGCTTTCATCTC<br>CGTT | TTTATTGGCTCCCGAA<br>CATC   | 60.3                             | 790                                           | INTRON                                            | Ca_14166                            | Z                     | MYB_related |
| Ca4_P4_29696963  | Ca4                                     | 29696963                      | AGGTGGT/AGGTGGTTTGGTGGT                                       | TCTGCAGTTTTCGATG<br>TTCC | GCTACCGAGTTGATT<br>GGAA    | 60.0                             | 482                                           | INTRON                                            | Ca_14166                            | Z                     | MYB_related |
| Ca4_P4_29697671  | Ca4                                     | 29697671                      | GAATCGGCCT/GAATCGGCCTCTAA<br>ATCGGCCT                         | AACGTATTCATCACCA<br>GCCA | ACCGACAATGCACATT<br>CCTT   | 59.0                             | 458                                           | INTRON                                            | Ca_14166                            | Z                     | MYB_related |
| Ca4_P4_29719863  | Ca4                                     | 29719863                      | ATTTTTTT/ATTTTTTTT                                            | GAGTTGCGCCCAAACT<br>TTTA | AGGAACAGCAAGAACG<br>GTGT   | 60.2                             | 883                                           | INTRON                                            | Ca_14167                            | --                    | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')      | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                                   |                              |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca4_P4_29907949  | Ca4                                     | 29907949                      | AATATATATATATATATAT/AAATATAT<br>ATATATATAT                        | CGAAGCTTTGGGATTAT<br>TTGC    | TGTTTAAAATTAAAACA<br>AAAGGTCA | 59.7                             | 736                                           | INTRON                                            | Ca_14176                            | --                    | M-type  |
| Ca4_P4_30188259  | Ca4                                     | 30188259                      | TAA/TA                                                            | CTCCAAAACATGGTAT<br>GCCC     | CACCATCAGCAGCCTA<br>AACA      | 60.2                             | 690                                           | INTRON                                            | Ca_14186                            | --                    | SAP     |
| Ca4_P4_30264884  | Ca4                                     | 30264884                      | AAGAGAGAGAGAGAGAGAGAGAGA<br>GAG/AAGAGAGAGAGAGAGAGAGA<br>GAGAGAGAG | GTTAACGTTGACGGTG<br>GCTT     | TCTTTCCAAAACCCCT<br>CTT       | 60.0                             | 211                                           | INTRON                                            | Ca_14191                            | --                    | --      |
| Ca4_P4_30310689  | Ca4                                     | 30310689                      | TAAAGATACAAAA/TAAA                                                | TCCAATTCGTCTTGCC<br>TTTC     | GGGTGTTTAGCAACCG<br>AAGA      | 60.2                             | 534                                           | INTRON                                            | Ca_14192                            | R                     | bHLH    |
| Ca4_P4_30466090  | Ca4                                     | 30466090                      | CTTTTTTTTT/CTTTTTTTTT                                             | TGCACAAAGCAGTCTT<br>CACC     | GTTGTAGGGGCAACTG<br>AGGA      | 60.0                             | 855                                           | INTRON                                            | Ca_14199                            | --                    | G2-like |
| Ca4_P4_30537523  | Ca4                                     | 30537523                      | CA/CATA                                                           | TTTGATTGCCATTGTAT<br>CCG     | CAAATGGAATGCAA<br>GAACAA      | 59.4                             | 803                                           | INTRON                                            | Ca_14204                            | --                    | NAC     |
| Ca4_P4_30604376  | Ca4                                     | 30604376                      | CT/CTT                                                            | AATGCCCCACTTTTAAT<br>CCC     | CGGAGGCTACCGATAC<br>CATA      | 60.0                             | 185                                           | INTRON                                            | Ca_14208                            | T                     | --      |
| Ca4_P4_31303190  | Ca4                                     | 31303190                      | CTTTTTTTTTTT/CTTTTTTTTTTT                                         | GAGGTCCCGTCCAACC<br>TAAC     | TCAGCACCGAGAGTGT<br>CAAC      | 60.7                             | 488                                           | INTRON                                            | Ca_14231                            | --                    | bHLH    |
| Ca4_P4_31484248  | Ca4                                     | 31484248                      | TAAAAA/TAAAAA                                                     | AACAGGCTCATAATCA<br>CTTTTGAA | GCATAACCACGTCTCT<br>CCTA      | 59.2                             | 693                                           | INTRON                                            | Ca_15435                            | --                    | C2H2    |
| Ca4_P4_31646885  | Ca4                                     | 31646885                      | GA/GAA                                                            | AAGGCCCGTAAAAGAC<br>TGGT     | TTACACGTGGGGAAC<br>ATAA       | 60.0                             | 686                                           | INTRON                                            | Ca_15442                            | U                     | EIL     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_31647747  | Ca4                                     | 31647747                      | ATT/AT                                                        | CACGTGTGAAGGTCGA<br>GAGA | AAGCTACCTGATCAAT<br>GCGG  | 60.0                             | 863                                           | INTRON                                            | Ca_15442                            | U                     | EIL |
| Ca4_P4_31647770  | Ca4                                     | 31647770                      | GTTTTTTTTT/GTTTTTTTTT                                         | CACGTGTGAAGGTCGA<br>GAGA | AAGCTACCTGATCAAT<br>GCGG  | 60.0                             | 863                                           | INTRON                                            | Ca_15442                            | U                     | EIL |
| Ca4_P4_31649942  | Ca4                                     | 31649942                      | CT/CTT                                                        | CGTGCCCTGCAGGTAT<br>TTAT | ATTGACCGGTGGAAGA<br>CATT  | 60.0                             | 454                                           | INTRON                                            | Ca_15442                            | U                     | EIL |
| Ca4_P4_31651386  | Ca4                                     | 31651386                      | ATTTTTTT/ATTTTTTTT                                            | GAATAGATATTTGGGC<br>GCGA | AATGCCTGCAATCCAA<br>AATC  | 60.0                             | 486                                           | INTRON                                            | Ca_15442                            | U                     | EIL |
| Ca4_P4_31723730  | Ca4                                     | 31723730                      | GAAAAAAAAA/GAAAAAAAAA                                         | CCCAGATCCGAAATCT<br>GAAA | TGTCACCATGTCAACC<br>ATCA  | 60.0                             | 593                                           | INTRON                                            | Ca_15445                            | G                     | --  |
| Ca4_P4_31967535  | Ca4                                     | 31967535                      | T/TC                                                          | TACCCTTAATGGCTGG<br>GATG | AAAAACACTTGCGATG<br>ACCC  | 59.8                             | 510                                           | INTRON                                            | Ca_15456                            | --                    | --  |
| Ca4_P4_32042126  | Ca4                                     | 32042126                      | TTTTATTTATTTATTTATTTATTTATTT<br>TATT/TTTTATTTATTTATTTATTT     | TGCTAATGGACCCCT<br>TATG  | TCAACACACTGAGCCG<br>CTAC  | 59.8                             | 606                                           | INTRON                                            | Ca_15459                            | --                    | --  |
| Ca4_P4_32042706  | Ca4                                     | 32042706                      | ATATTA/ATATTATTAATATTATTATT<br>A                              | CTTGCTTCGGTGGTTA<br>GCTC | TTTTGGTTGCACACATG<br>ACA  | 60.0                             | 419                                           | INTRON                                            | Ca_15459                            | --                    | --  |
| Ca4_P4_32043714  | Ca4                                     | 32043714                      | GTTTTTTTTT/GTTTTTTTTT                                         | ATTTTGATCGGTGGCT<br>TACG | CAAACCTCGAATTGCTG<br>GACA | 60.0                             | 237                                           | INTRON                                            | Ca_15459                            | --                    | --  |
| Ca4_P4_32044292  | Ca4                                     | 32044292                      | T/TG                                                          | CCTTTAATGCCCTGAC<br>TGCT | ATTTTCCAATGGAGTTC<br>CCC  | 59.3                             | 480                                           | INTRON                                            | Ca_15459                            | --                    | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca4_P4_32100622  | Ca4                                     | 32100622                      | A/AGT                                                         | TCCGTGTACATCCAA<br>CACTTC | ACACATGCCATTTCTT<br>CCC   | 59.9                             | 950                                           | INTRON                                            | Ca_15462                            | --                    | --       |
| Ca4_P4_32214848  | Ca4                                     | 32214848                      | ATTTTT/ATTTTTT                                                | CGCATGTGTATCCCTT<br>TGTG  | CGTTCTCGGAACCTTT<br>CTTTC | 60.0                             | 471                                           | INTRON                                            | Ca_15467                            | T                     | HB-other |
| Ca4_P4_32623906  | Ca4                                     | 32623906                      | TAAAA/TAAAA                                                   | TACTTGTGAACCACG<br>CAGC   | TGGGCATACATCTGGT<br>TTCA  | 59.9                             | 530                                           | INTRON                                            | Ca_15485                            | O                     | --       |
| Ca4_P4_33924249  | Ca4                                     | 33924249                      | ATAGT/ATAGTAGT                                                | CCGTATTACATGTTG<br>CTGG   | TCGAGAGTTGCTCCTG<br>GTTT  | 60.0                             | 729                                           | INTRON                                            | Ca_20365                            | O                     | GATA     |
| Ca4_P4_348520    | Ca4                                     | 348520                        | CATATATATATATATATA/CATATA<br>TATATATATATA                     | CTTGCCCCAACTTTC<br>CATA   | TTGAAAAATGCGAGCA<br>AATG  | 59.9                             | 539                                           | INTRON                                            | Ca_07667                            | R                     | B3       |
| Ca4_P4_35345914  | Ca4                                     | 35345914                      | GTTTT/GTTTTT                                                  | TTTGTGAAGGGATTG<br>GCTC   | ATGCCTCTCTATGCAG<br>CGTT  | 60.1                             | 763                                           | INTRON                                            | Ca_20018                            | Z                     | NAC      |
| Ca4_P4_36455905  | Ca4                                     | 36455905                      | A/AC                                                          | GGTGGAGAGCTATTTG<br>AGCG  | AAGCAAACTTCAGGA<br>GCGA   | 60.0                             | 668                                           | INTRON                                            | Ca_14832                            | T                     | YABBY    |
| Ca4_P4_36462059  | Ca4                                     | 36462059                      | ACCC/ACC                                                      | CAGCAGCTCCAAAAG<br>AACC   | TTTGTCAGTGTGGTGG<br>TGGT  | 60.0                             | 719                                           | INTRON                                            | Ca_14831                            | --                    | --       |
| Ca4_P4_36494393  | Ca4                                     | 36494393                      | A/AT                                                          | AAACCTTTATGTTGCG<br>GCTG  | GGGTTTCTTCCCAACA<br>CTGA  | 60.1                             | 701                                           | INTRON                                            | Ca_14828                            | --                    | --       |
| Ca4_P4_36535469  | Ca4                                     | 36535469                      | CTTT/CTT                                                      | CTCGCGCGTGTTAAGT<br>ATGA  | ACACATGGTTTCTGGT<br>GCAA  | 60.0                             | 451                                           | INTRON                                            | Ca_14825                            | --                    | B3       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                      | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                                    |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca4_P4_36622112  | Ca4                                     | 36622112                      | AGTGTACGTGTTACGTGTT/AGTG<br>TTACGTGTT                                                              | ACAAGTCAAAACCGCC<br>TGAC | ATGCTGCCATCAGTAG<br>GTCC | 60.2                             | 427                                           | INTRON                                            | Ca_14818                            | I                     | WRKY     |
| Ca4_P4_36644531  | Ca4                                     | 36644531                      | ACTCTC/ACTC                                                                                        | CAACACCAAATTGCCA<br>AGTG | AGCTGCCTCAGTTCCA<br>CTGT | 60.0                             | 870                                           | INTRON                                            | Ca_14816                            | H                     | --       |
| Ca4_P4_36952734  | Ca4                                     | 36952734                      | ATTTTTTT/ATTTTTT                                                                                   | AACTCATGTGGTTTGT<br>GGCA | ATGGGCCCTCTTTTGT<br>CTTT | 60.0                             | 896                                           | INTRON                                            | Ca_14797                            | R                     | C2H2     |
| Ca4_P4_36953946  | Ca4                                     | 36953946                      | AAT/AATAATAATAATTATTAT                                                                             | AGTGTGTTCCCAATG<br>CACA  | GCGTGGGTTTTAGTGG<br>AAGA | 60.0                             | 180                                           | INTRON                                            | Ca_14797                            | R                     | C2H2     |
| Ca4_P4_3695491   | Ca4                                     | 3695491                       | AATATATATATATATATATAT/AATAT<br>ATATATATATATATATATAT                                                | CCGAAATTGGTCCGAT<br>AAAA | CCCAATTCATTGATT<br>TCTGA | 59.8                             | 461                                           | INTRON                                            | Ca_12166                            | --                    | --       |
| Ca4_P4_37268106  | Ca4                                     | 37268106                      | TCC/TC                                                                                             | CAGAAGCTGCATGGAA<br>CAAA | CCCTGTGTTTCCCATT<br>CTT  | 60.0                             | 210                                           | INTRON                                            | Ca_15149                            | UR                    | HB-other |
| Ca4_P4_37299801  | Ca4                                     | 37299801                      | CATATATATATATATATATATATATA<br>TATATATATATATATA/CATATATATA<br>TATATATATATATATATATATATATA<br>ATATATA | TCACCATGTTGGTCCT<br>TTGA | CATGCTTTGGGAGAG<br>AAAC  | 59.9                             | 431                                           | INTRON                                            | Ca_15146                            | A                     | --       |
| Ca4_P4_37303497  | Ca4                                     | 37303497                      | ATTTTTT/ATTTT                                                                                      | CAGTCGAAATACCAGC<br>CCAT | TTTCATTGCGGGACAT<br>ACAA | 60.0                             | 113                                           | INTRON                                            | Ca_15145                            | J                     | --       |
| Ca4_P4_37361673  | Ca4                                     | 37361673                      | T/TC                                                                                               | TGCCAGTGCTACAGAG<br>TTGG | CAAAAACCAATGGCAG<br>ACCT | 60.0                             | 492                                           | INTRON                                            | Ca_15140                            | S                     | --       |
| Ca4_P4_37362171  | Ca4                                     | 37362171                      | GTTGT/GTTGTTTGT                                                                                    | CCATTGGTTTTTGCTTC<br>GTT | CCACGCCTGGAGTTTA<br>TTGT | 60.0                             | 947                                           | INTRON                                            | Ca_15140                            | S                     | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_37370975  | Ca4                                     | 37370975                      | ATT/AT                                                        | ATCCAATAACCAACCC<br>CACA | TGCAGAATGATGCTGG<br>AGAG | 59.9                             | 545                                           | INTRON                                            | Ca_15139                            | R                     | NF-YA |
| Ca4_P4_37646806  | Ca4                                     | 37646806                      | C/CAA                                                         | GCTCTGGTGGGTGATT<br>TGTT | ATGTTCCGTTGGAAG<br>CATC  | 60.0                             | 641                                           | INTRON                                            | Ca_15117                            | T                     | LBD   |
| Ca4_P4_37688621  | Ca4                                     | 37688621                      | ATCTTCTC/ATCTTC                                               | GGATTTCCTGTGAGCT<br>GCAT | AGAATTGGAATGCCTG<br>AACG | 60.2                             | 492                                           | INTRON                                            | Ca_15113                            | S                     | --    |
| Ca4_P4_37693476  | Ca4                                     | 37693476                      | CAAA/CAAAA                                                    | CAATCAAATTGGGGCT<br>CTTT | GTGAAGGTGGAAGACA<br>CGGT | 59.0                             | 840                                           | INTRON                                            | Ca_15112                            | --                    | --    |
| Ca4_P4_37698241  | Ca4                                     | 37698241                      | GATATGAAT/GATATGAATATGAAT                                     | ATGCATAACATTGGCC<br>GTTT | TTCTTGAGCTTGCAATT<br>CCT | 60.2                             | 576                                           | INTRON                                            | Ca_15111                            | F                     | --    |
| Ca4_P4_37700126  | Ca4                                     | 37700126                      | CTATGTATGT/CTATGT                                             | GAGTGCCAGGTCAGCC<br>TAGT | TTGATAAGCTCGATTG<br>CGTG | 59.5                             | 893                                           | INTRON                                            | Ca_15111                            | F                     | --    |
| Ca4_P4_37711634  | Ca4                                     | 37711634                      | ATTTT/ATTTT                                                   | CCTTCACTGATACGAA<br>GGGG | TGCTTGCAACCTTCTG<br>ACAC | 59.5                             | 479                                           | INTRON                                            | Ca_15109                            | --                    | --    |
| Ca4_P4_37726921  | Ca4                                     | 37726921                      | TT/TTCTCTCTCT                                                 | TGGACTCAAACCTGCA<br>GCAC | CCTCTTCTTGATCTG<br>CTGG  | 60.0                             | 521                                           | INTRON                                            | Ca_15107                            | R                     | --    |
| Ca4_P4_37826612  | Ca4                                     | 37826612                      | GA/G                                                          | CCTTGCGTTGTTTTA<br>GGAA  | GAGCAAATCTGCCCAT<br>TGAT | 60.1                             | 517                                           | INTRON                                            | Ca_15093                            | A                     | --    |
| Ca4_P4_37860521  | Ca4                                     | 37860521                      | CTTA/CTTAATTA                                                 | TGGTCCCTTGTTGCCT<br>TTAG | AATGGACGGCTATGAG<br>TTGC | 60.1                             | 739                                           | INTRON                                            | Ca_15089                            | --                    | --    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca4_P4_37860655  | Ca4                                     | 37860655                      | CATATATATATATAT/CATATATATAT<br>ATATATATAT                     | TGGTCCCTTGTGCCT<br>TTAG      | AATGGACGGCTATGAG<br>TTGC    | 60.1                             | 739                                           | INTRON                                            | Ca_15089                            | --                    | --          |
| Ca4_P4_37938389  | Ca4                                     | 37938389                      | CATT/CATTAAATT                                                | GTTAATTTTCAGAGCG<br>GGCA     | GGGTGTTAGAGTTTGT<br>CTCTTCG | 60.2                             | 443                                           | INTRON                                            | Ca_15084                            | --                    | --          |
| Ca4_P4_38004324  | Ca4                                     | 38004324                      | TAA/TAAA                                                      | GAGAAAACGCGTTGA<br>GAAG      | CCTCCTGCAGTCTCAC<br>ACAA    | 60.0                             | 437                                           | INTRON                                            | Ca_13146                            | F                     | --          |
| Ca4_P4_38021208  | Ca4                                     | 38021208                      | TA/TAAAAA                                                     | AAGATTGATTTTCATGG<br>ATTGACA | TTGGTGATGTGAGGA<br>AACA     | 59.7                             | 584                                           | INTRON                                            | Ca_13143                            | E                     | --          |
| Ca4_P4_38039526  | Ca4                                     | 38039526                      | T/TATCGG                                                      | ATCTGTCAAGCGCATA<br>GCCT     | CGCTCTCTCTCCCTT<br>GTTG     | 60.0                             | 659                                           | INTRON                                            | Ca_13141                            | --                    | MYB_related |
| Ca4_P4_38039882  | Ca4                                     | 38039882                      | TAT/TATTGAAAT                                                 | CGAATTCGCCCTAAAC<br>AAAA     | CGCTCTCTCTCCCTT<br>GTTG     | 60.1                             | 178                                           | INTRON                                            | Ca_13141                            | --                    | MYB_related |
| Ca4_P4_38054541  | Ca4                                     | 38054541                      | CTTT/CTT                                                      | TTGTACCGCGATCTA<br>CTGA      | ATGGACTGTGATGGGT<br>GTGA    | 59.6                             | 433                                           | INTRON                                            | Ca_13140                            | P                     | --          |
| Ca4_P4_38135317  | Ca4                                     | 38135317                      | AATT/AATTCATT                                                 | ACATTGTACAAAGGCC<br>CTGC     | TTCAGCCAAGACAACA<br>GCAC    | 60.0                             | 627                                           | INTRON                                            | Ca_13139                            | --                    | ERF         |
| Ca4_P4_38196929  | Ca4                                     | 38196929                      | TA/TACATAATAATAATAAA                                          | ATATGTCCAGGTGCAC<br>GACA     | TTCTTCAATGGTGGGC<br>TTTC    | 60.0                             | 559                                           | INTRON                                            | Ca_13134                            | GE                    | HB-other    |
| Ca4_P4_38207067  | Ca4                                     | 38207067                      | GTTT/GTT                                                      | CTCGTTGCAAGCAAT<br>TTGA      | CAGGCTCTAAGCACAC<br>CACA    | 60.0                             | 334                                           | INTRON                                            | Ca_13133                            | R                     | C2H2        |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_38225619  | Ca4                                     | 38225619                      | T/TGATCTAAG                                                   | GAGAGGTGATCCGCAT<br>GATT | GTTGTGGCTATGGAGG<br>GAAA   | 60.0                             | 547                                           | INTRON                                            | Ca_13131                            | --                    | --   |
| Ca4_P4_38226662  | Ca4                                     | 38226662                      | GTATAT/GTAT                                                   | CCAAAATGATCTTGCC<br>CCTA | AGCCGCTGTTGTTAAG<br>TCAA   | 59.9                             | 480                                           | INTRON                                            | Ca_13131                            | --                    | --   |
| Ca4_P4_38237743  | Ca4                                     | 38237743                      | CTTTTTTTTT/CTTTTTTTTTTTTT                                     | CTCCATAGCCACAACA<br>AGCA | TCCACAGTTGCAATC<br>ACAT    | 59.9                             | 604                                           | INTRON                                            | Ca_13131                            | --                    | --   |
| Ca4_P4_38240819  | Ca4                                     | 38240819                      | ACCC/ACC                                                      | CTGGTGAACTCCGTA<br>TCCAA | TTGGATGTGCACGATG<br>TTTT   | 60.0                             | 258                                           | INTRON                                            | Ca_13131                            | --                    | --   |
| Ca4_P4_38484127  | Ca4                                     | 38484127                      | TTTATT/TTT                                                    | TCATCTTTGCTGCTTCT<br>GGA | CTACCTCATGCTTGGC<br>ATCC   | 59.7                             | 299                                           | INTRON                                            | Ca_13111                            | K                     | MIKC |
| Ca4_P4_38484269  | Ca4                                     | 38484269                      | ATTG/ATTGTTG                                                  | TCATCTTTGCTGCTTCT<br>GGA | TGCCAGATCTGTTTCAT<br>GGAT  | 59.7                             | 523                                           | INTRON                                            | Ca_13111                            | K                     | MIKC |
| Ca4_P4_38484870  | Ca4                                     | 38484870                      | CATATA/CATA                                                   | AATGATGGCATGCAAG<br>TTGA | GCCTGTTTCTCCCGGA<br>TAGT   | 60.1                             | 268                                           | INTRON                                            | Ca_13111                            | K                     | MIKC |
| Ca4_P4_38485192  | Ca4                                     | 38485192                      | ATTTTTTT/ATTTTTTTTTTTTT                                       | AATGATGGCATGCAAG<br>TTGA | GGAGGTCTCACATTG<br>TACTTGG | 60.1                             | 755                                           | INTRON                                            | Ca_13111                            | K                     | MIKC |
| Ca4_P4_38485235  | Ca4                                     | 38485235                      | TG/T                                                          | AATGATGGCATGCAAG<br>TTGA | GGAGGTCTCACATTG<br>TACTTGG | 60.1                             | 755                                           | INTRON                                            | Ca_13111                            | K                     | MIKC |
| Ca4_P4_38508596  | Ca4                                     | 38508596                      | CAAGAA/CAAGAAGAA                                              | CCTTTGATTCCCCCAA<br>TTT  | ACCGGGGTCTCTAAAG<br>GAAA   | 60.0                             | 346                                           | INTRON                                            | Ca_13110                            | G                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                         |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_38514660  | Ca4                                     | 38514660                      | TAC/TACAAAC                                                             | TGCCTACGTTTTAGG<br>CCAC  | GGAAAAACCCGAGCAA<br>TGTA | 60.1                             | 448                                           | INTRON                                            | Ca_13110                            | G                     | --  |
| Ca4_P4_38515365  | Ca4                                     | 38515365                      | AGT/AGTGT                                                               | TACATTGCTCGGGTTT<br>TTCC | TCCACATCTTTTCCCC<br>ATC  | 59.9                             | 412                                           | INTRON                                            | Ca_13110                            | G                     | --  |
| Ca4_P4_38527668  | Ca4                                     | 38527668                      | ATCATT/ATCATTTTCATT                                                     | GCTTAATTGAGCCAAT<br>CCCA | TCAACGAATGGCTACC<br>AAAA | 60.0                             | 678                                           | INTRON                                            | Ca_13110                            | G                     | --  |
| Ca4_P4_38613792  | Ca4                                     | 38613792                      | AC/A                                                                    | TTGCAGCAAGGACCAT<br>AACA | GATGCGGTACAGAGGA<br>GAGC | 60.3                             | 815                                           | INTRON                                            | Ca_13104                            | O                     | NAC |
| Ca4_P4_38665428  | Ca4                                     | 38665428                      | CA/CATA                                                                 | TGCGATTGTTCAAAA<br>ACA   | AGTCATAACAGGTGA<br>GGGG  | 60.1                             | 632                                           | INTRON                                            | Ca_13100                            | L                     | CPP |
| Ca4_P4_38677141  | Ca4                                     | 38677141                      | GAA/GAAA                                                                | CTATTCCTCCATCTG<br>CCAA  | GCTCTGATGCCTTCAC<br>TTCC | 60.0                             | 824                                           | INTRON                                            | Ca_13099                            | --                    | --  |
| Ca4_P4_3868034   | Ca4                                     | 3868034                       | GATNNNNNNNNNAT/GAT                                                      | AGGAAGGGAACCTCAG<br>GCAT | GCGCTTCCTGTTATCC<br>AGAG | 60.1                             | 426                                           | INTRON                                            | Ca_03867                            | --                    | --  |
| Ca4_P4_3871012   | Ca4                                     | 3871012                       | GTATATATATATATATATATATAT<br>ATATATA/GTATATATATATATATATA<br>TATATATATATA | GCGTTGAAATGGACTA<br>AGGC | AAAGATGTTGAGCCCC<br>AGTG | 59.7                             | 486                                           | INTRON                                            | Ca_03867                            | --                    | --  |
| Ca4_P4_38757469  | Ca4                                     | 38757469                      | TG/T                                                                    | CTGTACGTTTTGTCCC<br>CGAC | CTTTAAAAAGATGGCG<br>TGGG | 60.4                             | 450                                           | INTRON                                            | Ca_13097                            | --                    | --  |
| Ca4_P4_38758073  | Ca4                                     | 38758073                      | GTTTTT/GTTT                                                             | TAGACAGGTTGGTCCC<br>TCCC | ACCGTACAATCAAACC<br>GCTC | 61.3                             | 840                                           | INTRON                                            | Ca_13097                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                         | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                                                       |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca4_P4_38965155  | Ca4                                     | 38965155                      | TATAATAA/TATAA                                                                                        | AGCCATGCCAGATTAT<br>TTGC    | CAGTGCATCCATCTC<br>TGAA  | 60.1                             | 221                                           | INTRON                                            | Ca_13082                            | O                     | MYB_related |
| Ca4_P4_39016793  | Ca4                                     | 39016793                      | C/CA                                                                                                  | GGTAGTTCAGGATTGG<br>GGGT    | AGGTCCATAAATGGCG<br>TGAA | 60.1                             | 774                                           | INTRON                                            | Ca_13079                            | R                     | DBB         |
| Ca4_P4_39033132  | Ca4                                     | 39033132                      | GAAA/GAA                                                                                              | GGATTTCCTCAACAGC<br>AAAA    | TGCCTTACCAAAGGAA<br>TTGG | 59.9                             | 523                                           | INTRON                                            | Ca_13078                            | A                     | --          |
| Ca4_P4_39034835  | Ca4                                     | 39034835                      | CTTTTT/CTTT                                                                                           | AATTCGTGTGGGCCAA<br>GTAG    | ACCATGGACAATTGG<br>CATT  | 60.0                             | 489                                           | INTRON                                            | Ca_13078                            | A                     | --          |
| Ca4_P4_39053363  | Ca4                                     | 39053363                      | TAAA/TAAAAATGAAAA                                                                                     | TTAATTGCAGTCCGTT<br>CCC     | ATGCAAAATTGTGTGC<br>CAAA | 59.9                             | 527                                           | INTRON                                            | Ca_13076                            | --                    | --          |
| Ca4_P4_39054440  | Ca4                                     | 39054440                      | ATTTTTTTTT/ATTTTTTTTTT                                                                                | ACCAACACAAACACCGA<br>CTCA   | ATTAGAGCACCGCTTC<br>CTCA | 60.0                             | 354                                           | INTRON                                            | Ca_13076                            | --                    | --          |
| Ca4_P4_39054543  | Ca4                                     | 39054543                      | TAAAAAGAAAAAGAAAA/TAAAAAG<br>AAAAAGAAAAAGAAAA                                                         | ACCAACACAAACACCGA<br>CTCA   | ATTAGAGCACCGCTTC<br>CTCA | 60.0                             | 354                                           | INTRON                                            | Ca_13076                            | --                    | --          |
| Ca4_P4_3912089   | Ca4                                     | 3912089                       | CTATATATATATATATAT/CTATATAT<br>ATATATATATATATATATAT                                                   | TCCCTTAATTTTGTGT<br>TGTTGAA | GTTTGCAAGTACGTGG<br>TGGA | 59.8                             | 457                                           | INTRON                                            | Ca_03861                            | --                    | --          |
| Ca4_P4_39393116  | Ca4                                     | 39393116                      | TTATATATATATATATATATATATATA<br>TATATATATATATATATAT/TTATATA<br>TATATATATATATATATATATATATAT<br>ATATATAT | GTTTGGGCTTCATGCA<br>ATTT    | CTACCAAAGTCCACT<br>GCGT  | 59.9                             | 799                                           | INTRON                                            | Ca_13052                            | T                     | bHLH        |
| Ca4_P4_3993392   | Ca4                                     | 3993392                       | CAAA/CAA                                                                                              | CTTGTTGGAAAATCGG<br>GAGA    | CCAATGAATGCATGT<br>CACC  | 60.0                             | 627                                           | INTRON                                            | Ca_03853                            | --                    | --          |





| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_40584112  | Ca4                                     | 40584112                      | ATATCGT/AT                                                    | TGATATGCGGTAGCCATCAA    | GACCCAAATCTGGCTTCAAA    | 60.1                             | 547                                           | INTRON                                            | Ca_14868                            | K                     | --   |
| Ca4_P4_40593121  | Ca4                                     | 40593121                      | CAAGT/CAAGTAAGT                                               | CATTCCCACCATCCTTCACT    | GGCCTATCGAACCACACAGT    | 59.8                             | 932                                           | INTRON                                            | Ca_14867                            | R                     | BES1 |
| Ca4_P4_40598412  | Ca4                                     | 40598412                      | GTATAT/GTAT                                                   | AGTGGATTGCGAAAGTGGAG    | ACCATGTCCATGCACGATAA    | 60.3                             | 326                                           | INTRON                                            | Ca_14866                            | --                    | NAC  |
| Ca4_P4_40641891  | Ca4                                     | 40641891                      | TCA/T                                                         | TTAAAAACAAGTGGGTGGGG    | TGGGTGTTTACTTTGCATTT    | 59.7                             | 357                                           | INTRON                                            | Ca_14865                            | --                    | --   |
| Ca4_P4_40706252  | Ca4                                     | 40706252                      | TA/TAAAA                                                      | CGGTTTTGTGTGAGGAGGTT    | AAAATTCCGCACCTGTCAAC    | 60.0                             | 499                                           | INTRON                                            | Ca_23911                            | BK                    | FAR1 |
| Ca4_P4_40727369  | Ca4                                     | 40727369                      | CAG/CAGAG                                                     | AAGACTCAAGCCCCCTTCAT    | TTGTGGTGCCAATGTATGCT    | 60.1                             | 282                                           | INTRON                                            | Ca_23910                            | S                     | C2H2 |
| Ca4_P4_40757421  | Ca4                                     | 40757421                      | TATCTA/T                                                      | ACCAAACCCAGCAAAACCTTG   | ATCTAAAACGTTGGGTTGCG    | 60.0                             | 764                                           | INTRON                                            | Ca_23905                            | J                     | --   |
| Ca4_P4_40767801  | Ca4                                     | 40767801                      | ACATCAT/ACATCATCAT                                            | TGGCATCAAATTCTCTGTCC    | AATCACCTCATTGCAAA       | 60.1                             | 334                                           | INTRON                                            | Ca_23904                            | Q                     | --   |
| Ca4_P4_40769312  | Ca4                                     | 40769312                      | GNNNNNNNNN/GNNNNNNN                                           | GATGCCTTGGTGTTTTCCAT    | GCCTTGTGGGTTTCATTTTG    | 59.8                             | 644                                           | INTRON                                            | Ca_23904                            | Q                     | --   |
| Ca4_P4_40769926  | Ca4                                     | 40769926                      | TCC/TCCC                                                      | CAAATGAACCCAACAAGGC     | GAGTTTGTGGCCGATGGTT     | 60.3                             | 633                                           | INTRON                                            | Ca_23904                            | Q                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca4_P4_40793708  | Ca4                                     | 40793708                      | CAAC/CAACTAAC                                                 | TATCCGTGCGCACCTA<br>TTTC   | CCTGCATCAACATTGA<br>CACC | 59.9                             | 157                                           | INTRON                                            | Ca_23903                            | --                    | --      |
| Ca4_P4_40801294  | Ca4                                     | 40801294                      | AAAA/AAAATACCACTAAA                                           | AGCTTGCCTCTGAGCT<br>CTTG   | TTTATGGCATGGGACC<br>AAAT | 60.0                             | 736                                           | INTRON                                            | Ca_23902                            | R                     | --      |
| Ca4_P4_40802414  | Ca4                                     | 40802414                      | AATAT/AATATAT                                                 | TGACAGGTGTCAAGTT<br>GTTGG  | CGCAGTGGACTTCAAA<br>ATGA | 59.6                             | 748                                           | INTRON                                            | Ca_23902                            | R                     | --      |
| Ca4_P4_40819629  | Ca4                                     | 40819629                      | TCAACAACAACAA/TCAACAACA<br>ACAA                               | GGCCTGGAACACTTTC<br>CATA   | CAAGGGGTGAAAAAT<br>CAGA  | 59.9                             | 407                                           | INTRON                                            | Ca_23900                            | R                     | --      |
| Ca4_P4_40891676  | Ca4                                     | 40891676                      | AA/AAATTA                                                     | GCACAAAAGCAGTGTA<br>GCCA   | CCCGAACCTCTCCACA<br>ATAA | 60.1                             | 869                                           | INTRON                                            | Ca_11020                            | R                     | G2-like |
| Ca4_P4_40891712  | Ca4                                     | 40891712                      | TCC/TC                                                        | ATCGAATCCTCGTTGG<br>AATG   | CCCGAACCTCTCCACA<br>ATAA | 59.9                             | 725                                           | INTRON                                            | Ca_11020                            | R                     | G2-like |
| Ca4_P4_4089388   | Ca4                                     | 4089388                       | TTATA/TTA                                                     | TGCTTCTTGCAATTGAT<br>GCTC  | TGGGATTTCATTTTTC<br>CAT  | 60.1                             | 370                                           | INTRON                                            | Ca_03847                            | R                     | SBP     |
| Ca4_P4_40929158  | Ca4                                     | 40929158                      | C/CA                                                          | TCCATCATATTTGCAAT<br>GGTTC | AAGAAGCGCGTATTGG<br>TGTT | 59.7                             | 506                                           | INTRON                                            | Ca_11015                            | --                    | bZIP    |
| Ca4_P4_40929349  | Ca4                                     | 40929349                      | AATATATATAT/AATATATAT                                         | TCCATCATATTTGCAAT<br>GGTTC | AAGAAGCGCGTATTGG<br>TGTT | 59.7                             | 506                                           | INTRON                                            | Ca_11015                            | --                    | bZIP    |
| Ca4_P4_4098326   | Ca4                                     | 4098326                       | GTTTTTCATTTTTCATTTT/GTTTT<br>CATTTT                           | AAGCTGAGAGAAAGCG<br>CAAG   | CCTTTCCTTGGCTACA<br>CCAT | 60.0                             | 447                                           | INTRON                                            | Ca_03846                            | T                     | --      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_4139678   | Ca4                                     | 4139678                       | T/TTCTTCTTCTA                                                 | GACTTGTGCTGTTGCG<br>TGTT  | CTGCTGTTGCAAAGCC<br>ACTA  | 60.0                             | 830                                           | INTRON                                            | Ca_03842                            | --                    | --   |
| Ca4_P4_41805831  | Ca4                                     | 41805831                      | CATATATATATATATAT/CATATATAT<br>ATATATATAT                     | GTTAAGGCCCTTCGAT<br>CCTC  | CACCTTGGAAGCTAAT<br>CGAAA | 60.0                             | 565                                           | INTRON                                            | Ca_10934                            | QR                    | B3   |
| Ca4_P4_41806206  | Ca4                                     | 41806206                      | CTA/CTAATA                                                    | TGCCTTGAATCTCTTCT<br>TGGA | TGGAAAACCATAATTGA<br>GCG  | 59.9                             | 905                                           | INTRON                                            | Ca_10934                            | QR                    | B3   |
| Ca4_P4_41806539  | Ca4                                     | 41806539                      | ATTTT/ATT                                                     | TGGTGCTTGTAGTTGA<br>TGAGG | TTTGGGTCAGGACAAG<br>AAGG  | 58.8                             | 949                                           | INTRON                                            | Ca_10934                            | QR                    | B3   |
| Ca4_P4_41806627  | Ca4                                     | 41806627                      | ATT/AT                                                        | AACACATCCAAATCACA<br>TGCT | ATTGGAGCCCACTTG<br>TTTG   | 57.9                             | 964                                           | INTRON                                            | Ca_10934                            | QR                    | B3   |
| Ca4_P4_41845729  | Ca4                                     | 41845729                      | ATT/ATTT                                                      | GCATGAAGTCTCCCAT<br>TGCT  | CTCTCCGGCGTACTA<br>TTCA   | 60.2                             | 378                                           | INTRON                                            | Ca_10933                            | QR                    | --   |
| Ca4_P4_42120439  | Ca4                                     | 42120439                      | TAAAAAAAA/TAAAAAAAA                                           | CACAAGCATTGGAGTC<br>CCTT  | AACTCGTGGGTTGGAT<br>TTTG  | 60.1                             | 495                                           | INTRON                                            | Ca_10910                            | --                    | C2H2 |
| Ca4_P4_42120574  | Ca4                                     | 42120574                      | C/CG                                                          | CACAAGCATTGGAGTC<br>CCTT  | AACTCGTGGGTTGGAT<br>TTTG  | 60.1                             | 495                                           | INTRON                                            | Ca_10910                            | --                    | C2H2 |
| Ca4_P4_42120639  | Ca4                                     | 42120639                      | AAA/AAAATAA                                                   | CACAAGCATTGGAGTC<br>CCTT  | AACTCGTGGGTTGGAT<br>TTTG  | 60.1                             | 495                                           | INTRON                                            | Ca_10910                            | --                    | C2H2 |
| Ca4_P4_42122308  | Ca4                                     | 42122308                      | TAGAGAGAGAGAGA/TAGAGAGAGA<br>GAGAGA                           | GCTCCCTCACTTTTTC<br>GTTC  | TGCGAGTTTGAATTTGT<br>CCA  | 58.9                             | 548                                           | INTRON                                            | Ca_10910                            | --                    | C2H2 |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_44582516  | Ca4                                     | 44582516                      | GCC/GC                                                        | TTATGTTGCACCCACC<br>AAAG | TCTCCTCCTCTTCTCC<br>TCC  | 59.4                             | 803                                           | INTRON                                            | Ca_09130                            | --                    | --    |
| Ca4_P4_44592697  | Ca4                                     | 44592697                      | GAA/GAAA                                                      | GGAGCATGATTCCCTC<br>TGAA | AACATCACGCAAAGTTT<br>CCC | 60.2                             | 651                                           | INTRON                                            | Ca_09131                            | T                     | B3    |
| Ca4_P4_44634106  | Ca4                                     | 44634106                      | TTTAATGGCTT/TTT                                               | TCCCCATTCTTTTAC<br>CTC   | TCCCGAAATAACTTCAA<br>CCG | 60.1                             | 578                                           | INTRON                                            | Ca_09135                            | R                     | MYB   |
| Ca4_P4_44656544  | Ca4                                     | 44656544                      | GAAAA/GAAAAA                                                  | AACCCAGCAATTATGC<br>AAGC | GATGGGATGCAAGAAA<br>AGGA | 60.1                             | 727                                           | INTRON                                            | Ca_09137                            | R                     | NF-YA |
| Ca4_P4_44658965  | Ca4                                     | 44658965                      | AT/A                                                          | GGGCCTAACAGTCAAA<br>ACCA | AGGGTCGCAGAGTTGC<br>TTTA | 60.0                             | 505                                           | INTRON                                            | Ca_09137                            | R                     | NF-YA |
| Ca4_P4_44675409  | Ca4                                     | 44675409                      | CGATTGATTGATTG/CGATTGATTG                                     | TGCTTCAGCACTCTGC<br>ATCT | GTTTTGGAAAGGTTTG<br>CAGC | 59.9                             | 519                                           | INTRON                                            | Ca_09140                            | E                     | --    |
| Ca4_P4_4468607   | Ca4                                     | 4468607                       | TACCAAA/TA                                                    | CTGCAGGAAATTTAG<br>GAGC  | CCGCATTGCTACTTTGT<br>GAA | 60.0                             | 471                                           | INTRON                                            | Ca_03810                            | GOT                   | --    |
| Ca4_P4_4469357   | Ca4                                     | 4469357                       | CAAAA/CAAA                                                    | ATGGGTGCAGGTTTCA<br>TAGC | ATCCATTGGTTAAGAG<br>GGGG | 60.0                             | 576                                           | INTRON                                            | Ca_03810                            | GOT                   | --    |
| Ca4_P4_44704530  | Ca4                                     | 44704530                      | C/CG                                                          | ACAACCTTCGAGGGA<br>AGTT  | CTTCGAATCAGAATT<br>GGGT  | 60.0                             | 857                                           | INTRON                                            | Ca_09141                            | O                     | --    |
| Ca4_P4_44705100  | Ca4                                     | 44705100                      | ATTT/ATT                                                      | ACCCAATTCTGATTGC<br>GAAG | AAGCAAAATGGTTGAA<br>ACGG | 60.1                             | 293                                           | INTRON                                            | Ca_09141                            | O                     | --    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |           |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----------|
|                  |                                         |                               |                                                                       |                            |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs       |
| Ca4_P4_44706474  | Ca4                                     | 44706474                      | CAAAAAAAAA/CAAAAAAAAA                                                 | ACTACTCCTCCCCTGG<br>GAAA   | GGTACTAGAGTTGCGG<br>TGCC | 59.9                             | 811                                           | INTRON                                            | Ca_09141                            | O                     | --        |
| Ca4_P4_44706655  | Ca4                                     | 44706655                      | GAAA/GAA                                                              | AATAACAAAGCACGC<br>CTGG    | GGTACTAGAGTTGCGG<br>TGCC | 60.1                             | 576                                           | INTRON                                            | Ca_09141                            | O                     | --        |
| Ca4_P4_4471743   | Ca4                                     | 4471743                       | TAAGAAAAATACAAG/TAAGAAAAAT<br>ACAAGAAAAATACAAG                        | ACATTTGATCACGGTC<br>CTCC   | AGGCATTGATTCTTCGT<br>TCG | 59.8                             | 615                                           | INTRON                                            | Ca_03810                            | GOT                   | --        |
| Ca4_P4_44733325  | Ca4                                     | 44733325                      | AT/ATT                                                                | ACGAGTTGTACGGATA<br>CGGG   | GGAAATGGAGCACCCA<br>CTAA | 59.9                             | 602                                           | INTRON                                            | Ca_09142                            | C                     | bHLH      |
| Ca4_P4_44785874  | Ca4                                     | 44785874                      | GATGCACATATACGCATGCACAT/G<br>ATGCACATATACGCATGCACATATA<br>CGCATGCACAT | TAACAACAACCTTGAG<br>GGGC   | GTTCCAAGTCACCAAG<br>GGAA | 60.0                             | 640                                           | INTRON                                            | Ca_09144                            | --                    | S1Fa-like |
| Ca4_P4_44786400  | Ca4                                     | 44786400                      | GTTTT/GTTTTT                                                          | TTCCCTTGGTGACTTG<br>GAAC   | AAGCGGCTTACAATGA<br>TGCT | 59.9                             | 364                                           | INTRON                                            | Ca_09144                            | --                    | S1Fa-like |
| Ca4_P4_44787096  | Ca4                                     | 44787096                      | GCC/GC                                                                | TGGCTTCATTTCCATG<br>TCA    | ATTCCAAGAATAGCCG<br>CCTT | 60.0                             | 246                                           | INTRON                                            | Ca_09144                            | --                    | S1Fa-like |
| Ca4_P4_44787142  | Ca4                                     | 44787142                      | CTGT/CTGTGT                                                           | TGGCTTCATTTCCATG<br>TCA    | ATTCCAAGAATAGCCG<br>CCTT | 60.0                             | 246                                           | INTRON                                            | Ca_09144                            | --                    | S1Fa-like |
| Ca4_P4_44799381  | Ca4                                     | 44799381                      | ATTTTTTT/ATTTTTTTT                                                    | CAACTTCATCTATTGTC<br>ACGCC | TTTCGCTGTTTCAGTGT<br>TCG | 59.6                             | 730                                           | INTRON                                            | Ca_09145                            | --                    | --        |
| Ca4_P4_44848176  | Ca4                                     | 44848176                      | G/GTC                                                                 | CCCCTGCAAGTTGAAA<br>ACAT   | GGGCGGATCTTCTCTA<br>GGAC | 60.0                             | 680                                           | INTRON                                            | Ca_09149                            | --                    | --        |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca4_P4_44848432  | Ca4                                     | 44848432                      | TAAA/TAA                                                      | TAGAGACAGTGGCGGA<br>GCTT   | TGGTCAGACAAATCCA<br>TCCA | 60.2                             | 636                                           | INTRON                                            | Ca_09149                            | --                    | --          |
| Ca4_P4_4489505   | Ca4                                     | 4489505                       | TTATA/TTA                                                     | AGTGGTCTGCAACATA<br>GGGG   | GAAATGCAAAATGCCTT<br>GGT | 60.0                             | 698                                           | INTRON                                            | Ca_03808                            | --                    | --          |
| Ca4_P4_44903376  | Ca4                                     | 44903376                      | CCCTTTA/CCCTTTAGTCCTTTA                                       | CAATTCAAAGGGGGAT<br>TCCT   | TGGATGAGGGTTTGG<br>AGAG  | 60.1                             | 254                                           | INTRON                                            | Ca_09153                            | --                    | --          |
| Ca4_P4_44909734  | Ca4                                     | 44909734                      | TGA/T                                                         | AGCTCTCATGAGGGGC<br>TACA   | TCAATTGAAGTGTCG<br>GTGC  | 60.0                             | 310                                           | INTRON                                            | Ca_09154                            | --                    | --          |
| Ca4_P4_4492925   | Ca4                                     | 4492925                       | A/AGTC                                                        | AATTGCATGACAAACA<br>CCGA   | AATTTGGGAGTTCTT<br>TTGG  | 60.0                             | 270                                           | INTRON                                            | Ca_03808                            | --                    | --          |
| Ca4_P4_44946194  | Ca4                                     | 44946194                      | AACA/AA                                                       | CTGCTCTGGTCACTGC<br>ACAT   | CAATTCCAAGGCAAGT<br>TTGG | 60.1                             | 512                                           | INTRON                                            | Ca_09157                            | G                     | --          |
| Ca4_P4_4497451   | Ca4                                     | 4497451                       | TAGGAAG/TAG                                                   | TAAACCACATCGACAC<br>GGAA   | TTATGGCATTCCATTCT<br>CCC | 60.0                             | 631                                           | INTRON                                            | Ca_03808                            | --                    | --          |
| Ca4_P4_45053251  | Ca4                                     | 45053251                      | ATTTTTTTTTTT/ATTTTTTTTTT                                      | CCTTGAGAGATTCATT<br>TGATGC | GAGGAACCAGCAAGAA<br>GTGC | 60.1                             | 820                                           | INTRON                                            | Ca_09167                            | K                     | GATA        |
| Ca4_P4_45083148  | Ca4                                     | 45083148                      | CATGAT/CAT                                                    | CTTGATGTCGCGGATC<br>TTTT   | AGACCATGAACCCTTT<br>GTGC | 60.2                             | 472                                           | INTRON                                            | Ca_09169                            | E                     | GATA        |
| Ca4_P4_45112028  | Ca4                                     | 45112028                      | AATTGTTC/A                                                    | TGTGGTGGCATTGTG<br>AAGT    | CATAAGCGACTCCCTC<br>GTTC | 60.0                             | 561                                           | INTRON                                            | Ca_09171                            | --                    | MYB_related |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_45118855  | Ca4                                     | 45118855                      | AAC TTACATA/AA                                                | GCTTGAGGAAAAAGCC<br>TGTG | ACAGACGGTGCACAAT<br>TGAA  | 60.0                             | 441                                           | INTRON                                            | Ca_09172                            | T                     | --   |
| Ca4_P4_45127760  | Ca4                                     | 45127760                      | CTTTGTTTTGTTT/CTTTGTTT                                        | AGGGTGGTATGATGGT<br>CAGG | GGACGCTGTCTCGTTA<br>TGGT  | 59.7                             | 284                                           | INTRON                                            | Ca_09174                            | --                    | --   |
| Ca4_P4_45143616  | Ca4                                     | 45143616                      | ATTTT/ATTTT                                                   | AGCTGGCTTGAAACAC<br>CACT | CATCAACGTTGCAGAT<br>ACGAA | 59.9                             | 543                                           | INTRON                                            | Ca_09177                            | T                     | --   |
| Ca4_P4_45151444  | Ca4                                     | 45151444                      | AATAT/AAT                                                     | CGCTTCCTTGTTTCTTT<br>TGG | CACTGAAAGCAAGGGT<br>CACA  | 59.9                             | 555                                           | INTRON                                            | Ca_09178                            | B                     | NAC  |
| Ca4_P4_45153925  | Ca4                                     | 45153925                      | ATGTGT/AT                                                     | ATGCCCTCTAAACCGC<br>AATG | TGCTCTCCCTCGTTTT<br>GATT  | 60.1                             | 587                                           | INTRON                                            | Ca_09178                            | B                     | NAC  |
| Ca4_P4_45161056  | Ca4                                     | 45161056                      | T/TG                                                          | GGATTGTGGAATTGGA<br>TTGG | CAAGACACGTGCACAC<br>ACAG  | 60.0                             | 496                                           | INTRON                                            | Ca_09179                            | P                     | --   |
| Ca4_P4_45163080  | Ca4                                     | 45163080                      | AT/A                                                          | CCATCAGTGACCTATG<br>GCCT | CAACGGTATCCCTGCA<br>ACTT  | 60.0                             | 516                                           | INTRON                                            | Ca_09179                            | P                     | --   |
| Ca4_P4_45185839  | Ca4                                     | 45185839                      | CT/C                                                          | TTCTGGTGTTAGAGGA<br>CGGG | AATGCGCATGTATTTGT<br>GGA  | 60.1                             | 768                                           | INTRON                                            | Ca_09180                            | K                     | TALE |
| Ca4_P4_45202888  | Ca4                                     | 45202888                      | CTTTGACACT/CTTTGACACTCTCG<br>GTTTGACACT                       | GACATGACTGGCCTTG<br>GTTT | ATTTAATCATGGGTCG<br>CAGC  | 60.0                             | 712                                           | INTRON                                            | Ca_09182                            | --                    | --   |
| Ca4_P4_45225608  | Ca4                                     | 45225608                      | ATAAGAATTAAGAA/ATAAGAA                                        | CGGTGCAGGGAAAGG<br>TATAA | GAAGCAACAAGCCGTC<br>TTTC  | 60.0                             | 427                                           | INTRON                                            | Ca_09185                            | S                     | --   |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_45236013  | Ca4                                     | 45236013                      | CATGTGCGAACAATG/CATGTGCGA<br>ACAATGTGCGAACAATG                | CAACCTGAAAAGGGC<br>ACAT  | TAACGATGGGATTGGT<br>CCAT  | 60.0                             | 461                                           | INTRON                                            | Ca_09187                            | A                     | --   |
| Ca4_P4_45267760  | Ca4                                     | 45267760                      | GT/GTAATCGTAATT                                               | ATTGATGGCAAGAAAG<br>GTGG | TTTCCAGGCATATAGG<br>GTGC  | 59.9                             | 758                                           | INTRON                                            | Ca_09190                            | --                    | --   |
| Ca4_P4_45268939  | Ca4                                     | 45268939                      | TTATATATA/TTATATATATA                                         | TGTTCATTTTGCACCGT<br>GTT | AACATGGCGGTGAGAA<br>AAAC  | 60.0                             | 718                                           | INTRON                                            | Ca_09190                            | --                    | --   |
| Ca4_P4_4529211   | Ca4                                     | 4529211                       | CTTCATTTTT/CTTCATTTTATAGTT<br>TCATTTTT                        | AAGGAGATGCCAAGAG<br>GGAT | AAGGGATGAACTACGT<br>TGGG  | 60.0                             | 346                                           | INTRON                                            | Ca_03806                            | --                    | --   |
| Ca4_P4_45335482  | Ca4                                     | 45335482                      | ATTTT/ATTT                                                    | GTTCCGATCACATGGC<br>TTCT | TGAGACGCTTTCGTCA<br>CAAC  | 60.1                             | 406                                           | INTRON                                            | Ca_09198                            | L                     | --   |
| Ca4_P4_45337315  | Ca4                                     | 45337315                      | AT/ATT                                                        | AGCTTGCAATTCCTGA<br>TGCT | TCAAATGAGCATGCCT<br>GGAG  | 60.0                             | 856                                           | INTRON                                            | Ca_09198                            | L                     | --   |
| Ca4_P4_45367732  | Ca4                                     | 45367732                      | A/AT                                                          | CCACACCGTTTAAGCC<br>CTAC | TTGCTCTTCCCATTGTT<br>TCA  | 59.5                             | 798                                           | INTRON                                            | Ca_09200                            | K                     | MYB  |
| Ca4_P4_45375885  | Ca4                                     | 45375885                      | TTATAT/TTATATAT                                               | ATGGCATGAAATTGGT<br>GGAT | GGAAATCGTTCTGCGT<br>TTGT  | 60.0                             | 397                                           | INTRON                                            | Ca_09201                            | --                    | --   |
| Ca4_P4_45415781  | Ca4                                     | 45415781                      | TAA/TA                                                        | CATCATCAAGGAGGAG<br>GGAG | CCCCTTGTAACCATGAA<br>TTGG | 59.6                             | 375                                           | INTRON                                            | Ca_09202                            | K                     | TALE |
| Ca4_P4_45416883  | Ca4                                     | 45416883                      | TTTTGTTT/TTTT                                                 | GCTTTCAAAATGGAAT<br>GGGA | TCAGGAATCAGGATCT<br>TGGG  | 59.9                             | 574                                           | INTRON                                            | Ca_09202                            | K                     | TALE |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                             |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_45417045  | Ca4                                     | 45417045                      | TA/T                                                          | GCTTTC AAAATGGAAT<br>GGGA   | TCAGGAATCAGGATCT<br>TGGG | 59.9                             | 574                                           | INTRON                                            | Ca_09202                            | K                     | TALE |
| Ca4_P4_4549797   | Ca4                                     | 4549797                       | TTTC/TTTCTTC                                                  | GGGCAATTTGGAAGTT<br>ACGA    | TCTGCGCTATAAGCTG<br>GGTT | 59.9                             | 383                                           | INTRON                                            | Ca_03803                            | --                    | --   |
| Ca4_P4_4561239   | Ca4                                     | 4561239                       | TTATTGAA/TTATTGAACTACTATTG<br>AA                              | GTGCGATAGCTTGTT<br>GGGT     | ACACTTCCTTGCCATGT<br>TCC | 60.1                             | 476                                           | INTRON                                            | Ca_03802                            | UZ                    | --   |
| Ca4_P4_4563881   | Ca4                                     | 4563881                       | CTTTTT/CTTTTTT                                                | TGCAGTTTGCTATGCC<br>ACTT    | GGCCAGTCATCAGATC<br>CAGT | 59.5                             | 605                                           | INTRON                                            | Ca_03802                            | UZ                    | --   |
| Ca4_P4_4563901   | Ca4                                     | 4563901                       | ATT/ATTT                                                      | TGCAGTTTGCTATGCC<br>ACTT    | GGCCAGTCATCAGATC<br>CAGT | 59.5                             | 605                                           | INTRON                                            | Ca_03802                            | UZ                    | --   |
| Ca4_P4_4564033   | Ca4                                     | 4564033                       | TAA/TAAAA                                                     | TTGCAAAATTTTCAATA<br>CACTCA | GGCCAGTCATCAGATC<br>CAGT | 59.7                             | 309                                           | INTRON                                            | Ca_03802                            | UZ                    | --   |
| Ca4_P4_4564093   | Ca4                                     | 4564093                       | CTG/CTGTG                                                     | TGGCATGGTAACAAA<br>GTCA     | TGTGTTCCAAAGCCAG<br>TGAG | 57.6                             | 539                                           | INTRON                                            | Ca_03802                            | UZ                    | --   |
| Ca4_P4_4569917   | Ca4                                     | 4569917                       | ATTTTTTTT/ATTTTTTTTTT                                         | ACCCCAAAAAGTTCCA<br>TTCC    | ATGCATACCTCACCAG<br>GAGC | 60.0                             | 230                                           | INTRON                                            | Ca_03801                            | --                    | --   |
| Ca4_P4_4584821   | Ca4                                     | 4584821                       | TAA/TATCTCATAAAA                                              | GGCTGGACTTCAAAT<br>GCTC     | CATTCTTGATGGACC<br>TTGG  | 59.8                             | 920                                           | INTRON                                            | Ca_03799                            | R                     | --   |
| Ca4_P4_4585016   | Ca4                                     | 4585016                       | T/TC                                                          | CGTGTGTGTTTGCTT<br>GCCT     | CATTCTTGATGGACC<br>TTGG  | 59.8                             | 757                                           | INTRON                                            | Ca_03799                            | R                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                                           |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_46151550  | Ca4                                     | 46151550                      | TAGAGAGAGAGAGAGAGAGAGA<br>GAGAGAGAGAGAGA/TAGAGAGAG<br>AGAGAGAGAGAGAGAGAGA | TCGCAAGAGCTAATCA<br>GGGT | GAAATGGGGTCATTG<br>GATG  | 60.0                             | 585                                           | INTRON                                            | Ca_18357                            | --                    | NF-X1 |
| Ca4_P4_46716677  | Ca4                                     | 46716677                      | TAAA/TAA                                                                  | AGATTGACGAGGAAGC<br>TGGA | CTCTGCTTGCAGGGTT<br>AAGG | 60.0                             | 947                                           | INTRON                                            | Ca_19246                            | S                     | --    |
| Ca4_P4_46730399  | Ca4                                     | 46730399                      | T/TGTTTCA                                                                 | GCACCTTGTCTCTCTC<br>CCA  | TAACAGACCCGTGCAA<br>TGAG | 60.2                             | 680                                           | INTRON                                            | Ca_19245                            | P                     | --    |
| Ca4_P4_46730464  | Ca4                                     | 46730464                      | CTTTTT/CTTTTTT                                                            | CATTAGTCCACGTTGC<br>TTCG | TAACAGACCCGTGCAA<br>TGAG | 59.3                             | 271                                           | INTRON                                            | Ca_19245                            | P                     | --    |
| Ca4_P4_46730888  | Ca4                                     | 46730888                      | AATAG/AATAGAAGATCATAG                                                     | CTCATTGCACGGGTCT<br>GTTA | TTCGCGTACATCTTTCA<br>GCA | 59.7                             | 727                                           | INTRON                                            | Ca_19245                            | P                     | --    |
| Ca4_P4_46735865  | Ca4                                     | 46735865                      | TC/T                                                                      | AGACAGCTGCAAAAGC<br>CATT | TTGCTCGTAGCGCAAA<br>AAGT | 60.0                             | 604                                           | INTRON                                            | Ca_19244                            | --                    | bZIP  |
| Ca4_P4_46736356  | Ca4                                     | 46736356                      | AGAAT/A                                                                   | GCGCTACGAGCAAGAA<br>GATT | GCTTTCATTGACCCCA<br>AAAA | 59.8                             | 274                                           | INTRON                                            | Ca_19244                            | --                    | bZIP  |
| Ca4_P4_46744931  | Ca4                                     | 46744931                      | TCACA/TCACACA                                                             | AAAACGCCCAACAAAA<br>ACAG | TCGTCAGATGAGATTT<br>CCCC | 60.0                             | 480                                           | INTRON                                            | Ca_19243                            | --                    | --    |
| Ca4_P4_46761914  | Ca4                                     | 46761914                      | GTTTTTTTTT/GTTTTTTTTT                                                     | GCATCATCATCAGCAC<br>CATC | AGGTTTTAAATCACGCT<br>CGC | 60.0                             | 631                                           | INTRON                                            | Ca_19242                            | R                     | bZIP  |
| Ca4_P4_46762039  | Ca4                                     | 46762039                      | A/AT                                                                      | GCATCATCATCAGCAC<br>CATC | TTTCCATCAATGAAGTG<br>CCA | 60.0                             | 728                                           | INTRON                                            | Ca_19242                            | R                     | bZIP  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_46768081  | Ca4                                     | 46768081                      | AT/A                                                          | TCAGAACAAGGGTCGA<br>ATCC | TGCTGCTAGCCCTACC<br>ACTT | 60.1                             | 135                                           | INTRON                                            | Ca_19241                            | OE                    | WRKY |
| Ca4_P4_46769290  | Ca4                                     | 46769290                      | TA/TAA                                                        | GGCTGTGCTATTGTCA<br>CCAA | CCTTAGCACGTGCATT<br>CTCA | 59.7                             | 864                                           | INTRON                                            | Ca_19241                            | OE                    | WRKY |
| Ca4_P4_47190628  | Ca4                                     | 47190628                      | CTTTTT/CTTTTTT                                                | CGTAGTGCTTCGGAAG<br>GAAG | GGCTGTTGTGGACTA<br>AGCAT | 60.0                             | 632                                           | INTRON                                            | Ca_10862                            | --                    | --   |
| Ca4_P4_47257066  | Ca4                                     | 47257066                      | GTGAATGAATGAAT/GTGAATGAAT                                     | CACACGACACTGACAC<br>ATCG | AGGACCTGCCTTCTCA<br>CAGA | 59.8                             | 612                                           | INTRON                                            | Ca_10855                            | --                    | B3   |
| Ca4_P4_47351262  | Ca4                                     | 47351262                      | GAAAAAAAA/GAAAAAAAAA                                          | TTGAGGAGGAGCCACA<br>CTCT | GACAACGGCTTTTCTT<br>CGAG | 60.0                             | 545                                           | INTRON                                            | Ca_10849                            | U                     | --   |
| Ca4_P4_47429657  | Ca4                                     | 47429657                      | GTATATATA/GTATATATATA                                         | GCATGTAAACCCCAAT<br>CATC | TCACTCTCACGTTTGTT<br>GGC | 60.1                             | 931                                           | INTRON                                            | Ca_10845                            | R                     | ERF  |
| Ca4_P4_47982618  | Ca4                                     | 47982618                      | TTTTTATTTTATTTTATTTTATTTT/TT<br>TTTATTTTATTTTATTTT            | CCAAACTCCAATCAAAT<br>GGG | CAATGAGAATTTTCTG<br>GGCA | 60.2                             | 483                                           | INTRON                                            | Ca_10790                            | U                     | ARF  |
| Ca4_P4_47982672  | Ca4                                     | 47982672                      | TC/TCC                                                        | CCAAACTCCAATCAAAT<br>GGG | CAATGAGAATTTTCTG<br>GGCA | 60.2                             | 483                                           | INTRON                                            | Ca_10790                            | U                     | ARF  |
| Ca4_P4_48057090  | Ca4                                     | 48057090                      | ANNNNNNNNN/ANNNNN                                             | ACAAGTCCCTGACC<br>TGTG   | CAACCAAGGAGGAATG<br>TCGT | 60.0                             | 597                                           | INTRON                                            | Ca_10782                            | I                     | bHLH |
| Ca4_P4_4814355   | Ca4                                     | 4814355                       | GTACATAC/GTACATACTACATAC                                      | TTTGGTGGCATCACAT<br>GACT | TACACTAGCCCCCGTT<br>TGAC | 60.0                             | 325                                           | INTRON                                            | Ca_03777                            | O                     | FAR1 |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca4_P4_48247972  | Ca4                                     | 48247972                      | TA/TACAA                                                      | AAAATTGCCCTGTTTCC<br>TTG  | TCCAGTAGCAAAATGG<br>CACA  | 59.1                             | 195                                           | INTRON                                            | Ca_10763                            | --                    | --     |
| Ca4_P4_48260377  | Ca4                                     | 48260377                      | TGG/TGGG                                                      | TGTTGCCATTTTGTTC<br>CAT   | ACCTGCACCACAAGAA<br>AACC  | 60.0                             | 635                                           | INTRON                                            | Ca_10761                            | K                     | B3     |
| Ca4_P4_48262957  | Ca4                                     | 48262957                      | CTTT/CTT                                                      | CATGGTCAGAAGGGGA<br>CAGT  | TCAAAACCACGCATTG<br>GTA   | 60.0                             | 600                                           | INTRON                                            | Ca_10761                            | K                     | B3     |
| Ca4_P4_48294920  | Ca4                                     | 48294920                      | TGG/TG                                                        | AGGTGTTTCTAGGGGA<br>TGTGA | TGGTTTTGACTTTTGAG<br>GACA | 58.5                             | 539                                           | INTRON                                            | Ca_10759                            | --                    | --     |
| Ca4_P4_48301458  | Ca4                                     | 48301458                      | TAAA/TAA                                                      | TAAGAGGATGGTTGT<br>CCCG   | CAATCTTCTCGCTTT<br>GCC    | 59.9                             | 384                                           | INTRON                                            | Ca_10758                            | J                     | --     |
| Ca4_P4_48330370  | Ca4                                     | 48330370                      | AC/A                                                          | GCAAAGGAGCTTCTCA<br>ATGG  | GCATCAGGAACAACCA<br>TCCT  | 60.0                             | 617                                           | INTRON                                            | Ca_10753                            | J                     | --     |
| Ca4_P4_48344615  | Ca4                                     | 48344615                      | TTTT/TTTTTATTTT                                               | CGAGGATGTTTGTGGT<br>TGTG  | ACCACAGCCCTAAATT<br>GTGC  | 60.0                             | 571                                           | INTRON                                            | Ca_10752                            | --                    | --     |
| Ca4_P4_4845603   | Ca4                                     | 4845603                       | CTTTTTTTTT/CTTTTTTTTT                                         | CTGCAGTGGTGTCTCT<br>TGGA  | GGTGGCCTGTGAAAC<br>AGAT   | 60.0                             | 331                                           | INTRON                                            | Ca_03774                            | G                     | --     |
| Ca4_P4_48503609  | Ca4                                     | 48503609                      | CAAAAAAAAA/CAAAAAAAAA                                         | GGTCCAAAATGCAAGG<br>AAAA  | TACTCAACGGCTCATG<br>GTTG  | 59.9                             | 472                                           | INTRON                                            | Ca_10741                            | J                     | E2F/DP |
| Ca4_P4_48505361  | Ca4                                     | 48505361                      | ACCCC/ACCCCC                                                  | CGGCAAAACCACAAAGA<br>AACT | ATTCTTCTCCGACGG<br>ACCT   | 60.1                             | 396                                           | INTRON                                            | Ca_10741                            | J                     | E2F/DP |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca4_P4_48505627  | Ca4                                     | 48505627                      | AATAAATACATAAATA/AATAAATA                                     | AGCTTCACCATGATTC<br>GGAC | TTTTCGCTCGTCTTTCA<br>CCT  | 60.1                             | 470                                           | INTRON                                            | Ca_10741                            | J                     | E2F/DP |
| Ca4_P4_48518535  | Ca4                                     | 48518535                      | AATAT/AATATAT                                                 | TGGTGGTTGACCACAA<br>AAGA | ATCATCTTTGGCAGTA<br>GCGG  | 60.0                             | 927                                           | INTRON                                            | Ca_10740                            | --                    | C2H2   |
| Ca4_P4_48520829  | Ca4                                     | 48520829                      | ATACTTATTA/ATA                                                | AGCATGGGTCACACAC<br>TCAA | CACCCCTCCTTTGTTTT<br>GAA  | 60.2                             | 976                                           | INTRON                                            | Ca_10740                            | --                    | C2H2   |
| Ca4_P4_48576925  | Ca4                                     | 48576925                      | AT/ATT                                                        | ATCTCACCCCAAGACA<br>ACCA | TCATTCCAGAAGGAGA<br>TGGG  | 60.4                             | 211                                           | INTRON                                            | Ca_23007                            | P                     | --     |
| Ca4_P4_4858835   | Ca4                                     | 4858835                       | G/GGT                                                         | TTCAGGCCAATTTTAC<br>GAGG | ATGTTCATTTTCTTCG<br>GCT   | 60.1                             | 753                                           | INTRON                                            | Ca_03773                            | --                    | --     |
| Ca4_P4_4859197   | Ca4                                     | 4859197                       | GTCT/GT                                                       | TCCAGTTTTGGTTGCT<br>GAGA | TAGGCATCACCGTTGT<br>GTGT  | 59.4                             | 737                                           | INTRON                                            | Ca_03773                            | --                    | --     |
| Ca4_P4_48673023  | Ca4                                     | 48673023                      | ATTTTTTT/ATTTTTTTT                                            | CGTGTAAGGCGGAAT<br>TTGT  | CCGCATGTTTCGGTAGC<br>TAGT | 60.0                             | 853                                           | INTRON                                            | Ca_23017                            | --                    | --     |
| Ca4_P4_48689311  | Ca4                                     | 48689311                      | TA/T                                                          | AATACCTGGACAGTGG<br>CTCG | TTTGACGCTTGAGTGG<br>CTTA  | 60.1                             | 500                                           | INTRON                                            | Ca_23019                            | R                     | --     |
| Ca4_P4_48689373  | Ca4                                     | 48689373                      | CATAT/CAT                                                     | AATACCTGGACAGTGG<br>CTCG | TTTGACGCTTGAGTGG<br>CTTA  | 60.1                             | 500                                           | INTRON                                            | Ca_23019                            | R                     | --     |
| Ca4_P4_48711156  | Ca4                                     | 48711156                      | T/TC                                                          | CTCTGGGCTGATCAGA<br>AAGG | ACTCTTTGGGCCCTCA<br>TTCT  | 59.9                             | 229                                           | INTRON                                            | Ca_23021                            | U                     | --     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_48716729  | Ca4                                     | 48716729                      | AATA/AATACATGGTTACATA                                         | GACCAGAAAGCCCAAT<br>TGAA   | CCGATTCGTGGTCTGT<br>TTTT  | 60.1                             | 576                                           | INTRON                                            | Ca_23021                            | U                     | --   |
| Ca4_P4_48740635  | Ca4                                     | 48740635                      | CTTTTT/CTTTTTTT                                               | TCAAGGAGGAATCCCA<br>ACAG   | TTACACCTGTGGCCAA<br>TTCA  | 60.0                             | 569                                           | INTRON                                            | Ca_23023                            | --                    | FAR1 |
| Ca4_P4_48740916  | Ca4                                     | 48740916                      | AATA/AA                                                       | TGAATTGGCCACAGGT<br>GTAA   | TGCCTGAATCATCAAG<br>TACCA | 60.0                             | 160                                           | INTRON                                            | Ca_23023                            | --                    | FAR1 |
| Ca4_P4_4874270   | Ca4                                     | 4874270                       | TTATATATATATATAT/TTATATAT<br>ATATATATATATAT                   | TGGATGGTCTTGGCAC<br>CTAT   | TGCAAAATGTTTCTTGCT<br>TGC | 60.3                             | 971                                           | INTRON                                            | Ca_03771                            | Z                     | NAC  |
| Ca4_P4_48759040  | Ca4                                     | 48759040                      | GCC/GC                                                        | CATGGAAAATCATGTTA<br>GTCGC | TTATGCAGCATGTCTCA<br>CGTC | 59.5                             | 462                                           | INTRON                                            | Ca_23023                            | --                    | FAR1 |
| Ca4_P4_48759217  | Ca4                                     | 48759217                      | TCC/TCCC                                                      | CATGGAAAATCATGTTA<br>GTCGC | TTATGCAGCATGTCTCA<br>CGTC | 59.5                             | 462                                           | INTRON                                            | Ca_23023                            | --                    | FAR1 |
| Ca4_P4_48769666  | Ca4                                     | 48769666                      | GTTTTTTTTT/GTTTTTTTTT                                         | TTTCAATGAAGCCTAGT<br>CCG   | TTAAGGGTCCGCATGA<br>TTGT  | 58.0                             | 605                                           | INTRON                                            | Ca_23023                            | --                    | FAR1 |
| Ca4_P4_48770331  | Ca4                                     | 48770331                      | AC/A                                                          | TTTTGTTACAATCATG<br>CGG    | TGTTTTAACGTGGCTG<br>ACCA  | 60.5                             | 675                                           | INTRON                                            | Ca_23023                            | --                    | FAR1 |
| Ca4_P4_48786645  | Ca4                                     | 48786645                      | TTA/T                                                         | TCAAGGAGGAATCCCA<br>ACAG   | TTACACCTGTGGCCAA<br>TTCA  | 60.0                             | 641                                           | INTRON                                            | Ca_23024                            | --                    | FAR1 |
| Ca4_P4_48826868  | Ca4                                     | 48826868                      | ATTTT/ATTT                                                    | GAATTGATCACGGGTG<br>TGTG   | CCACATTCGCACCCAT<br>TTAT  | 59.8                             | 909                                           | INTRON                                            | Ca_23025                            | --                    | FAR1 |

[illegible]



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca4_P4_7415395   | Ca4                                     | 7415395                       | TAA/TA                                                        | TTTCTGTCTCACCT<br>CACC   | TGTAGGTTTGGACGGT<br>AGGC | 60.1                             | 535                                           | INTRON                                            | Ca_03496                            | F                     | YABBY |
| Ca4_P4_8187438   | Ca4                                     | 8187438                       | CATATAT/CATAT                                                 | CTAAGCCGAGCAGAAG<br>CAAT | TCCCTTTAATGCAAAG<br>GTGG | 59.8                             | 363                                           | INTRON                                            | Ca_08308                            | T                     | --    |
| Ca4_P4_8187730   | Ca4                                     | 8187730                       | TCC/TC                                                        | CTAAGCCGAGCAGAAG<br>CAAT | TCCCTTTAATGCAAAG<br>GTGG | 59.8                             | 499                                           | INTRON                                            | Ca_08308                            | T                     | --    |
| Ca4_P4_8195012   | Ca4                                     | 8195012                       | A/AT                                                          | TCAGCATTGATTGCTT<br>CCTG | GTTGCATTGTTTACGCA<br>TGG | 59.9                             | 660                                           | INTRON                                            | Ca_08309                            | R                     | --    |
| Ca4_P4_8195277   | Ca4                                     | 8195277                       | AA/AAATA                                                      | CCATGCGTAAACAATG<br>CAAC | GTATTCTCCGCGAAA<br>ATCA  | 60.0                             | 185                                           | INTRON                                            | Ca_08309                            | R                     | --    |
| Ca4_P4_8243001   | Ca4                                     | 8243001                       | CTTTTTTT/CTTTTTTTT                                            | CAGCCCAGGATATCTC<br>CAAA | GTCCAACACATGTCGG<br>TGTC | 60.0                             | 553                                           | INTRON                                            | Ca_08314                            | KB                    | --    |
| Ca4_P4_8258153   | Ca4                                     | 8258153                       | CTATTA/CTATTATTA                                              | CACCCCAAATATGATA<br>CCCG | CAGGGAAAGAAACCGT<br>TGAA | 59.9                             | 460                                           | INTRON                                            | Ca_08315                            | S                     | --    |
| Ca4_P4_8265723   | Ca4                                     | 8265723                       | ACCCC/ACCCCCCCCCACCCCCC<br>C                                  | ATTGGGAAAAACCCAA<br>GTCC | ACAACCCAATTGCTCTT<br>TGC | 60.0                             | 759                                           | INTRON                                            | Ca_08315                            | S                     | --    |
| Ca4_P4_8271274   | Ca4                                     | 8271274                       | TAAAAAAAAA/TAAAAAAAAA                                         | ATTCAACGGGCCTATA<br>CGGT | TTAGTGGTGTACGTTG<br>CGGA | 60.6                             | 794                                           | INTRON                                            | Ca_08315                            | S                     | --    |
| Ca4_P4_8275681   | Ca4                                     | 8275681                       | TAAA/TAA                                                      | GCAAGCAATCAAAACA<br>AGCA | ACCTCACCATGACGTT<br>CTCC | 60.0                             | 357                                           | INTRON                                            | Ca_08315                            | S                     | --    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca4_P4_8305796   | Ca4                                     | 8305796                       | TTACTACCATACTACCAT/TTACTAC<br>CATACTACCATACTACCAT             | CATCATGCAGTCGCCT<br>CTAA | ACCACATCTGCCATCA<br>ATCA  | 60.0                             | 510                                           | INTRON                                            | Ca_08319                            | S                     | --   |
| Ca4_P4_8339338   | Ca4                                     | 8339338                       | CAA/CA                                                        | AAAAACTGCCGCAAAA<br>GCTA | GTTTGAAGATGGCGAT<br>GGTT  | 60.0                             | 641                                           | INTRON                                            | Ca_08321                            | --                    | --   |
| Ca4_P4_8340348   | Ca4                                     | 8340348                       | T/TATAAAG                                                     | AGGAAAGGAAATGAAA<br>GGGC | CCAAATACGCATTGGT<br>TAAAG | 59.5                             | 734                                           | INTRON                                            | Ca_08321                            | --                    | --   |
| Ca4_P4_8342083   | Ca4                                     | 8342083                       | AATCATCAT/AATCAT                                              | TGATCAAATCCCAAG<br>AAGC  | CCAATCTCTTCTGCTCC<br>CCT  | 60.0                             | 951                                           | INTRON                                            | Ca_08321                            | --                    | --   |
| Ca4_P4_8342338   | Ca4                                     | 8342338                       | TC/T                                                          | ACTTGTTTGACCGGG<br>TATC  | TGTGCTTGTGGTTGAA<br>GCTC  | 59.9                             | 752                                           | INTRON                                            | Ca_08321                            | --                    | --   |
| Ca4_P4_8344016   | Ca4                                     | 8344016                       | CTT/CTTT                                                      | TAAGAATTTCCGCATC<br>CCTG | CCTTTCACCTCGTTCTGC<br>TCC | 60.0                             | 336                                           | INTRON                                            | Ca_08321                            | --                    | --   |
| Ca4_P4_8353215   | Ca4                                     | 8353215                       | ATT/ATTT                                                      | GAAAAATGGGGTCAAG<br>GGAT | GAGAGAAAGGCTGCAA<br>CCAC  | 60.0                             | 487                                           | INTRON                                            | Ca_08323                            | --                    | --   |
| Ca4_P4_8357483   | Ca4                                     | 8357483                       | CTATA/CTATATA                                                 | GCGATGCCAAATGAGA<br>AAAT | AACTTGGGTGATCCTG<br>AACG  | 60.0                             | 559                                           | INTRON                                            | Ca_08324                            | T                     | bZIP |
| Ca4_P4_8381452   | Ca4                                     | 8381452                       | TAAAAAAA/TAAAAAAA                                             | CAATCCGTTAAGGACC<br>TGGA | GATGATTCCCTTGCTG<br>GAAA  | 59.9                             | 388                                           | INTRON                                            | Ca_08327                            | KL                    | --   |
| Ca4_P4_8387546   | Ca4                                     | 8387546                       | TAAA/TAA                                                      | CATTGCCTGATTTTCC<br>CAAT | GGGCTTTGAACCCGAT<br>AAAT  | 59.8                             | 460                                           | INTRON                                            | Ca_08327                            | KL                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca4_P4_8400908   | Ca4                                     | 8400908                       | TAAAAAAA/TAAAAA                                               | CTTAAGCATCAAAGCC<br>CGAG | CCTCAATTGCCACCAA<br>AACT | 60.0                             | 469                                           | INTRON                                            | Ca_08329                            | O                     | B3  |
| Ca4_P4_8405694   | Ca4                                     | 8405694                       | TAA/TAA                                                       | GACCAGATTTCCGGTT<br>TTCA | AACAAGCTTCGTGCTG<br>GAAT | 59.9                             | 175                                           | INTRON                                            | Ca_08330                            | O                     | B3  |
| Ca4_P4_8433584   | Ca4                                     | 8433584                       | ATTTTTTTT/ATTTTTTT                                            | AAAAAGTGGAGGAGGC<br>CATT | GGGACCTCGAAGTTGT<br>GTGT | 59.9                             | 174                                           | INTRON                                            | Ca_08335                            | R                     | --  |
| Ca4_P4_8437768   | Ca4                                     | 8437768                       | A/AT                                                          | TTGCTCTTCAAACCC<br>ATTC  | TTTGAGAACAAATCCAA<br>GCC | 60.1                             | 624                                           | INTRON                                            | Ca_08335                            | R                     | --  |
| Ca4_P4_8441953   | Ca4                                     | 8441953                       | GTTTGTA/GTTTGATTTTGTA                                         | AGCAGGAGAGCTGAGA<br>TTGG | TACTGTGTATCGGGC<br>AACA  | 59.7                             | 731                                           | INTRON                                            | Ca_08335                            | R                     | --  |
| Ca4_P4_8474416   | Ca4                                     | 8474416                       | CA/C                                                          | TGAGGTGGCTTTTAGG<br>ATGC | TGGAAGGGGATGAATC<br>TGAG | 60.2                             | 178                                           | INTRON                                            | Ca_08339                            | G                     | --  |
| Ca4_P4_8476596   | Ca4                                     | 8476596                       | GAAAAA/GAAAAA                                                 | ACCTGCAGATGGAAGC<br>TTGT | TGCAGTGTGTGCGTGA<br>TAGA | 59.9                             | 459                                           | INTRON                                            | Ca_08339                            | G                     | --  |
| Ca4_P4_8477719   | Ca4                                     | 8477719                       | TTATTTACAC/T                                                  | AAGGGGAAAGCGTCTA<br>GCTC | GGGTTCAAAAACCCA<br>ACAC  | 60.0                             | 208                                           | INTRON                                            | Ca_08339                            | G                     | --  |
| Ca4_P4_8483876   | Ca4                                     | 8483876                       | TG/T                                                          | CAACAGAAGGCAATGA<br>GCAA | AATTGAAGGCGTATTC<br>GGTG | 60.0                             | 125                                           | INTRON                                            | Ca_08340                            | R                     | --  |
| Ca4_P4_8486971   | Ca4                                     | 8486971                       | AT/ATT                                                        | CAACTGCACATGCACA<br>CAAG | ACAGCAGGGCTGAATA<br>TTGG | 59.9                             | 733                                           | INTRON                                            | Ca_08340                            | R                     | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca4_P4_8497257   | Ca4                                     | 8497257                       | TAAACTGAAGAACT/TAAACTGAAG<br>AAACTGAAGAACT                    | AGCGTGAGAGGAACCT<br>GTGT | GACTGGCAACAGCAAT<br>TTGA  | 59.9                             | 564                                           | INTRON                                            | Ca_08341                            | --                    | CPP     |
| Ca4_P4_8509176   | Ca4                                     | 8509176                       | CTTTT/CTT                                                     | GCCTTCTGGACAAAAC<br>GAAG | TCTGCAGGTGAAGCAA<br>CATC  | 59.9                             | 578                                           | INTRON                                            | Ca_08343                            | YU                    | --      |
| Ca4_P4_8524426   | Ca4                                     | 8524426                       | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA                                 | AATTGTTGGGTTGTGA<br>GGGA | TTGGTCGATTCCAACG<br>TGTA  | 60.2                             | 704                                           | INTRON                                            | Ca_08345                            | --                    | bZIP    |
| Ca4_P4_8605380   | Ca4                                     | 8605380                       | ATAGTAGTAGTAGTAGTA/ATAG<br>TAGTAGTAGTAGTAGTA                  | GAAATGAATTGGAGCG<br>CATT | AGGATGAGACCAGATG<br>CAAGA | 60.0                             | 417                                           | INTRON                                            | Ca_08354                            | U                     | GRAS    |
| Ca4_P4_8647972   | Ca4                                     | 8647972                       | A/AG                                                          | GACCAATAGGCCGTAC<br>ATGC | AAGGACTGCGAACCTC<br>AAAA  | 60.4                             | 591                                           | INTRON                                            | Ca_08358                            | --                    | G2-like |
| Ca4_P4_8698891   | Ca4                                     | 8698891                       | AAGAGTAGTAGAGTAGT/AAGAGTA<br>GT                               | AAGCTGGCCACTGTAA<br>GCAT | TCACAATCTCGACAAC<br>CCAA  | 59.9                             | 246                                           | INTRON                                            | Ca_08365                            | G                     | --      |
| Ca4_P4_8770957   | Ca4                                     | 8770957                       | AT/ATGTT                                                      | CTTCGAGAAGAGTGGT<br>TCGG | CGCAGATGCCTATCAT<br>TCAA  | 60.0                             | 505                                           | INTRON                                            | Ca_08372                            | --                    | NAC     |
| Ca4_P4_8787589   | Ca4                                     | 8787589                       | TA/T                                                          | CCAAGGGTTTTCTTC<br>ACAA  | ATCAATCAAATGGGT<br>GGGA   | 59.9                             | 436                                           | INTRON                                            | Ca_08375                            | R                     | NF-YA   |
| Ca4_P4_8846872   | Ca4                                     | 8846872                       | ATTTTT/ATTTTTT                                                | ACAACGACACACGGTC<br>TCTG | CGCAGAACATAGATGA<br>GCCA  | 59.8                             | 729                                           | INTRON                                            | Ca_08381                            | --                    | --      |
| Ca4_P4_8876702   | Ca4                                     | 8876702                       | A/AAGGAAT                                                     | ACTTCCCATGCCTTTG<br>TGTC | TTGGTGGTGTGATGC<br>TGTT   | 60.0                             | 393                                           | INTRON                                            | Ca_08385                            | U                     | B3      |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca5_P4_140338    | Ca5                                     | 140338                        | ATCTCTCT/ATCTCT                                               | CTCTCTGACACATGCC<br>CTCA   | TGGTGATTTCCCTTC<br>AGC    | 60.0                             | 558                                           | INTRON                                            | Ca_18170                            | --                    | --          |
| Ca5_P4_16126632  | Ca5                                     | 16126632                      | CTATATATATATATA/CTATATATA<br>TATATATATA                       | GCCACGATTTATACCG<br>CTTT   | ATGGAAGAAAAGATGC<br>CACG  | 59.1                             | 388                                           | INTRON                                            | Ca_17911                            | C                     | MYB         |
| Ca5_P4_17939380  | Ca5                                     | 17939380                      | ATTTTTTTTTTT/ATTTTTTTTTTT                                     | TCTAGGAACGAAAGCC<br>TGGA   | CGGAATTGATCCCCCT<br>ATTT  | 59.9                             | 562                                           | INTRON                                            | Ca_22850                            | I                     | bZIP        |
| Ca5_P4_17960147  | Ca5                                     | 17960147                      | GTTTTTTTTT/GTTTTTTTTT                                         | TGCATTTTACAGCGCT<br>TTTG   | GCTGTTAGGCAAGGGA<br>TCTG  | 60.0                             | 556                                           | INTRON                                            | Ca_22850                            | I                     | bZIP        |
| Ca5_P4_195727    | Ca5                                     | 195727                        | GC/GCC                                                        | CAACTCAACATCCCCT<br>GCTT   | TGAGGGGAAAGAACAG<br>AGAGA | 60.1                             | 875                                           | INTRON                                            | Ca_18174                            | L                     | --          |
| Ca5_P4_197674    | Ca5                                     | 197674                        | CA/CATA                                                       | TGAATTTTCTGTTTGG<br>GGC    | GAACCCGATTCATAAC<br>CCCT  | 59.9                             | 309                                           | INTRON                                            | Ca_18174                            | L                     | --          |
| Ca5_P4_20024873  | Ca5                                     | 20024873                      | GC/GCC                                                        | ATGTGGTGGGCTCAGG<br>TAAG   | ATTCCCCGACCAACAT<br>ACAA  | 60.0                             | 320                                           | INTRON                                            | Ca_22809                            | M                     | MYB_related |
| Ca5_P4_202535    | Ca5                                     | 202535                        | TAAAAAA/TAAAAAA                                               | TTGGAATTGAAGTTGA<br>CATTGC | ACGAGTTGGATTGGGT<br>TGAC  | 60.2                             | 269                                           | INTRON                                            | Ca_18175                            | --                    | --          |
| Ca5_P4_206513    | Ca5                                     | 206513                        | ATT/AT                                                        | ATCACGCAGATGATGG<br>CATA   | AAAGGCAAAAGGATGG<br>GAGT  | 60.1                             | 426                                           | INTRON                                            | Ca_18175                            | --                    | --          |
| Ca5_P4_206789    | Ca5                                     | 206789                        | AATTGATTGATTGATTGAT/AA<br>TTGATTGATTGATTGAT                   | ATCACGCAGATGATGG<br>CATA   | AAAGGCAAAAGGATGG<br>GAGT  | 60.1                             | 426                                           | INTRON                                            | Ca_18175                            | --                    | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca5_P4_233377    | Ca5                                     | 233377                        | ATTTTT/ATTTT                                                  | TGCTCACGTGGCTGTT<br>TAAG | GAGCCTTTTCTCTGCA<br>CACC | 60.1                             | 580                                           | INTRON                                            | Ca_18178                            | S                     | --  |
| Ca5_P4_2375405   | Ca5                                     | 2375405                       | AATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATA<br>TAT | ATGTTTTGGATTTTGG<br>CTCG | AGGAAGAGTGGAGTTG<br>CGAA | 59.9                             | 571                                           | INTRON                                            | Ca_18664                            | --                    | B3  |
| Ca5_P4_2418306   | Ca5                                     | 2418306                       | ATTTTTTTTTTTTT/ATTTTTTTTTT<br>TT                              | GCTCTGCATTTTCCTT<br>GAGC | TGAGAAATTTTCCGCT<br>GCT  | 60.1                             | 328                                           | INTRON                                            | Ca_18664                            | --                    | B3  |
| Ca5_P4_25600693  | Ca5                                     | 25600693                      | A/AT                                                          | CGTGCACTTTCACGAC<br>AAAT | TTGCTGTACTTGGTTG<br>CTCG | 59.8                             | 801                                           | INTRON                                            | Ca_09030                            | E                     | --  |
| Ca5_P4_26249256  | Ca5                                     | 26249256                      | TAAAAAAAAA/TAAAAAAAAA                                         | TTGCCACATAATTTGCC<br>TGA | TGCTTACACGATGAAC<br>CCAA | 60.1                             | 571                                           | INTRON                                            | Ca_08995                            | GC                    | HSF |
| Ca5_P4_27537316  | Ca5                                     | 27537316                      | G/GATCA                                                       | CAAAGTCTTCGGCAC<br>AGTA  | TGCTCCAGTTGAGAGG<br>GAGT | 60.1                             | 527                                           | INTRON                                            | Ca_08901                            | L                     | --  |
| Ca5_P4_276846    | Ca5                                     | 276846                        | T/TGCATCGGTTCA                                                | TTGTGTCTTTTCTTCG<br>GCT  | ACAGGCACTCCAGGAT<br>CAAC | 60.0                             | 330                                           | INTRON                                            | Ca_18181                            | D                     | --  |
| Ca5_P4_28850506  | Ca5                                     | 28850506                      | TTTGTGTGTGTGTGTGTG/TTTGT<br>GTTG                              | CACAAACGGTACAATG<br>CCTG | TATCAACCAACAAGGG<br>CACA | 60.0                             | 597                                           | INTRON                                            | Ca_13347                            | KL                    | --  |
| Ca5_P4_289542    | Ca5                                     | 289542                        | CATATATATATATA/CATATATATA<br>TATATATA                         | GCAAGAACAGGTGTCA<br>TGGA | AAAATGCGAGAAAATG<br>TGCC | 59.7                             | 611                                           | INTRON                                            | Ca_18185                            | R                     | B3  |
| Ca5_P4_289898    | Ca5                                     | 289898                        | ATT/ATTT                                                      | AAAGTGCCGAAGTTTG<br>CAGT | TTTCCCTTCAACAGTC<br>ATGG | 59.9                             | 351                                           | INTRON                                            | Ca_18185                            | R                     | B3  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                       | Forward primers (5'-3')   | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------|---------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                                     |                           |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca5_P4_291054    | Ca5                                     | 291054                        | TAAAAAAAAA/TAAAAAAAAA                                                                               | TGCTTCATATGCTTGA<br>CCACA | TGGTGCTTCTTTGGCT<br>CTTT    | 60.3                             | 476                                           | INTRON                                            | Ca_18185                            | R                     | B3       |
| Ca5_P4_29111048  | Ca5                                     | 29111048                      | AGNNNNNNNNNG/AG                                                                                     | TGCGAGTGAATCTGAG<br>GATG  | TGCGCAGCATTATCTG<br>AAAC    | 59.9                             | 548                                           | INTRON                                            | Ca_23826                            | I                     | --       |
| Ca5_P4_29753906  | Ca5                                     | 29753906                      | TTATATATATATATATATATATATA<br>T/TTATATATATATATATATATATA<br>TATAT                                     | CACCTCAATTGGGTC<br>GAGT   | TTAGAGAGGAGGAATT<br>CAAAAGC | 60.0                             | 250                                           | INTRON                                            | Ca_16657                            | G                     | G2-like  |
| Ca5_P4_30551642  | Ca5                                     | 30551642                      | AT/ATT                                                                                              | CAAGAGCCATCGTCAT<br>CAGA  | AGCTGATGCCAAGCTC<br>AAAT    | 59.9                             | 838                                           | INTRON                                            | Ca_04744                            | R                     | C3H      |
| Ca5_P4_31092589  | Ca5                                     | 31092589                      | CG/CGG                                                                                              | AAGTAAGCGGCTCTCA<br>CAACA | TTTCCAACGATTTCGGT<br>TTC    | 60.1                             | 843                                           | INTRON                                            | Ca_04809                            | O                     | --       |
| Ca5_P4_31136023  | Ca5                                     | 31136023                      | AAAAT/A                                                                                             | TCACAATTTCCAACC<br>CAAT   | AATTTCTACCAATGCGT<br>CCG    | 60.0                             | 796                                           | INTRON                                            | Ca_04816                            | G                     | Trihelix |
| Ca5_P4_31689383  | Ca5                                     | 31689383                      | GTTTATTTATTTATTTATTT/GT<br>TTATTTATTTATTTATTT                                                       | GCTGGGTTTCATGGTC<br>AGTT  | TCGTCCATGTTGGATC<br>TCAG    | 60.0                             | 422                                           | INTRON                                            | Ca_04871                            | OJ                    | bZIP     |
| Ca5_P4_31952645  | Ca5                                     | 31952645                      | TTATATATATATATATATATATATA<br>TATATATATATATAT/TTATATATA<br>TATATATATATATATATATATATAT<br>ATATATATATAT | CCAAACCACAAGCAAC<br>ACTG  | TGGAGAGCTGGGATAT<br>GGAC    | 60.2                             | 502                                           | INTRON                                            | Ca_04899                            | S                     | ARF      |
| Ca5_P4_32166090  | Ca5                                     | 32166090                      | GATATATATATATATATATATAT/G<br>ATATATATATATATATATATAT                                                 | AATGCGCTAAGAGCAC<br>TGAAA | TCGGGATGAGCCTGTT<br>TATT    | 60.2                             | 710                                           | INTRON                                            | Ca_04917                            | G                     | C2H2     |
| Ca5_P4_32555066  | Ca5                                     | 32555066                      | TAAAAAAAAA/TAAAAAAAAA                                                                               | TCAAACACGGCACCAA<br>TTTA  | CGAATTTTGTGTGATT<br>GGG     | 60.0                             | 550                                           | INTRON                                            | Ca_04963                            | --                    | BES1     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                                                              |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca5_P4_327512    | Ca5                                     | 327512                        | ATTTTTTTTT/ATTTTTTTTT                                                                        | GCTTCTGCATGTTTT<br>GTCA  | AGGATCATCCATTGGA<br>GCAG | 59.8                             | 466                                           | INTRON                                            | Ca_18189                            | G                     | --      |
| Ca5_P4_33794381  | Ca5                                     | 33794381                      | AATATATATATATAT/AATATATATAT<br>ATATAT                                                        | GCAAGGGTACCCACGT<br>CTAA | TAATTTCCACCACACCC<br>CAT | 60.0                             | 439                                           | INTRON                                            | Ca_01877                            | Q                     | --      |
| Ca5_P4_34263941  | Ca5                                     | 34263941                      | TTCAGCTATAGTGATATCAGCTATA<br>GTGATAT/TTCAGCTATAGTGATATC<br>AGCTATAGTGATATCAGCTATAGTG<br>ATAT | CAAGTGGATTCTTCCC<br>CTCA | CCTTTTGTGGATTGCG<br>TTTT | 60.0                             | 825                                           | INTRON                                            | Ca_01820                            | --                    | --      |
| Ca5_P4_37086090  | Ca5                                     | 37086090                      | AGGGGGGGGG/AGGGGGGGGG                                                                        | CCGTGCAAAGGATGAA<br>AAGT | TACTCGGCCCAAATTA<br>ACG  | 60.1                             | 614                                           | INTRON                                            | Ca_01507                            | --                    | G2-like |
| Ca5_P4_37112216  | Ca5                                     | 37112216                      | CTTATTTATTTATTTATTTATTTATTT<br>AT/CTTATTTATTTATTTATTTATTTA<br>TTTATTTATTTAT                  | TTCTTCCAGGGACATC<br>CAAG | AGGAGGTGCCCATTTA<br>GGAT | 60.0                             | 648                                           | INTRON                                            | Ca_01505                            | R                     | --      |
| Ca5_P4_37167592  | Ca5                                     | 37167592                      | TCCC/TCCCC                                                                                   | GGCTGTTGAATTAGCT<br>GCAA | ATCGACGGACATTCCA<br>TTTC | 59.1                             | 878                                           | INTRON                                            | Ca_01500                            | T                     | NAC     |
| Ca5_P4_37991428  | Ca5                                     | 37991428                      | A/ATTT                                                                                       | GAGCGCTACTCTGCTC<br>CATC | TTCAATCCCAAAAGAGT<br>GGC | 60.3                             | 835                                           | INTRON                                            | Ca_01421                            | B                     | --      |
| Ca5_P4_38016624  | Ca5                                     | 38016624                      | TAAGAAA/TAA                                                                                  | ATCCTCGAGAAGGAAG<br>GAGC | CCTTTTCCCTCCAATGT<br>CAA | 59.9                             | 276                                           | INTRON                                            | Ca_01419                            | A                     | --      |
| Ca5_P4_38017775  | Ca5                                     | 38017775                      | CTTTTT/CTTTTT                                                                                | TGATCCCATGTGCACA<br>AACT | CTATCCACACAACGTC<br>GAGC | 60.0                             | 405                                           | INTRON                                            | Ca_01419                            | A                     | --      |
| Ca5_P4_38064856  | Ca5                                     | 38064856                      | CT/CTATAGTATTAATGT                                                                           | AAACGGAAATCGCATG<br>AATC | ACACACAACCCAATCC<br>CCTA | 59.9                             | 352                                           | INTRON                                            | Ca_01414                            | --                    | NAC     |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                           |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca5_P4_38072280  | Ca5                                     | 38072280                      | TGG/TG                                                                    | TAGGGCTAGGGTTTC<br>GGTT   | TGGCGCAAAATGATGA<br>AATA | 60.0                             | 475                                           | INTRON                                            | Ca_01412                            | O                     | MYB_related |
| Ca5_P4_38078782  | Ca5                                     | 38078782                      | ACC/AC                                                                    | TGATCTTGCTCCTAGG<br>CGTT  | GCAAACGCTGTTTTCC<br>ATTT | 60.0                             | 419                                           | INTRON                                            | Ca_01411                            | D                     | WRKY        |
| Ca5_P4_38079677  | Ca5                                     | 38079677                      | ACTGCTCT/ACT                                                              | GCAAAAGCAAAGCATG<br>ACAA  | AGCCCCTACCTTATGC<br>CACT | 60.0                             | 346                                           | INTRON                                            | Ca_01411                            | D                     | WRKY        |
| Ca5_P4_38080854  | Ca5                                     | 38080854                      | A/AC                                                                      | AATAGATCCTGATGGC<br>CGTG  | TCGATTCACCATGACA<br>GCAT | 59.9                             | 813                                           | INTRON                                            | Ca_01411                            | D                     | WRKY        |
| Ca5_P4_38150908  | Ca5                                     | 38150908                      | CAAAAAAA/CAAAAAAA                                                         | GTTGTTGGATCGGCAA<br>AAGT  | TCACTGGAAAGGCCCT<br>TATG | 60.0                             | 571                                           | INTRON                                            | Ca_01402                            | --                    | bHLH        |
| Ca5_P4_39557215  | Ca5                                     | 39557215                      | GATATATATATATATATAT/GATAT<br>ATATATATATATATATAT                           | GCAAAAAGGGGCACAA<br>TAAA  | AATGTCAATCCTCCATT<br>GCC | 59.9                             | 357                                           | INTRON                                            | Ca_07489                            | TBLD                  | --          |
| Ca5_P4_39569272  | Ca5                                     | 39569272                      | ACTCTTNNNNNNNNNNCTCTT/A<br>CTCTT                                          | TAGACAAGCCCATTTTC<br>CAGG | TTATGCAAAACATTGGT<br>GCT | 60.1                             | 450                                           | INTRON                                            | Ca_07489                            | TBLD                  | --          |
| Ca5_P4_395817    | Ca5                                     | 395817                        | TAAAAAAAAA/TAAAAAAAAA                                                     | AAAGGCATCAAAGTCT<br>TGGG  | GCTTCTATTCACCG<br>ATGA   | 59.2                             | 809                                           | INTRON                                            | Ca_18194                            | A                     | bHLH        |
| Ca5_P4_41678103  | Ca5                                     | 41678103                      | TCT/TCTTCCCTTAAAGGACT                                                     | CAGTGGGTCCTCTTCC<br>ACAT  | CCCGAACTCCTGTAC<br>TCCA  | 60.0                             | 551                                           | INTRON                                            | Ca_19215                            | J                     | C3H         |
| Ca5_P4_42146197  | Ca5                                     | 42146197                      | GATATATATATATATATATATATA<br>TATATATATAT/GATATATATATATAT<br>ATATATATATATAT | GCAGGCTCACATGTCT<br>TTGA  | CTGCATATCCAGCAGT<br>GGAA | 60.0                             | 403                                           | INTRON                                            | Ca_11399                            | L                     | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                             | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                                           |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca5_P4_42822040  | Ca5                                     | 42822040                      | AGCGNNNNNNNNNGCG/AGCG                                                                     | TCCATTGCAGTCAGCA<br>ACTC   | GCTTGGTCCTAGAAGA<br>TGCG  | 60.0                             | 433                                           | INTRON                                            | Ca_11327                            | R                     | MYB  |
| Ca5_P4_42868600  | Ca5                                     | 42868600                      | CAAAAA/CAAAAAA                                                                            | CTGGCGTCAGAGAAAA<br>GTCC   | ATACGGGACGCTAACC<br>ATGA  | 60.0                             | 887                                           | INTRON                                            | Ca_11321                            | L                     | --   |
| Ca5_P4_43051982  | Ca5                                     | 43051982                      | ATCTCTCTCTCTCT/ATCTCTCTC<br>TCTCTCTCT                                                     | TGCACTGTTTACCAATC<br>CGA   | TCCCAATGCAGAAACA<br>TCAA  | 60.1                             | 523                                           | INTRON                                            | Ca_11302                            | --                    | B3   |
| Ca5_P4_43230818  | Ca5                                     | 43230818                      | T/TAAGATCTTTCCC                                                                           | ACATTACGTGTTTGGC<br>CTTG   | GATTCCCAAGGACACT<br>CCAA  | 59.8                             | 455                                           | INTRON                                            | Ca_12734                            | T                     | MYB  |
| Ca5_P4_43456554  | Ca5                                     | 43456554                      | TTCTTGGGCAGTCTTGGGCAG/TT<br>TTGGGCAGTCTTGGGCAGTCTTGG<br>GCAG                              | TCTGGATGATAATTC<br>GGGC    | TTGAATTCACCTTTGAC<br>CCC  | 59.9                             | 520                                           | INTRON                                            | Ca_12708                            | O                     | MYB  |
| Ca5_P4_44136905  | Ca5                                     | 44136905                      | GTTTTTTTTTTT/GTTTTTTTTTTT                                                                 | GGTTTGATGCCATTTT<br>GCTT   | TTTTTCCCAACTTGCTC<br>CTTT | 59.9                             | 680                                           | INTRON                                            | Ca_12643                            | G                     | C2H2 |
| Ca5_P4_44244203  | Ca5                                     | 44244203                      | AA/AATTTAGA                                                                               | CAATGAACACATTGC<br>CACC    | GGACGATCAAGCTCAA<br>CCAT  | 59.8                             | 747                                           | INTRON                                            | Ca_03869                            | P                     | --   |
| Ca5_P4_460106    | Ca5                                     | 460106                        | ATTT/ATTTT                                                                                | ACACATACCCAAAGGG<br>ATGC   | CCCCAGCAGTCGGTAA<br>AATA  | 59.7                             | 541                                           | INTRON                                            | Ca_18199                            | --                    | --   |
| Ca5_P4_46318825  | Ca5                                     | 46318825                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATT/TTTATTATTATTAT<br>TATTATTATTATTATTATTATTATT<br>T | TGCCATTTCATTCAAA<br>ATTGTT | TGGGTTGTAAGGCACT<br>AATCG | 58.4                             | 338                                           | INTRON                                            | Ca_04085                            | QI                    | bHLH |
| Ca5_P4_471069    | Ca5                                     | 471069                        | GAAATTAAATTAAGAAATTAATTA<br>AATTAAA                                                       | GTGACACCGTCTCGTT<br>GGTA   | AACTGGGTGAGAGCCT<br>GAGA  | 59.6                             | 314                                           | INTRON                                            | Ca_18200                            | U                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca5_P4_47714017  | Ca5                                     | 47714017                      | GATATATATATATATATATATATA<br>TA/GATATATATATATATATATATA<br>TA   | ATGCGTGTGAAATTGT<br>GCAT | TCAGCTCAGTGGATGA<br>TTGG | 60.0                             | 402                                           | INTRON                                            | Ca_04232                            | G                     | C2H2 |
| Ca5_P4_48112115  | Ca5                                     | 48112115                      | ATTTTTTTTTT/ATTTTTTTTTT                                       | TTGAAGAATGGCATCA<br>GCAG | AAAACCGTTCCAAACTC<br>ACG | 59.9                             | 658                                           | INTRON                                            | Ca_04273                            | K                     | --   |
| Ca5_P4_7524783   | Ca5                                     | 7524783                       | ATTTTT/ATTTTTTT                                               | TGGTGGCGTTCAATTA<br>GTCA | TTGTCATCTGGCAATC<br>CTGA | 60.1                             | 606                                           | INTRON                                            | Ca_18747                            | O                     | --   |
| Ca5_P4_8949616   | Ca5                                     | 8949616                       | AATATATATATATATATATATAT/A<br>ATATATATATATATATATATATAT         | GCTCATGCTCAAGTTC<br>TCCC | CGACTCCCGTATCCTC<br>TTCA | 60.0                             | 631                                           | INTRON                                            | Ca_20342                            | --                    | --   |
| Ca6_P4_10374395  | Ca6                                     | 10374395                      | ATTTTTTTTTT/ATTTTTTTTTT                                       | TGATCCCTCGTTGTGG<br>TACA | CAATCATGCACAGCCC<br>TAAA | 60.0                             | 650                                           | INTRON                                            | Ca_08555                            | --                    | ERF  |
| Ca6_P4_10498080  | Ca6                                     | 10498080                      | TAAAAAAAA/TAAAAAAAA                                           | TGTCCTGATTCAATGG<br>TGGA | CTATGCCTGTGCTGAG<br>TGGA | 59.9                             | 555                                           | INTRON                                            | Ca_08547                            | G                     | C2H2 |
| Ca6_P4_10501710  | Ca6                                     | 10501710                      | ACC/AC                                                        | TTGATTGCTTTTGTTC<br>TGC  | GAAGTCACTCCACC<br>CAAT   | 60.0                             | 461                                           | INTRON                                            | Ca_08546                            | --                    | --   |
| Ca6_P4_10510710  | Ca6                                     | 10510710                      | AGG/AG                                                        | CGACTAGATGTCGCTG<br>ACCA | CACATTTTGGTGTGCT<br>TGG  | 60.0                             | 385                                           | INTRON                                            | Ca_08544                            | S                     | --   |
| Ca6_P4_10512345  | Ca6                                     | 10512345                      | CTTTTTTTTT/CTTTTTTTTT                                         | CTTGACGTGCAAAACG<br>ATGT | GACCTGGGGAAGTCGT<br>AACA | 59.8                             | 540                                           | INTRON                                            | Ca_08544                            | S                     | --   |
| Ca6_P4_10512634  | Ca6                                     | 10512634                      | CAA/CA                                                        | TGTTACGACTTCCCCA<br>GGTC | TATGCGTTTGCATTTC<br>TCA  | 60.0                             | 388                                           | INTRON                                            | Ca_08544                            | S                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca6_P4_10513025  | Ca6                                     | 10513025                      | GTA/GTATATA                                                   | TGAAAAATCGAAACG<br>CATA   | ATTGTTCAGCCACTG<br>GAGG   | 60.2                             | 433                                           | INTRON                                            | Ca_08544                            | S                     | --          |
| Ca6_P4_10652240  | Ca6                                     | 10652240                      | TA/T                                                          | TTCGAATTTTCATGGTG<br>GGT  | GATAAGCGACGTCTTG<br>GAGC  | 60.2                             | 804                                           | INTRON                                            | Ca_08531                            | I                     | --          |
| Ca6_P4_10660274  | Ca6                                     | 10660274                      | TTTTGGGGAAGGCGAAAAATT/TTT                                     | CTAGTGAGCATTGCGA<br>GCAG  | CTTGTGAGGCAGTCCA<br>ATCA  | 59.9                             | 372                                           | INTRON                                            | Ca_08531                            | I                     | --          |
| Ca6_P4_10660543  | Ca6                                     | 10660543                      | G/GCC                                                         | TGATTGGA CTGCCTCA<br>CAAG | GGCCTCAGATCAGTGG<br>AAAA  | 59.8                             | 617                                           | INTRON                                            | Ca_08531                            | I                     | --          |
| Ca6_P4_10671034  | Ca6                                     | 10671034                      | GAAAA/GAAA                                                    | GGAGATCCCAAAATCC<br>CAAT  | ACAGGTTCAACTCCAAT<br>GCC  | 60.0                             | 219                                           | INTRON                                            | Ca_08530                            | --                    | bHLH        |
| Ca6_P4_10675712  | Ca6                                     | 10675712                      | ATTT/ATTTT                                                    | TCCAATTCTCACGTGTT<br>CCA  | TTAGCCGGATGAGAG<br>GAAA   | 60.1                             | 112                                           | INTRON                                            | Ca_08530                            | --                    | bHLH        |
| Ca6_P4_1195895   | Ca6                                     | 1195895                       | CATATATATATATATATATA/CATATA<br>TATATATATATATATA               | GCATCTGAGGGTAAAG<br>CAGG  | TGTTTCATCAAGCAGGA<br>ACCA | 59.8                             | 786                                           | INTRON                                            | Ca_13325                            | U                     | LBD         |
| Ca6_P4_12534444  | Ca6                                     | 12534444                      | GTTTTTTTTT/GTTTTTTTTT                                         | GCTTTCTCTGCTGGAA<br>TTGG  | TGGAGCCACGTGTTG<br>TATC   | 60.0                             | 188                                           | INTRON                                            | Ca_05031                            | R                     | --          |
| Ca6_P4_12905966  | Ca6                                     | 12905966                      | T/TGA                                                         | AGAGTTGTTGCGGAAA<br>AGGA  | TTACGCACCGGACATA<br>ATGA  | 60.0                             | 203                                           | INTRON                                            | Ca_05064                            | T                     | bHLH        |
| Ca6_P4_12959033  | Ca6                                     | 12959033                      | ATTTTTTT/ATTTTTTTT                                            | GATGGCAAATCGGTTT<br>ATCT  | TGAGCATGTGATTGAG<br>GGAA  | 59.9                             | 571                                           | INTRON                                            | Ca_05068                            | --                    | MYB_related |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca6_P4_12970311  | Ca6                                     | 12970311                      | TA/T                                                                          | CACAGACACGTTGACA<br>CTGCT | CAACAGTGCCAACCA<br>CAAC   | 60.0                             | 730                                           | INTRON                                            | Ca_05069                            | S                     | --     |
| Ca6_P4_12982515  | Ca6                                     | 12982515                      | ATTTTTTTTT/ATTTTTTTT                                                          | TCATGAAATGTTGCCT<br>GGAA  | ATCTTTTGTTGCCATC<br>AGG   | 60.0                             | 220                                           | INTRON                                            | Ca_05071                            | O                     | E2F/DP |
| Ca6_P4_12993014  | Ca6                                     | 12993014                      | CGGGGGGG/CGGGGGG                                                              | CCATCATTTTCGACATC<br>ATCA | TGGGACAAATGGGTT<br>TATG   | 59.3                             | 365                                           | INTRON                                            | Ca_05073                            | O                     | E2F/DP |
| Ca6_P4_12994324  | Ca6                                     | 12994324                      | AAATAATAATAATAATAA/AA<br>ATAATAATAATAATAA                                     | CCCAAAACCATACCA<br>AACC   | TGCCTAGAACTGCAGA<br>ACCAT | 59.0                             | 559                                           | INTRON                                            | Ca_05073                            | O                     | E2F/DP |
| Ca6_P4_13178173  | Ca6                                     | 13178173                      | TGCA/TGCAGCGTAACAGCA                                                          | CGACATGCAAAGTCAC<br>CAAC  | AATCAGCAGAGACACC<br>CCAC  | 60.2                             | 404                                           | INTRON                                            | Ca_05088                            | --                    | --     |
| Ca6_P4_14027918  | Ca6                                     | 14027918                      | GACATGCCCTAAAGTAACAACATGC<br>/GACATGCCCTAAAGTAACAACATG<br>CCCTAAAGTAACAACATGC | CCCCCACTCAACTTTTT<br>GAA  | GGACATTGGTGCTTTG<br>GAGT  | 59.9                             | 690                                           | INTRON                                            | Ca_05168                            | A                     | --     |
| Ca6_P4_1491943   | Ca6                                     | 1491943                       | CT/CTT                                                                        | TGGTTTTCGTACCGGA<br>CTCT  | CAATGTCATCAAATAGC<br>GGC  | 59.6                             | 772                                           | INTRON                                            | Ca_27033                            | H                     | --     |
| Ca6_P4_1492349   | Ca6                                     | 1492349                       | GC/GCGCCGCTATAAC                                                              | CCGTGCATATGACAGA<br>AATGA | ATGCACCGTTGAAACA<br>ACAA  | 59.6                             | 510                                           | INTRON                                            | Ca_27033                            | H                     | --     |
| Ca6_P4_1492728   | Ca6                                     | 1492728                       | AT/ATT                                                                        | TTGTTGTTTCAACGGT<br>GCAT  | ATGGTTGGGGATAAA<br>AAGG   | 60.0                             | 651                                           | INTRON                                            | Ca_27033                            | H                     | --     |
| Ca6_P4_15868992  | Ca6                                     | 15868992                      | AATATATATATAT/AATATATATAT<br>AT                                               | GGCTGTGTACCAATTT<br>GCCT  | AATGTAGGGTTGCGAA<br>GGTG  | 60.0                             | 604                                           | INTRON                                            | Ca_22021                            | K                     | MYB    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                           | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                                                                                         |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca6_P4_16547931  | Ca6                                     | 16547931                      | GA/GAGAGCTTA                                                                                                                            | TTCTTCCTGCTCGT<br>CTAT     | TTCTTTGGCTGAAATG<br>GTCC | 60.0                             | 640                                           | INTRON                                            | Ca_06284                            | A                     | --          |
| Ca6_P4_17094586  | Ca6                                     | 17094586                      | TAAAAAA/TAAAAAA                                                                                                                         | CATGTGTTGGTGTCG<br>GTCA    | GCAGGAAGCTGGTCAT<br>TTGT | 60.0                             | 755                                           | INTRON                                            | Ca_06327                            | C                     | --          |
| Ca6_P4_17259878  | Ca6                                     | 17259878                      | TAAA/TAAAA                                                                                                                              | ACACCCCAAAGCCTCC<br>TAAT   | TGCAAACACAGTTG<br>ACAT   | 59.8                             | 392                                           | INTRON                                            | Ca_06343                            | --                    | HB-other    |
| Ca6_P4_17655734  | Ca6                                     | 17655734                      | G/GCT                                                                                                                                   | GGTTGATGTTGAATG<br>TCCC    | ACAGATGGTCCCAGAT<br>GGTC | 60.0                             | 211                                           | INTRON                                            | Ca_06382                            | --                    | MYB_related |
| Ca6_P4_18207034  | Ca6                                     | 18207034                      | CATATATATATATAT/CATATATAT<br>ATATATATAT                                                                                                 | CACGCAGACAACCACC<br>TAGA   | GGCTTTTCTGTTGC<br>AATA   | 59.9                             | 441                                           | INTRON                                            | Ca_06439                            | R                     | bHLH        |
| Ca6_P4_1828999   | Ca6                                     | 1828999                       | TA/TAA                                                                                                                                  | GAGATGAGCAGCTTGC<br>AGTG   | CAGTTGGACCTCCCAT<br>GTCT | 59.9                             | 622                                           | INTRON                                            | Ca_10310                            | G                     | --          |
| Ca6_P4_18331022  | Ca6                                     | 18331022                      | G/GTTCGGGTATC                                                                                                                           | TATATTGCTGCCACAAT<br>CGC   | TTTCCTCCTTGAATCA<br>TGG  | 59.7                             | 402                                           | INTRON                                            | Ca_06449                            | QI                    | B3          |
| Ca6_P4_19259151  | Ca6                                     | 19259151                      | TGATTTGCAGAATTATTTAGATTTG<br>CAGAATTATTTAGATTTGCAGAATT/<br>TGATTTGCAGAATTATTTAGATTTG<br>CAGAATTATTTAGATTTGCAGAATT<br>ATTTAGATTTGCAGAATT | TTGTGCTTTTGTGTTG<br>GCA    | TCCCATCCGAATGAAG<br>TCTC | 60.3                             | 216                                           | INTRON                                            | Ca_06531                            | I                     | --          |
| Ca6_P4_19334085  | Ca6                                     | 19334085                      | AAATAATAATAATAATAATAATA<br>ATA/AAATAATAATAATAATAATA<br>ATAATAATA                                                                        | GGAATAGAAATTGTTG<br>GCGTTT | ATTTTGGCCACACTG<br>AGTC  | 59.4                             | 220                                           | INTRON                                            | Ca_06539                            | --                    | ERF         |
| Ca6_P4_1978360   | Ca6                                     | 1978360                       | A/ATCG                                                                                                                                  | CGTGGAGCATCCGAG<br>TATT    | GGAGTTAGGCGGTGTG<br>ATGT | 60.1                             | 575                                           | INTRON                                            | Ca_10322                            | --                    | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                         | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                       |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_2063027   | Ca6                                     | 2063027                       | GGAAAGAAAGAAAGAAAGAAAGAA<br>GAAA/GGAAAGAAAGAAAGAAAGAA<br>AGAAA                        | AGGCAAAGAAAGGAGC<br>AACA | GCATGACACGACAATG<br>GAAG   | 60.0                             | 807                                           | INTRON                                            | Ca_10326                            | A                     | --  |
| Ca6_P4_21582119  | Ca6                                     | 21582119                      | CCTCTCTCTCTCTCTCTCTCTCTCT<br>CTCTCTC/CCTCTCTCTCTCTCTCTC<br>TCTCTCTCTCTCTCTC           | TGAAGCGAATTGCGTA<br>TCTG | CCTCATGTAGCATGTG<br>GACC   | 60.0                             | 513                                           | INTRON                                            | Ca_11282                            | IQ                    | --  |
| Ca6_P4_21891223  | Ca6                                     | 21891223                      | TTCTC/TTC                                                                             | GGGAAGACCTTGGATT<br>CACA | CAATACCGTCCTGCAC<br>ATTG   | 59.9                             | 517                                           | INTRON                                            | Ca_11250                            | S                     | --  |
| Ca6_P4_23040308  | Ca6                                     | 23040308                      | TT/TTTTAT                                                                             | ACTCCTACGGATTGTG<br>CAGC | CGGTGAAGAGAGATGA<br>AACGA  | 60.3                             | 702                                           | INTRON                                            | Ca_11143                            | --                    | ERF |
| Ca6_P4_23042823  | Ca6                                     | 23042823                      | CATATATATATATAT/CATATATATAT<br>AT                                                     | CAACGATCTGCACCAC<br>ACAT | GGTGCAGCAAGTGAGC<br>AATA   | 60.6                             | 665                                           | INTRON                                            | Ca_11143                            | --                    | ERF |
| Ca6_P4_23042859  | Ca6                                     | 23042859                      | TCAATCCAATCCAATCCAAT/TCAAT<br>CCAATCCAATCCAATCCAAT                                    | CAACGATCTGCACCAC<br>ACAT | GGTGCAGCAAGTGAGC<br>AATA   | 60.6                             | 665                                           | INTRON                                            | Ca_11143                            | --                    | ERF |
| Ca6_P4_23042981  | Ca6                                     | 23042981                      | TAAA/TAA                                                                              | CAACGATCTGCACCAC<br>ACAT | GGTGCAGCAAGTGAGC<br>AATA   | 60.6                             | 665                                           | INTRON                                            | Ca_11143                            | --                    | ERF |
| Ca6_P4_23227711  | Ca6                                     | 23227711                      | TAGAG/TAG                                                                             | GCTAGTAATTCGAAT<br>GGGGA | CATGACCGAGGATAAA<br>TCACTG | 58.2                             | 227                                           | INTRON                                            | Ca_11132                            | R                     | --  |
| Ca6_P4_23642077  | Ca6                                     | 23642077                      | T/TTTCC                                                                               | GATTACCATGGTTGGG<br>ATCG | CAATTCGGTGCTTGTT<br>CCT    | 60.0                             | 137                                           | INTRON                                            | Ca_11091                            | R                     | --  |
| Ca6_P4_23889247  | Ca6                                     | 23889247                      | TTATATATATATATATATATATATATA<br>TATATAT/TTATATATATATATATATA<br>TATATATATATATATATATATAT | ATAGCAGCGAGTAGGC<br>CAAA | AGAGGGGGAATCGAAA<br>GAAA   | 60.0                             | 619                                           | INTRON                                            | Ca_11072                            | K                     | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                 | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                                                               |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca6_P4_2514023   | Ca6                                     | 2514023                       | A/AG                                                                                                          | TCTAATGAGGCTTGG<br>AGGA   | CTTTTGTGACAGCTTT<br>CCC      | 59.8                             | 841                                           | INTRON                                            | Ca_10383                            | A                     | --  |
| Ca6_P4_2516623   | Ca6                                     | 2516623                       | ATTTTT/ATTTTTTT                                                                                               | GGGTTCTTGCCATGAT<br>GAGT  | TGAAAACCATCAATGAC<br>CCA     | 59.9                             | 114                                           | INTRON                                            | Ca_10384                            | --                    | --  |
| Ca6_P4_25971601  | Ca6                                     | 25971601                      | TTTAACATAATCAAATTACTTAACAT<br>AATCAAATTACTT/TTTAACATAATCA<br>AATTACTTAACATAATCAAATTACTT<br>AACATAATCAAATTACTT | AGTGC GTTGCTCATCC<br>TCTT | GGTAGAGACCCACAT<br>TGGA      | 60.0                             | 568                                           | INTRON                                            | Ca_25500                            | --                    | --  |
| Ca6_P4_2674985   | Ca6                                     | 2674985                       | ATGTT/AT                                                                                                      | GAAACTTCGTGCCTTT<br>TTGC  | ACGATAGTAGATGTGG<br>CGGC     | 59.9                             | 152                                           | INTRON                                            | Ca_10401                            | V                     | --  |
| Ca6_P4_27122116  | Ca6                                     | 27122116                      | ATATTATTATTATTATTATTATTA<br>TTATTATTATTATTAT/ATATTATTAT<br>TATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTAT  | ATGCAATTCACGCAAC<br>CATA  | GTTACATGGGCTCACC<br>GAGT     | 60.0                             | 873                                           | INTRON                                            | Ca_14630                            | --                    | MYB |
| Ca6_P4_27128473  | Ca6                                     | 27128473                      | CATATATATATATAT/CATATATAT<br>ATATATATATATAT                                                                   | TGGTTTTCTCCTTTGG<br>GTCT  | CAAGTGGCAAGAACAC<br>GTTG     | 58.6                             | 668                                           | INTRON                                            | Ca_14630                            | --                    | MYB |
| Ca6_P4_27134190  | Ca6                                     | 27134190                      | ACACCCACC/ACACC                                                                                               | CAAAGGGAGTTGACAC<br>CAAAA | AAAAGACAAAACTGTG<br>AAATCG   | 60.0                             | 916                                           | INTRON                                            | Ca_14630                            | --                    | MYB |
| Ca6_P4_27148781  | Ca6                                     | 27148781                      | GATATATATATATATAT/GATATATAT<br>ATATATATATATATAT                                                               | AATAAGGCACGGTGT<br>GGAG   | CGACTCCCCAAATGTG<br>AGAT     | 60.0                             | 473                                           | INTRON                                            | Ca_14630                            | --                    | MYB |
| Ca6_P4_2751162   | Ca6                                     | 2751162                       | TAAAAAAAAA/TAAAAAAAAA                                                                                         | GTGGGACATGCAATTT<br>CCTT  | AAAAATTTCTTGTGTG<br>GATTGTCA | 59.8                             | 451                                           | INTRON                                            | Ca_10408                            | --                    | --  |
| Ca6_P4_2854436   | Ca6                                     | 2854436                       | CAAGAAAGAAAGAAAGAAAGAA<br>AAGAAAGAAA/CAAGAAAGAAAGAA<br>AGAAAGAAAGAAAGAAAGAAAGAA                               | CATGCCATAATTTTGG<br>GGAC  | TCGTGAAGAGGAGATG<br>CGAT     | 60.0                             | 692                                           | INTRON                                            | Ca_10421                            | C                     | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                           |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca6_P4_29006122  | Ca6                                     | 29006122                      | AGG/AG                                                                    | CTGACAGCCTGGGATC<br>ATT   | ATGCTGGACACTTTGTT<br>CCC | 60.1                             | 579                                           | INTRON                                            | Ca_17468                            | OE                    | WRKY     |
| Ca6_P4_29374587  | Ca6                                     | 29374587                      | ATTTTTTTT/ATTTTTTT                                                        | AAAATGGCGAGAGCTT<br>GAAA  | TTGCCCATGTTTGTC<br>AGTA  | 60.0                             | 830                                           | INTRON                                            | Ca_17447                            | U                     | C2H2     |
| Ca6_P4_30130392  | Ca6                                     | 30130392                      | CTATATATATATATATATATATATAT<br>ATATATATAT/CTATATATATATATAT<br>ATATATATATAT | TGTTGAAATAGGACCG<br>GAGG  | CATCAGAAGCACCAGG<br>TTGA | 59.9                             | 259                                           | INTRON                                            | Ca_24048                            | --                    | --       |
| Ca6_P4_30578950  | Ca6                                     | 30578950                      | CTATATATATATATAT/CTATATATAT<br>ATATATATAT                                 | TGCACATTCTCCTCACT<br>TGC  | CCTCTCGGTACTCTGT<br>TCGC | 60.0                             | 593                                           | INTRON                                            | Ca_16460                            | --                    | --       |
| Ca6_P4_32294748  | Ca6                                     | 32294748                      | TCTG/T                                                                    | TCGAATCAAGCAAAAT<br>GCAC  | ATGGTTGAAGATGGAT<br>TGCC | 59.8                             | 496                                           | INTRON                                            | Ca_15222                            | --                    | bZIP     |
| Ca6_P4_3395635   | Ca6                                     | 3395635                       | GTT/GT                                                                    | GGCAGGAACGATACCA<br>CAGT  | TTGCCCGTACAAAAGA<br>ATCC | 60.0                             | 428                                           | INTRON                                            | Ca_05973                            | U                     | Trihelix |
| Ca6_P4_35719325  | Ca6                                     | 35719325                      | AATAGAATACTTTATTAT/AATAGAAT<br>ACTTTATTATAGAATACTTTATTAT                  | TGCATCGTTTTTCATCT<br>TTCA | GCGGCTAATTCAACC<br>AAAT  | 59.3                             | 630                                           | INTRON                                            | Ca_15773                            | --                    | --       |
| Ca6_P4_3756968   | Ca6                                     | 3756968                       | TAAAAAAAAA/TAAAAAAAAA                                                     | TCCGTTACCACTCACA<br>CCAA  | ACCCCTCAAATCTGTT<br>GTGC | 60.0                             | 640                                           | INTRON                                            | Ca_05928                            | --                    | bZIP     |
| Ca6_P4_4048315   | Ca6                                     | 4048315                       | AATATATATATATATATATATATAT/A<br>ATATATATATATATATATATATATAT                 | TAGGTTATCACCGTGG<br>AGCC  | AGCAGCAGTTCACCGA<br>GTTT | 60.0                             | 872                                           | INTRON                                            | Ca_05894                            | R                     | --       |
| Ca6_P4_42540850  | Ca6                                     | 42540850                      | AATATATATATATATATATATATATAT<br>AT/AATATATATATATATATATATATA<br>TAT         | GACAGGGGAGTGAAGA<br>TGGA  | CTGAAATCTTGTGCCT<br>GCAA | 60.0                             | 312                                           | INTRON                                            | Ca_23239                            | U                     | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)           | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                         |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca6_P4_4315739   | Ca6                                     | 4315739                       | AG/AGGGAAAGAATATTG                                                      | CACGATATTTGTGAGC<br>CGAA | CAAATACCATTGGGTA<br>CGGG  | 59.7                             | 261                                           | INTRON                                            | Ca_05869                            | R                     | --          |
| Ca6_P4_44418513  | Ca6                                     | 44418513                      | CCTCTCTCTCTCTCTCTCT/CCTCTC<br>TCTCTCTCTCTCTCT                           | ATAGGTGGCCATTGTT<br>CCAA | TGTGGAGTGAAAGCAT<br>GAGG  | 60.2                             | 543                                           | INTRON                                            | Ca_24238                            | --                    | MYB_related |
| Ca6_P4_44421954  | Ca6                                     | 44421954                      | ATTTTTTTTT/ATTTTTTTTTT                                                  | CTATGGCACCTCATTT<br>GCAC | ACGAAATTTGGGATTT<br>ACG   | 59.2                             | 479                                           | INTRON                                            | Ca_24238                            | --                    | MYB_related |
| Ca6_P4_44446594  | Ca6                                     | 44446594                      | TG/T                                                                    | ACGTGAAAGCGCAAGT<br>CTTT | GCGCCTAGGGAGATCA<br>TGTA  | 60.1                             | 672                                           | INTRON                                            | Ca_24238                            | --                    | MYB_related |
| Ca6_P4_44613043  | Ca6                                     | 44613043                      | AAATAATAATAATAATAATAATA/<br>AAATAATAATAATAATAATAATA<br>ATA              | TGTCCGGTAGCCTGAA<br>AATC | GAGCTGGTCTTGCTCT<br>TGCT  | 60.1                             | 899                                           | INTRON                                            | Ca_24242                            | TZ                    | --          |
| Ca6_P4_45336183  | Ca6                                     | 45336183                      | TTTATTATTATTATTATTATTATT<br>ATTA/TTTATTATTATTATTATTATTA<br>TTATTATTATTA | TTGCCACAAACAGAAC<br>GTGT | CCAAAAACACCAACTG<br>GCTT  | 60.2                             | 688                                           | INTRON                                            | Ca_13834                            | T                     | --          |
| Ca6_P4_45817671  | Ca6                                     | 45817671                      | TATAATAATAATAATAATAATAA<br>T/TATAATAATAATAATAATAATA<br>ATAAT            | GCCCCGTGTCCTTAT<br>AAAT  | TGGGGCTTTAGGTGAG<br>AGAA  | 60.0                             | 271                                           | INTRON                                            | Ca_13861                            | Q                     | --          |
| Ca6_P4_45948426  | Ca6                                     | 45948426                      | A/ACAGCTTTTAG                                                           | GAGGCTGAATTGTGTG<br>AGCA | AACAACATTCGTGTGA<br>CGGA  | 60.0                             | 388                                           | INTRON                                            | Ca_13867                            | --                    | --          |
| Ca6_P4_46026053  | Ca6                                     | 46026053                      | CGTGTGTGTGTGTGT/CGTGTGT<br>GTGTGTGT                                     | TGCTGATGTCTCACCT<br>CCAG | GCCAAAGATGATCAAG<br>GTGAA | 60.0                             | 540                                           | INTRON                                            | Ca_13871                            | Q                     | GeBP        |
| Ca6_P4_47028363  | Ca6                                     | 47028363                      | CT/CTCTTT                                                               | CAGACATGGCTGTGGA<br>GCTA | TTTGAAACATGAAGG<br>CAACT  | 60.0                             | 477                                           | INTRON                                            | Ca_17726                            | G                     | NAC         |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                                              | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                  |                                         |                               |                                                                                                                                                            |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| Ca6_P4_4759449   | Ca6                                     | 4759449                       | ATT/AT                                                                                                                                                     | GAGAAGCTGAGAAGGA<br>GCGA | GCTGCTGCTTGGTTGT<br>ATCA | 60.0                             | 635                                           | INTRON                                            | Ca_05820                            | --                    | WRKY   |
| Ca6_P4_47872131  | Ca6                                     | 47872131                      | T/TTATTATTATTA                                                                                                                                             | GGGGTGTCTGAGGTGT<br>GAGT | AAAATTGGGCCAGTT<br>GGAT  | 60.0                             | 695                                           | INTRON                                            | Ca_23445                            | --                    | WRKY   |
| Ca6_P4_48247002  | Ca6                                     | 48247002                      | TTTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATCATTATTATTAT/TTTATTATT<br>ATTATTATTATTATTATTATTATT<br>ATTATTATTATTATTATTATTATC<br>ATTATTATTAT | GAATTTAGGGCAATGG<br>CTCA | TTTTTGGCACCAGTAG<br>GAGG | 60.0                             | 632                                           | INTRON                                            | Ca_24603                            | A                     | HD-ZIP |
| Ca6_P4_49524074  | Ca6                                     | 49524074                      | T/TCCGGTGG                                                                                                                                                 | CGGCTTTAAGAAATGC<br>TTCG | GGTCCATGAAAATCAAT<br>GGG | 60.0                             | 287                                           | INTRON                                            | Ca_13512                            | --                    | Dof    |
| Ca6_P4_53304390  | Ca6                                     | 53304390                      | TAAA/TAAAA                                                                                                                                                 | TCTCTTGTGCTTTGCC<br>ATTG | GGCTACCCCAAGAATA<br>CACG | 60.0                             | 676                                           | INTRON                                            | Ca_22925                            | G                     | --     |
| Ca6_P4_53305336  | Ca6                                     | 53305336                      | ATTTTTTTTT/ATTTTTTTTT                                                                                                                                      | CAAGATTTCGTGGTGC<br>AAGA | TTGAGGACAAAAGCTG<br>CTGA | 59.8                             | 660                                           | INTRON                                            | Ca_22925                            | G                     | --     |
| Ca6_P4_5504837   | Ca6                                     | 5504837                       | AA/AAATTA                                                                                                                                                  | AACCACTTTTGGAGG<br>GCTT  | GGGTGACCATTTGCAT<br>TTCC | 60.0                             | 372                                           | INTRON                                            | Ca_05750                            | --                    | bHLH   |
| Ca6_P4_57132721  | Ca6                                     | 57132721                      | CAAAAAAAAA/CAAAAAAAAA                                                                                                                                      | ACAAGATCGGAGGGAG<br>GAGT | TTTTGTGTTTTTGGTTC<br>GTG | 60.1                             | 580                                           | INTRON                                            | Ca_17439                            | --                    | --     |
| Ca6_P4_57600323  | Ca6                                     | 57600323                      | AT/A                                                                                                                                                       | CGACACAACCACTTCC<br>ATTG | AATTGGTGGGAACG<br>ACAG   | 60.0                             | 887                                           | INTRON                                            | Ca_13685                            | IE                    | --     |
| Ca6_P4_58827188  | Ca6                                     | 58827188                      | GAAAAA/GAAAAA                                                                                                                                              | GTGCAAACCACTGGAA<br>TCCT | TTGGTTTGGGTGGAA<br>CATT  | 60.0                             | 600                                           | INTRON                                            | Ca_15424                            | S                     | --     |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca6_P4_6433713   | Ca6                                     | 6433713                       | CTT/CTTT                                                      | TGTATGCGTTTTTCATC<br>CCA | TCGGAACATATTTTCGC<br>CTTC   | 59.9                             | 197                                           | INTRON                                            | Ca_16912                            | --                    | --   |
| Ca6_P4_667186    | Ca6                                     | 667186                        | AAT/AATAATTAT                                                 | GCAAAGGGATGCTATT<br>TCCA | TACCCAATTTACCTGCT<br>ACC    | 60.0                             | 546                                           | INTRON                                            | Ca_13284                            | T                     | --   |
| Ca6_P4_7123488   | Ca6                                     | 7123488                       | A/ACGAAGAGCG                                                  | TTGGGTTGGGTATGAA<br>CCTC | AGGATTTAGGGTTTCAG<br>AGGAGA | 59.6                             | 905                                           | INTRON                                            | Ca_09670                            | R                     | --   |
| Ca6_P4_7350878   | Ca6                                     | 7350878                       | TAAAAATAAAAAATAAAAAATA/TAAAA<br>TAAAAATA                      | TTGCAAATCCTCCCAA<br>AAAC | CACCTTCTGCAACTTTG<br>GCTG   | 59.9                             | 666                                           | INTRON                                            | Ca_09644                            | --                    | GRAS |
| Ca6_P4_7487802   | Ca6                                     | 7487802                       | CATTATT/CATT                                                  | CATTCTCCCAGGCTCA<br>ACAT | GATCCGTTGAATCACTT<br>TTTGA  | 60.1                             | 297                                           | INTRON                                            | Ca_09634                            | D                     | WRKY |
| Ca6_P4_7557330   | Ca6                                     | 7557330                       | A/AT                                                          | ATGGAAAGTGACATCT<br>CGGG | GTTGAGAGGAAAAATG<br>GGCA    | 59.9                             | 377                                           | INTRON                                            | Ca_09627                            | S                     | --   |
| Ca6_P4_7564789   | Ca6                                     | 7564789                       | AATTTTATATTTT/AATTTT                                          | TGCTCTGGAAGTTGAC<br>GATG | ACGAGCCAAAAGAGCT<br>ACCA    | 60.0                             | 939                                           | INTRON                                            | Ca_09627                            | S                     | --   |
| Ca6_P4_7571538   | Ca6                                     | 7571538                       | TAA/T                                                         | TGCTTGTAAGGTAGGG<br>GTGC | AGCAAGGGACATGATG<br>GAAG    | 60.1                             | 897                                           | INTRON                                            | Ca_09627                            | S                     | --   |
| Ca6_P4_7576438   | Ca6                                     | 7576438                       | ATAAGTTAAGT/ATAAGT                                            | CTTCAACTGGATGGCG<br>AAAT | TCATGGGAAGAATC<br>GTCA      | 60.1                             | 422                                           | INTRON                                            | Ca_09627                            | S                     | --   |
| Ca6_P4_7586160   | Ca6                                     | 7586160                       | GT/GTAAAAAT                                                   | GCACCTCTTGACCAT<br>CAAT  | ACAGTGTCAGTGCCTA<br>CCCC    | 59.9                             | 454                                           | INTRON                                            | Ca_09626                            | C                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca6_P4_7597943   | Ca6                                     | 7597943                       | TAA/TAACAA                                                    | CTGCCACTGGGAATTT<br>GATT  | CCTAAGCGAAACACCC<br>AAAA  | 59.9                             | 580                                           | INTRON                                            | Ca_09624                            | R                     | --   |
| Ca6_P4_7599551   | Ca6                                     | 7599551                       | CT/C                                                          | GCAACCAAGAGCTCCT<br>TCTG  | GTCATTTCTGTTGGGG<br>CACT  | 60.1                             | 212                                           | INTRON                                            | Ca_09624                            | R                     | --   |
| Ca6_P4_7626387   | Ca6                                     | 7626387                       | CATATATATATATATAT/CATATATAT<br>ATAT                           | GTTTCAGTTTGAGGGGC<br>ACAT | GTACACCGGATACCT<br>CCCT   | 60.0                             | 598                                           | INTRON                                            | Ca_09620                            | P                     | --   |
| Ca6_P4_7646083   | Ca6                                     | 7646083                       | AC/A                                                          | CGATGGAAATGGGGAA<br>TTTA  | ACGCGCAGAGCCTATA<br>AAAA  | 59.6                             | 676                                           | INTRON                                            | Ca_09618                            | --                    | --   |
| Ca6_P4_7648423   | Ca6                                     | 7648423                       | ATTTTTT/ATTTTTTT                                              | ACAAGAGGAAGCAGTG<br>GGAA  | GAACAACAAGTGGAGA<br>AACCG | 59.8                             | 627                                           | INTRON                                            | Ca_09618                            | --                    | --   |
| Ca6_P4_7694977   | Ca6                                     | 7694977                       | ATTTTTTTTTTTT/ATTTTTTTTT                                      | CTGCTGCAATGGATGC<br>TAAA  | GCCACTACAATTGTTC<br>GGCT  | 60.0                             | 575                                           | INTRON                                            | Ca_09611                            | --                    | --   |
| Ca6_P4_7723105   | Ca6                                     | 7723105                       | T/TACTC                                                       | CACTTGTAGGCAAGGG<br>AAGC  | TAACCAGCCAGGAAAA<br>TTGC  | 59.9                             | 458                                           | INTRON                                            | Ca_09607                            | --                    | --   |
| Ca6_P4_7748396   | Ca6                                     | 7748396                       | TAA/TA                                                        | CTTTTTTACAGGAGCA<br>AGGC  | ACATGCCAGGTCACCT<br>ACAA  | 60.0                             | 415                                           | INTRON                                            | Ca_09604                            | R                     | --   |
| Ca6_P4_7829258   | Ca6                                     | 7829258                       | ATTTT/ATTT                                                    | AAGATTGAGAGCCCC<br>AACT   | ATGCATCCTCCAAGCA<br>AGAC  | 60.1                             | 742                                           | INTRON                                            | Ca_09595                            | S                     | GRAS |
| Ca6_P4_7872493   | Ca6                                     | 7872493                       | CTTATTA/CTTA                                                  | AATAACGCCACCACTT<br>ACCG  | GCTGATATGCAGACCG<br>TTTGA | 59.9                             | 915                                           | INTRON                                            | Ca_09590                            | E                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca6_P4_7894773   | Ca6                                     | 7894773                       | A/AC                                                          | AGGATGGTAGCAACAG<br>GGTG  | GTGGCGGACAGTAAGA<br>GAGC  | 60.0                             | 318                                           | INTRON                                            | Ca_09586                            | I                     | --       |
| Ca6_P4_7897379   | Ca6                                     | 7897379                       | TTCACATGTC/TTC                                                | ATCCAACTCCGTTCTGA<br>CATC | GGAGGAAATTTATGCC<br>CCAT  | 59.9                             | 319                                           | INTRON                                            | Ca_09586                            | I                     | --       |
| Ca6_P4_7906219   | Ca6                                     | 7906219                       | ACTCT/ACT                                                     | CCACCATAAATTCAATC<br>CCG  | CCTTGAAATTGTAAGGT<br>GCGA | 60.0                             | 581                                           | INTRON                                            | Ca_09585                            | G                     | --       |
| Ca6_P4_7984507   | Ca6                                     | 7984507                       | ATTTTCTTGATTTTATTTT/ATTTT                                     | AGAATCACAAATTTTGC<br>GCC  | CCCACGAGGTATAGGT<br>GTCG  | 60.1                             | 649                                           | INTRON                                            | Ca_09577                            | G                     | --       |
| Ca6_P4_7985102   | Ca6                                     | 7985102                       | TTT/TTTAATT                                                   | TCAACAGGATTTGCCA<br>ACTG  | CACACCACCAACGTT<br>GAAG   | 59.7                             | 473                                           | INTRON                                            | Ca_09577                            | G                     | --       |
| Ca6_P4_7985386   | Ca6                                     | 7985386                       | TTTT/TTTTTAAAAAATATAAATTT                                     | TCCCCCAATTTTATTT<br>CCC   | CACACCACCAACGTT<br>GAAG   | 59.8                             | 365                                           | INTRON                                            | Ca_09577                            | G                     | --       |
| Ca6_P4_8003918   | Ca6                                     | 8003918                       | TC/T                                                          | CATCCCTAACCCCTAG<br>CTCC  | CGGTCTTCACCCACAA<br>ACTT  | 59.9                             | 828                                           | INTRON                                            | Ca_09574                            | C                     | --       |
| Ca6_P4_8008294   | Ca6                                     | 8008294                       | TA/TACA                                                       | TGTTAGTTGTTGCGCT<br>CTGG  | TCCAATGCCATTTAAGC<br>CTC  | 60.1                             | 549                                           | INTRON                                            | Ca_09573                            | G                     | --       |
| Ca6_P4_8037044   | Ca6                                     | 8037044                       | ATTT/ATT                                                      | TTAGGTGTTAGCCACC<br>CCAG  | TGCAGAATTGGCTTCT<br>GATG  | 60.0                             | 312                                           | INTRON                                            | Ca_09570                            | --                    | --       |
| Ca6_P4_8075760   | Ca6                                     | 8075760                       | CTTCATTCTTTCATTCT/CTTCATTCT                                   | GCGTGTGTAATTGGTC<br>ATCG  | AGAACAAGCTCTTCGT<br>CCCA  | 60.0                             | 683                                           | INTRON                                            | Ca_09564                            | U                     | Trihelix |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca6_P4_8077664   | Ca6                                     | 8077664                       | CTTTTT/CTTTT                                                  | AGGTACGTCAAGAAGC<br>TGGC   | ATGAGGGCACAGAAC<br>CAAC  | 60.2                             | 941                                           | INTRON                                            | Ca_09564                            | U                     | Trihelix |
| Ca6_P4_8087315   | Ca6                                     | 8087315                       | GTATATATATATATAT/ATATATAT<br>ATATATAT                         | CTCACAACCACCTTCA<br>CCCT   | ATCCACACTTCCAGCC<br>TGAT | 60.0                             | 639                                           | INTRON                                            | Ca_09562                            | S                     | CAMTA    |
| Ca6_P4_8087365   | Ca6                                     | 8087365                       | ATAATTAA/ATAA                                                 | CGTTCAACTGAAATTTG<br>CCA   | ATCCACACTTCCAGCC<br>TGAT | 59.7                             | 450                                           | INTRON                                            | Ca_09562                            | S                     | CAMTA    |
| Ca6_P4_8103334   | Ca6                                     | 8103334                       | GCCCTCCCATCCCCT/GCCCTCCCA<br>TCCCCTCCCATCCCCT                 | ATTGTGTTCTCGCAGC<br>CTCT   | GGGATTCTGTTGTGCT<br>GGAT | 60.0                             | 434                                           | INTRON                                            | Ca_09560                            | J                     | --       |
| Ca6_P4_8141464   | Ca6                                     | 8141464                       | GAAAAAAAAA/GAAAAAAAAA                                         | TTTGCTTGGGAAATTTG<br>GAG   | TCTCTCCATGCAAGTC<br>AGGA | 60.2                             | 509                                           | INTRON                                            | Ca_09555                            | P                     | GRAS     |
| Ca6_P4_8194523   | Ca6                                     | 8194523                       | AATATATATATATATA/AATATATATA<br>TATATATATATATA                 | CTTTCAACCCGTTTTCC<br>TCA   | GATGTCCTGCGTGGTT<br>ACCT | 60.1                             | 450                                           | INTRON                                            | Ca_09551                            | --                    | --       |
| Ca6_P4_8248948   | Ca6                                     | 8248948                       | AATATATATATATATATATATA/AA<br>TATATATATATATATATATATA           | GAACCAACTGCCCTTG<br>TCAT   | AAATGCGTAGGTTGTC<br>CGTC | 60.0                             | 538                                           | INTRON                                            | Ca_09545                            | J                     | --       |
| Ca6_P4_8252016   | Ca6                                     | 8252016                       | ATGTGTGTGT/ATGTGTGT                                           | CATCCAAGAATAGCGG<br>AGGA   | GCTTGTTTTCCCTGTTT<br>GGA | 60.2                             | 569                                           | INTRON                                            | Ca_09545                            | J                     | --       |
| Ca6_P4_8796967   | Ca6                                     | 8796967                       | A/AG                                                          | GCCAAACAATAGTTGA<br>AACCAA | AACGTTACGCATGAAC<br>CTCC | 59.0                             | 588                                           | INTRON                                            | Ca_16754                            | E                     | --       |
| Ca6_P4_8809776   | Ca6                                     | 8809776                       | GGTG/GG                                                       | TGTGCATTGAGTGCTG<br>CATA   | GGAAGCCACTCATCTT<br>TTGG | 60.0                             | 739                                           | INTRON                                            | Ca_16753                            | --                    | --       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca6_P4_9873238   | Ca6                                     | 9873238                       | GTTCAAC/GTTCAACTCAAC                                          | AACGTGGAACAGAC<br>AGGG   | AACATCGACCGATT<br>AACG    | 60.0                             | 544                                           | INTRON                                            | Ca_08602                            | F                     | --       |
| Ca7_P4_1040581   | Ca7                                     | 1040581                       | A/ATTATTATTATTAT                                              | AGAGATGGCATTGTTT<br>CGGT | TGGCACCAAATTTGTC<br>AAGA  | 59.6                             | 520                                           | INTRON                                            | Ca_03373                            | --                    | Dof      |
| Ca7_P4_11534309  | Ca7                                     | 11534309                      | TAA/TTGAA                                                     | AATGCCATCACTGTCC<br>ACAA | ATTTACGCACCGTTGG<br>AGAT  | 60.0                             | 781                                           | INTRON                                            | Ca_09343                            | --                    | --       |
| Ca7_P4_12365777  | Ca7                                     | 12365777                      | TTATATATATATATATAT/TTATAT<br>ATATATATATATATATAT               | TTCGGGAACAGATTTT<br>GGAG | TTCAAAAGAATCGGAG<br>GAAGA | 60.0                             | 434                                           | INTRON                                            | Ca_09277                            | K                     | HSF      |
| Ca7_P4_13828258  | Ca7                                     | 13828258                      | AAAATTCAAATTCAAATT/AAAATTCA<br>AATT                           | ATATTTGGGACTGCTG<br>CGAC | GCAGGATACTTTGGGC<br>GTAA  | 60.1                             | 737                                           | INTRON                                            | Ca_16059                            | R                     | --       |
| Ca7_P4_1423751   | Ca7                                     | 1423751                       | GTAATTAATTAA/GTAATTAATTAATT<br>AA                             | CGAGCTTTAAGCCACC<br>TTTG | GGATTGACCCCTTGTC<br>CTTA  | 60.0                             | 706                                           | INTRON                                            | Ca_03325                            | --                    | --       |
| Ca7_P4_14894607  | Ca7                                     | 14894607                      | CTATATATATATAT/CTATATATATAT<br>ATAT                           | ACTCAATTCGACAAAC<br>GGGT | TGGTAAATGCAAAAGG<br>GCAT  | 59.5                             | 719                                           | INTRON                                            | Ca_09961                            | P                     | --       |
| Ca7_P4_16414718  | Ca7                                     | 16414718                      | TGTCAATAAAAT/TGTCAATAAAATA<br>TTATAGTCAATAAAAT                | GTGGTTCTTTTGTGTC<br>CGTT | GATAGCTGACGTTTGC<br>GACA  | 60.0                             | 607                                           | INTRON                                            | Ca_09848                            | --                    | --       |
| Ca7_P4_16729879  | Ca7                                     | 16729879                      | CATATATATATATATATAT/CATAT<br>ATATATATATATAT                   | GTTCCATTGATGACCC<br>TGCT | GCATTTGAATTTGAAGC<br>CGT  | 59.9                             | 403                                           | INTRON                                            | Ca_20573                            | --                    | --       |
| Ca7_P4_16881273  | Ca7                                     | 16881273                      | GAAAAAAA/GAAAAAAA                                             | TGCACAGCTGAAGTTT<br>GCAT | AAACCCACATGTAGC<br>CTCC   | 60.6                             | 383                                           | INTRON                                            | Ca_15888                            | --                    | Trihelix |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                            | Forward primers (5'-3')     | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|------------------------------------------------------------------------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                                          |                             |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_17596965  | Ca7                                     | 17596965                      | GACTTAACTTAA/GACTTAA                                                                     | CATCTATGCCACCTCC<br>ACCT    | GATCCAGAAGAAGGCT<br>GCAC  | 60.0                             | 789                                           | INTRON                                            | Ca_15849                            | --                    | --   |
| Ca7_P4_18153348  | Ca7                                     | 18153348                      | CATATATATATATATATATATAT/C<br>ATATATATATATATATATATATAT                                    | GATCGAAAGCGGGTTG<br>TTTA    | TATTTTCAAATGGTCC<br>CGC   | 60.1                             | 442                                           | INTRON                                            | Ca_22140                            | --                    | --   |
| Ca7_P4_19241060  | Ca7                                     | 19241060                      | TAATAAAATAAATAAATAAATAAC<br>ATAAAATAAATAAATAAATAAATA<br>AATAAAATAAATAACATAAATAAA<br>TAAA | TGCCTAGAACCATAGG<br>GACG    | GGTTTTCTGACTGGGT<br>GCAT  | 60.1                             | 592                                           | INTRON                                            | Ca_12331                            | ABO                   | --   |
| Ca7_P4_1932018   | Ca7                                     | 1932018                       | ACTCTCTCTCTCTCTC/ACTCTCTCT<br>CTCTCTCTC                                                  | AAGGAAGATGGTTGGC<br>AGTG    | AAGAGGCATGATGAGG<br>TTGG  | 60.1                             | 326                                           | INTRON                                            | Ca_03280                            | S                     | --   |
| Ca7_P4_19534402  | Ca7                                     | 19534402                      | TTATATATATATATATATATATATA<br>TATAT/TTATATATATATATATATA<br>TATATAT                        | GCCCAAATTCTAAATG<br>GCAA    | CACCCTCGGTCTAAAG<br>TCCA  | 59.9                             | 448                                           | INTRON                                            | Ca_12348                            | --                    | --   |
| Ca7_P4_20318275  | Ca7                                     | 20318275                      | TAAAAAAAAA/TAAAAAAAAA                                                                    | TGTTGATGATTGAGTG<br>ATCGAAG | TGCACACTCCAATACC<br>AAGG  | 60.1                             | 537                                           | INTRON                                            | Ca_12387                            | --                    | C2H2 |
| Ca7_P4_20498976  | Ca7                                     | 20498976                      | AATTTTCCATTTTC/AATTTTCCATT<br>TCCATTTTC                                                  | GATGATGTGGTCAAAC<br>GCAG    | GCACAGATGGACGGGT<br>AGAT  | 60.1                             | 615                                           | INTRON                                            | Ca_12400                            | --                    | AP2  |
| Ca7_P4_20499984  | Ca7                                     | 20499984                      | AAAATAAATAAATAAATAAATA<br>AATAAATAAATAAATAAATAA                                          | AGAAATCGACTGCGC<br>TTGT     | GGTGTGTGCATTTTCGT<br>CAAC | 60.0                             | 403                                           | INTRON                                            | Ca_12400                            | --                    | AP2  |
| Ca7_P4_20532551  | Ca7                                     | 20532551                      | TAAAAAAA/TAAAAAAA                                                                        | GGTGATGATGCACAAG<br>ATGG    | TGTGTTTTTGCTTCGGT<br>TCA  | 59.9                             | 607                                           | INTRON                                            | Ca_12402                            | --                    | --   |
| Ca7_P4_20553747  | Ca7                                     | 20553747                      | GTTTTTTTT/GTTTTTTTTT                                                                     | AGGGGAAGTGGGAA<br>GTCTA     | TTGATCCACATCAAGG<br>TCCA  | 59.9                             | 366                                           | INTRON                                            | Ca_12405                            | K                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                  |                                         |                               |                                                               |                            |                                |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| Ca7_P4_20572925  | Ca7                                     | 20572925                      | TAAAAAAAAA/TAAAAAA                                            | AATGCAAGCAACCAAA<br>AACC   | ATAGACCTGGCTGCAA<br>GGAA       | 60.0                             | 617                                           | INTRON                                            | Ca_12407                            | --                    | --      |
| Ca7_P4_20615652  | Ca7                                     | 20615652                      | TAAAAAAAAAAAAAAAAA/TAAAAA<br>AAAAAAA                          | GAGCTTTCACCTCCGC<br>AAAC   | TCATTGGAAGGGTCAA<br>AAGG       | 60.0                             | 347                                           | INTRON                                            | Ca_12414                            | --                    | MIKC    |
| Ca7_P4_21637949  | Ca7                                     | 21637949                      | GATATATATATATATATATATAT/G<br>ATATATATATATATATATATATA<br>TATAT | TGGCTCCTACAACCTCC<br>ACCT  | TCATTATGGGACAAC<br>TTTTTG      | 59.7                             | 284                                           | INTRON                                            | Ca_14515                            | U                     | --      |
| Ca7_P4_2168224   | Ca7                                     | 2168224                       | CATA/CATATA                                                   | TTCTGAGATTGGCAAA<br>AGGG   | CGCGATCGTTCACCTGA<br>TATG      | 60.2                             | 820                                           | INTRON                                            | Ca_03253                            | P                     | --      |
| Ca7_P4_2169903   | Ca7                                     | 2169903                       | T/TA                                                          | CAGGCCTTACTGCTA<br>CAGG    | CAACGGAAAACATCGT<br>TCAA       | 59.9                             | 397                                           | INTRON                                            | Ca_03253                            | P                     | --      |
| Ca7_P4_21715335  | Ca7                                     | 21715335                      | GTTTTTTTTT/GTTTTTTTTT                                         | TTTCCTTCACCTTTGT<br>TGC    | TGGGCGCTAATCTAGC<br>CTAA       | 60.1                             | 443                                           | INTRON                                            | Ca_14519                            | --                    | --      |
| Ca7_P4_21745626  | Ca7                                     | 21745626                      | TTTTATATTAT/TTTTAT                                            | ATAGGGCCCATTTTAC<br>AGCG   | CCAGTTGCCCTGTCCA<br>TACT       | 61.2                             | 455                                           | INTRON                                            | Ca_14522                            | O                     | MYB     |
| Ca7_P4_23262295  | Ca7                                     | 23262295                      | ATTTTTTTTT/ATTTTTTTTT                                         | TCCGAATTTGAACCTA<br>GTAGCA | AAATTCGTGTAATTTT<br>ATGGAGTTTT | 58.9                             | 529                                           | INTRON                                            | Ca_19506                            | E                     | BBR-BPC |
| Ca7_P4_24744404  | Ca7                                     | 24744404                      | ATT/AT                                                        | TGCGTAATCGTTGAAT<br>GTTGA  | TCGAAATCACGTTCCAA<br>ACA       | 60.1                             | 354                                           | INTRON                                            | Ca_19898                            | --                    | --      |
| Ca7_P4_28222527  | Ca7                                     | 28222527                      | CTTTTTTTTT/CTTTTTTTTTT                                        | GCGATCATGTTAAGGG<br>CAAT   | CCAAATAGTGGAACCC<br>AACA       | 59.9                             | 654                                           | INTRON                                            | Ca_26609                            | PT                    | FAR1    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')   | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|---------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                                     |                           |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca7_P4_28335175  | Ca7                                     | 28335175                      | AAAATATA/AA                                                         | GGTACTGTCTCACTGCG<br>CAAA | TCAACCAAAATCCCCCA<br>ATA      | 59.9                             | 236                                           | INTRON                                            | Ca_18921                            | --                    | --    |
| Ca7_P4_28346061  | Ca7                                     | 28346061                      | GA/GAA                                                              | GATGAAGGCGAAAGTG<br>GAAC  | GGCAAAGGGATAGACA<br>TGGA      | 59.7                             | 616                                           | INTRON                                            | Ca_18921                            | --                    | --    |
| Ca7_P4_28557231  | Ca7                                     | 28557231                      | AACCTACTTA/AACCTTA                                                  | TGCGATGGAAATGGTA<br>TTGA  | CACAACACCGAGAGAA<br>CGAA      | 59.9                             | 233                                           | INTRON                                            | Ca_18943                            | L                     | C3H   |
| Ca7_P4_28648459  | Ca7                                     | 28648459                      | TTATATATATATATATAT/TTATAT<br>ATATATATATAT                           | CCCAATTTTCAAGCCA<br>AGAA  | TTGCACATGAAGCAC<br>TGAA       | 60.0                             | 633                                           | INTRON                                            | Ca_18950                            | GC                    | HSF   |
| Ca7_P4_28698838  | Ca7                                     | 28698838                      | TTATATATATATATATATATAT/TT<br>ATATATATATATATATATAT                   | TCCACACAAAAACCCA<br>ATCA  | CCTGTGCAGAAGTTGC<br>TTGA      | 59.8                             | 691                                           | INTRON                                            | Ca_18957                            | --                    | --    |
| Ca7_P4_29666663  | Ca7                                     | 29666663                      | CATATATATATATATATATATATA<br>TATA/CATATATATATATATATATA<br>TATATATATA | AAATCATCTTCAAGGG<br>CACG  | TGCTATAATGGGATGG<br>GTGG      | 60.1                             | 442                                           | INTRON                                            | Ca_11758                            | --                    | NF-YC |
| Ca7_P4_30059154  | Ca7                                     | 30059154                      | AGG/AGGG                                                            | GTGCAGTGCTGTTTT<br>TGGA   | CAAAATTGGCAACCTGG<br>TTCT     | 60.0                             | 481                                           | INTRON                                            | Ca_11722                            | P                     | NF-YB |
| Ca7_P4_30129956  | Ca7                                     | 30129956                      | CAAAA/CAAAAA                                                        | CCACGTGAGTTACCAT<br>GCTG  | TCCACGTACGTTTAGC<br>CACC      | 60.2                             | 674                                           | INTRON                                            | Ca_11715                            | U                     | --    |
| Ca7_P4_30130333  | Ca7                                     | 30130333                      | CTTT/CT                                                             | GGTACGGTACGGTGG<br>CTAAA  | TCTCCGATCCATAATAA<br>TTGACCTA | 59.9                             | 302                                           | INTRON                                            | Ca_11715                            | U                     | --    |
| Ca7_P4_30130717  | Ca7                                     | 30130717                      | AATTATTATTATTATTATTATTAT<br>TAT/AATTATTATTATTATTATTAT<br>TTAT       | GGTACGGTACGGTGG<br>CTAAA  | TTTCAATTTAATTTGGT<br>GGCAA    | 59.9                             | 860                                           | INTRON                                            | Ca_11715                            | U                     | --    |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca7_P4_30131573  | Ca7                                     | 30131573                      | ATTTTT/ATTT                                                   | TGTTTTCGGCTAACAC<br>ATCG  | TGCAATGTCCAACCTCA<br>CTTGT | 59.7                             | 372                                           | INTRON                                            | Ca_11715                            | U                     | --          |
| Ca7_P4_30132171  | Ca7                                     | 30132171                      | AATATATATATATATATAT/AATATAT<br>ATATATATATATAT                 | GATCTCGGAGTTGCAT<br>GTGA  | TGATGACCGTGTAGGA<br>ACCA   | 59.8                             | 256                                           | INTRON                                            | Ca_11715                            | U                     | --          |
| Ca7_P4_30132559  | Ca7                                     | 30132559                      | TC/T                                                          | TGGTTCCTACACGGTC<br>ATCA  | GACCCACCCATAAAG<br>GATT    | 60.0                             | 413                                           | INTRON                                            | Ca_11715                            | U                     | --          |
| Ca7_P4_30161236  | Ca7                                     | 30161236                      | TAAAAA/TAAAAA                                                 | TTGTATTCCCATCGGA<br>GTTTG | GAGCCGACAAATTGAG<br>GAAA   | 59.8                             | 499                                           | INTRON                                            | Ca_11712                            | Q                     | B3          |
| Ca7_P4_30190946  | Ca7                                     | 30190946                      | ATTTTTTTTT/ATTTTTTT                                           | CTCAATCTCGTGGTTG<br>GACA  | GCCAACAAGCATTTC<br>CCTA    | 59.7                             | 560                                           | INTRON                                            | Ca_11709                            | U                     | --          |
| Ca7_P4_30192094  | Ca7                                     | 30192094                      | GAA/GAAA                                                      | CATCGTTGGTTGTTTG<br>GTTG  | TGCAAAAATGACTCGG<br>ACAA   | 59.9                             | 279                                           | INTRON                                            | Ca_11709                            | U                     | --          |
| Ca7_P4_30192122  | Ca7                                     | 30192122                      | TTTATTAT/TTTATTATTAT                                          | CATCGTTGGTTGTTTG<br>GTTG  | TGCAAAAATGACTCGG<br>ACAA   | 59.9                             | 279                                           | INTRON                                            | Ca_11709                            | U                     | --          |
| Ca7_P4_30208302  | Ca7                                     | 30208302                      | CGA/C                                                         | TTGGACGATGTGGATT<br>GAAA  | CCATCTCAGCATGTGT<br>TTGG   | 59.9                             | 642                                           | INTRON                                            | Ca_11706                            | --                    | --          |
| Ca7_P4_30208770  | Ca7                                     | 30208770                      | ATTT/ATT                                                      | CCAAACACATGCTGAG<br>ATGG  | CTTCCTTTGCACGACC<br>GTAT   | 60.1                             | 707                                           | INTRON                                            | Ca_11706                            | --                    | --          |
| Ca7_P4_30394911  | Ca7                                     | 30394911                      | TAAAAAAA/TAAAAAA                                              | TCATCTTCGATGCAAA<br>CCA   | TTTTCTCACCAATCAAG<br>CTGTC | 60.2                             | 783                                           | INTRON                                            | Ca_11690                            | --                    | MYB_related |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)         | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                       |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_30814492  | Ca7                                     | 30814492                      | CA/CATTCATGA                                                          | GACGCAATTTGCATGA<br>TACG | CCGACACTTGGGAGAT<br>GACT | 60.1                             | 659                                           | INTRON                                            | Ca_23321                            | O                     | --   |
| Ca7_P4_30824305  | Ca7                                     | 30824305                      | TTATATATATATATATATATATATA<br>TA/TTATATATATATATATATATAT<br>ATATATATATA | GGGAAAAGGAGTCACC<br>ACAA | GGCGCTTAAATTTTGG<br>AATG | 59.9                             | 773                                           | INTRON                                            | Ca_23321                            | O                     | --   |
| Ca7_P4_30824379  | Ca7                                     | 30824379                      | AAT/AATGAT                                                            | GGGAAAAGGAGTCACC<br>ACAA | GGCGCTTAAATTTTGG<br>AATG | 59.9                             | 773                                           | INTRON                                            | Ca_23321                            | O                     | --   |
| Ca7_P4_31201587  | Ca7                                     | 31201587                      | T/TG                                                                  | TGTCCGACATCGACAC<br>ATTT | CTCACCTGATTCCATG<br>AGCA | 60.0                             | 445                                           | INTRON                                            | Ca_10137                            | --                    | bHLH |
| Ca7_P4_31202147  | Ca7                                     | 31202147                      | TA/TAA                                                                | CATGCTCATGGAATCA<br>GGTG | ATTGGCGTTGTCCTTT<br>TTG  | 60.1                             | 370                                           | INTRON                                            | Ca_10137                            | --                    | bHLH |
| Ca7_P4_31216552  | Ca7                                     | 31216552                      | AG/AGG                                                                | GCCGTCCTGACCGTA<br>TCTT  | AACACCTGACATGTCT<br>GCCA | 60.1                             | 464                                           | INTRON                                            | Ca_10135                            | G                     | --   |
| Ca7_P4_31217391  | Ca7                                     | 31217391                      | A/AT                                                                  | GGGACAAAATTGAACT<br>GGGA | CCCTGGTGAACAGGTG<br>TCTT | 59.8                             | 938                                           | INTRON                                            | Ca_10135                            | G                     | --   |
| Ca7_P4_31217521  | Ca7                                     | 31217521                      | GATACAT/GATACATCATACT                                                 | GACCAGTGCAAAGGGA<br>TGTT | CCCTGGTGAACAGGTG<br>TCTT | 60.0                             | 460                                           | INTRON                                            | Ca_10135                            | G                     | --   |
| Ca7_P4_3186369   | Ca7                                     | 3186369                       | TTA/TTACTA                                                            | ACCACCATCCAAATCC<br>AAAA | GCGAAGGTGACGTCAA<br>AGA  | 60.0                             | 660                                           | INTRON                                            | Ca_03151                            | CR                    | NAC  |
| Ca7_P4_31969575  | Ca7                                     | 31969575                      | TAAAAAAAA/TAAAAAAAAA                                                  | ACATTTAATTGCCACT<br>GGC  | GATTGATCCTCGTCAC<br>CGTT | 59.8                             | 536                                           | INTRON                                            | Ca_10067                            | --                    | FAR1 |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_32451105  | Ca7                                     | 32451105                      | ATTTTTTTTT/ATTTTTTTTT                                         | GGAGTTCAGCAGTTCA<br>AGCC | TGAGTAGATTGCATGC<br>CAGG     | 60.0                             | 615                                           | INTRON                                            | Ca_10034                            | --                    | --  |
| Ca7_P4_32601479  | Ca7                                     | 32601479                      | A/AGGAATGCT                                                   | CAGCAACAGCGCAAAG<br>ATTA | GGATGACAAAGAAAGG<br>CCAA     | 60.2                             | 543                                           | INTRON                                            | Ca_10025                            | TU                    | --  |
| Ca7_P4_33219414  | Ca7                                     | 33219414                      | GT/GTT                                                        | GGGGAAAGTTGTCGTT<br>TTCA | AAGACCCAAAACAAAG<br>AGCTAAAA | 59.9                             | 246                                           | INTRON                                            | Ca_16150                            | --                    | --  |
| Ca7_P4_33219780  | Ca7                                     | 33219780                      | CA/CAA                                                        | GGGGAAAGTTGTCGTT<br>TTCA | GAGAAAAATTGCATG<br>CCGT      | 59.9                             | 848                                           | INTRON                                            | Ca_16150                            | --                    | --  |
| Ca7_P4_33255045  | Ca7                                     | 33255045                      | TTTGAGTTGGGTCTAAATTGAGTTG<br>GGTCTAAAT/TTTGAGTTGGGTCTAA<br>AT | GGGCCAGTTTGTAAAG<br>TGAA | TGTTTCTGAGTACCC<br>CAGC      | 60.0                             | 628                                           | INTRON                                            | Ca_16153                            | S                     | --  |
| Ca7_P4_33361891  | Ca7                                     | 33361891                      | TAAT/TAATAAAT                                                 | GAGCAAGTGCTTGGTT<br>GTGA | TAGAGGGTGACAGGGC<br>AAAC     | 60.0                             | 591                                           | INTRON                                            | Ca_16162                            | YU                    | --  |
| Ca7_P4_33366145  | Ca7                                     | 33366145                      | CTG/CTGTG                                                     | TGGGGAAAAGGTGTTT<br>TCTG | TCGTGACTGCTCAAAA<br>ATGG     | 59.9                             | 811                                           | INTRON                                            | Ca_16162                            | YU                    | --  |
| Ca7_P4_33375549  | Ca7                                     | 33375549                      | T/TC                                                          | GCTGTTGGGTTGAGCA<br>ATTT | AACCTCGATAATCACG<br>CACC     | 60.1                             | 659                                           | INTRON                                            | Ca_16163                            | --                    | --  |
| Ca7_P4_33378141  | Ca7                                     | 33378141                      | CAA/CAAAA                                                     | ACATGGGGATAAGCTC<br>AACG | TGTTATCAGTTGATGG<br>CGGA     | 60.0                             | 619                                           | INTRON                                            | Ca_16163                            | --                    | --  |
| Ca7_P4_33378174  | Ca7                                     | 33378174                      | T/TC                                                          | ACATGGGGATAAGCTC<br>AACG | TGTTATCAGTTGATGG<br>CGGA     | 60.0                             | 619                                           | INTRON                                            | Ca_16163                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                               |                          |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca7_P4_33421552  | Ca7                                     | 33421552                      | AATATATATATATATATA/AATATA<br>TATATATATATA                     | GTCTTGGGTGATGGCA<br>AAGT | GATTCTGCCTACTCAT<br>GTTTCAA | 60.0                             | 479                                           | INTRON                                            | Ca_16165                            | U                     | Dof      |
| Ca7_P4_33426751  | Ca7                                     | 33426751                      | CTTATATTATATT/CTTATATT                                        | CAAATTTACGGCAGCC<br>ACTT | CGTGCATACCCCAAGA<br>AACT    | 60.1                             | 603                                           | INTRON                                            | Ca_16165                            | U                     | Dof      |
| Ca7_P4_33457322  | Ca7                                     | 33457322                      | GAAAAAA/GAAAAAA                                               | CAACCATCCCAATCTG<br>ATCC | AATCCTGAGGGTGGGA<br>AACT    | 60.1                             | 838                                           | INTRON                                            | Ca_16167                            | Q                     | Nin-like |
| Ca7_P4_33467367  | Ca7                                     | 33467367                      | GA/GAA                                                        | GAAGATCCCTATCATC<br>GCCA | GGTTCCCATCGCTTGA<br>AGTA    | 60.0                             | 569                                           | INTRON                                            | Ca_16168                            | --                    | --       |
| Ca7_P4_33485739  | Ca7                                     | 33485739                      | ATATAT/ATATATCTTTTATAT                                        | TAGTTGCGAATGGATG<br>GTCA | ATCGGAACCCACTTCT<br>CCTT    | 60.1                             | 246                                           | INTRON                                            | Ca_16169                            | --                    | --       |
| Ca7_P4_33485861  | Ca7                                     | 33485861                      | TAGAG/TAGAGAGAGAGAG                                           | TAGTTGCGAATGGATG<br>GTCA | ATCGGAACCCACTTCT<br>CCTT    | 60.1                             | 246                                           | INTRON                                            | Ca_16169                            | --                    | --       |
| Ca7_P4_33524828  | Ca7                                     | 33524828                      | A/AAATGTC                                                     | CCGAGAACACGAGATG<br>GATT | ACCAGGTCCTTGCTGAG<br>CACT   | 60.1                             | 316                                           | INTRON                                            | Ca_16172                            | S                     | M-type   |
| Ca7_P4_33526924  | Ca7                                     | 33526924                      | A/ACGTAG                                                      | TGGCATTGGAAGAA<br>AAGG   | GATGCCACCACCTGAA<br>AGAT    | 60.0                             | 721                                           | INTRON                                            | Ca_16172                            | S                     | M-type   |
| Ca7_P4_33527005  | Ca7                                     | 33527005                      | TAATCATACAAAATCATACAA/TAA<br>TCATACAA                         | TGGCATTGGAAGAA<br>AAGG   | GATGCCACCACCTGAA<br>AGAT    | 60.0                             | 721                                           | INTRON                                            | Ca_16172                            | S                     | M-type   |
| Ca7_P4_33561568  | Ca7                                     | 33561568                      | AT/A                                                          | GGCCCTGCCTGTATAA<br>TCAA | GGATGATGTGTTGCCA<br>GATG    | 59.9                             | 541                                           | INTRON                                            | Ca_16175                            | QI                    | B3       |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)     | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                                   |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33562209  | Ca7                                     | 33562209                      | CTG/CTGTG                                                         | CATCTGGCAACACATC<br>ATCC  | TGTGACAAAGATGAGC<br>CAGG | 59.9                             | 599                                           | INTRON                                            | Ca_16175                            | QI                    | B3  |
| Ca7_P4_33618037  | Ca7                                     | 33618037                      | AT/ATT                                                            | GACCGCCGATTAACAA<br>CACT  | CGACTCCATAAATGCC<br>CTGT | 60.0                             | 392                                           | INTRON                                            | Ca_16179                            | J                     | --  |
| Ca7_P4_33642513  | Ca7                                     | 33642513                      | ATTTTTT/ATTTTT                                                    | TTCATAAAAAGGGACG<br>GCTG  | TGCACGTGATTTTCGG<br>ATTA | 60.1                             | 509                                           | INTRON                                            | Ca_16180                            | --                    | ERF |
| Ca7_P4_33642641  | Ca7                                     | 33642641                      | ATTTTTTTTTT/ATTTTTTTTTT                                           | CCAGGCAAAGCTAGGT<br>GAAC  | GGGTTCTGCTGTCAA<br>TTTT  | 59.9                             | 166                                           | INTRON                                            | Ca_16180                            | --                    | ERF |
| Ca7_P4_33643277  | Ca7                                     | 33643277                      | CAAAAAAAAA/CAAAAAAAAA                                             | CCCAATAAATGTGGG<br>GAAA   | ATCTTGTGGCCGAATT<br>GAG  | 59.5                             | 312                                           | INTRON                                            | Ca_16180                            | --                    | ERF |
| Ca7_P4_33766667  | Ca7                                     | 33766667                      | TATACTACAA/TA                                                     | TGGCAGGAAGTTTGTA<br>ACCC  | ACCCCCAAGCACTAAT<br>TTCC | 60.0                             | 533                                           | INTRON                                            | Ca_16185                            | --                    | --  |
| Ca7_P4_3377629   | Ca7                                     | 3377629                       | GTTTTTT/GTTTTTTTT                                                 | ATAACCGCAAGCAAAA<br>CCAA  | GGGGATTTTGGAGTTG<br>GAGT | 60.5                             | 649                                           | INTRON                                            | Ca_03127                            | T                     | C3H |
| Ca7_P4_3379457   | Ca7                                     | 3379457                       | AATATATATATATATATATATATAT<br>ATAT/AATATATATATATATATATATA<br>TATAT | AAAAACCATCTTGCATC<br>CTTT | TCCTTGGGCCTTGACT<br>TCTA | 57.7                             | 330                                           | INTRON                                            | Ca_03127                            | T                     | C3H |
| Ca7_P4_33795076  | Ca7                                     | 33795076                      | TAAAAAAAA/TAAAAAAAA                                               | GGTGTAAACAAAGGCC<br>CAAA  | AAGGATATGATGAAGG<br>GCCA | 59.8                             | 408                                           | INTRON                                            | Ca_16187                            | --                    | --  |
| Ca7_P4_33817388  | Ca7                                     | 33817388                      | CATAA/CATAAATAA                                                   | GCGTTTGCAATAGAAG<br>GCAT  | CTCGCGAAAAATTCAA<br>AGC  | 60.2                             | 282                                           | INTRON                                            | Ca_16190                            | E                     | --  |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_33817972  | Ca7                                     | 33817972                      | CAG/CAGAG                                                     | TCATCTCCAACCTGCA<br>GAAA  | ATGCTAGAATGTTCCG<br>TGCC | 59.4                             | 585                                           | INTRON                                            | Ca_16190                            | E                     | --  |
| Ca7_P4_33820036  | Ca7                                     | 33820036                      | GA/GATA                                                       | AGGGTATTGAGGGATG<br>GGAC  | ATAGAGCGAGCATGGC<br>AGAT | 60.0                             | 452                                           | INTRON                                            | Ca_16190                            | E                     | --  |
| Ca7_P4_33846722  | Ca7                                     | 33846722                      | T/TA                                                          | GCTGTGCTCCAACCTC<br>TTTC  | CAGCGTGCACATGGAT<br>TAGT | 60.0                             | 544                                           | INTRON                                            | Ca_16192                            | --                    | NAC |
| Ca7_P4_33846814  | Ca7                                     | 33846814                      | A/AG                                                          | GCTGTGCTCCAACCTC<br>TTTC  | CAGCGTGCACATGGAT<br>TAGT | 60.0                             | 544                                           | INTRON                                            | Ca_16192                            | --                    | NAC |
| Ca7_P4_33870660  | Ca7                                     | 33870660                      | CAAATAATTTAA/CAAA                                             | GCGGTTCCAACATGC<br>TAAT   | TGTCACCGCGGATATC<br>ATAA | 60.0                             | 180                                           | INTRON                                            | Ca_16193                            | U                     | --  |
| Ca7_P4_33877621  | Ca7                                     | 33877621                      | TACAATG/TACAATGTGTACTACAAC<br>AATG                            | TTGTGCATGTATTGGG<br>CTTG  | CGGGGGTATTCTGTG<br>AAGA  | 60.5                             | 544                                           | INTRON                                            | Ca_16194                            | O                     | --  |
| Ca7_P4_34053646  | Ca7                                     | 34053646                      | GTTTTTTTTT/GTTTTTTTTT                                         | TGTGAATGTGTGATT<br>GCTTTT | GGTCTCTTGATCTCTC<br>CCCC | 58.2                             | 859                                           | INTRON                                            | Ca_16200                            | --                    | --  |
| Ca7_P4_34080547  | Ca7                                     | 34080547                      | AT/A                                                          | AGGCAGGGGCAACTAA<br>AGAT  | TTGTGGGGGTGCTTA<br>GTTC  | 60.1                             | 446                                           | INTRON                                            | Ca_16200                            | --                    | --  |
| Ca7_P4_34087820  | Ca7                                     | 34087820                      | GAAAAAA/GAAAAAAA                                              | AACTGGAGCAACCCCT<br>TTTT  | AGGTTTTCAACCTAGC<br>GGGT | 60.0                             | 448                                           | INTRON                                            | Ca_16200                            | --                    | --  |
| Ca7_P4_34132402  | Ca7                                     | 34132402                      | TAAAAA/TAAAAA                                                 | TGTGTTCTGAAACAATC<br>GGC  | CCACATCTTCTCCCTTT<br>CCA | 59.7                             | 486                                           | INTRON                                            | Ca_21006                            | K                     | ERF |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_34136882  | Ca7                                     | 34136882                      | TCAA/TCAACAA                                                  | TTGAGTTCGTTGGCTT<br>GTTG | CTCCCGGTCTCATTCA<br>CAAT | 59.9                             | 219                                           | INTRON                                            | Ca_21006                            | K                     | ERF |
| Ca7_P4_34142469  | Ca7                                     | 34142469                      | TG/T                                                          | ACAATCCTGGTGGTT<br>GCTC  | ATTCTCCCACTACAC<br>CGC   | 60.0                             | 796                                           | INTRON                                            | Ca_21006                            | K                     | ERF |
| Ca7_P4_34143500  | Ca7                                     | 34143500                      | CA/CAA                                                        | AATGAGATGCCGATTT<br>TTGC | AATGTTACCTTGCAGG<br>ACCG | 60.0                             | 615                                           | INTRON                                            | Ca_21006                            | K                     | ERF |
| Ca7_P4_34144763  | Ca7                                     | 34144763                      | CTT/CTTT                                                      | GGCCATAGAGTCAAG<br>AAGC  | CTCACCCAAAACCTG<br>AAAA  | 60.0                             | 388                                           | INTRON                                            | Ca_21006                            | K                     | ERF |
| Ca7_P4_34152194  | Ca7                                     | 34152194                      | TAA/TAAAGAA                                                   | AAGCTTGGAGCAGGAC<br>AGAA | CTGCAAGATCGCAGGT<br>GTAA | 60.1                             | 775                                           | INTRON                                            | Ca_21006                            | K                     | ERF |
| Ca7_P4_34152239  | Ca7                                     | 34152239                      | TAAA/TAA                                                      | AAGCTTGGAGCAGGAC<br>AGAA | CTGCAAGATCGCAGGT<br>GTAA | 60.1                             | 775                                           | INTRON                                            | Ca_21006                            | K                     | ERF |
| Ca7_P4_34152655  | Ca7                                     | 34152655                      | CTG/CTGGTG                                                    | TCCCTTTAAATGCAACC<br>AGG | CGCTTATGGAGAAGCC<br>AGAT | 59.9                             | 358                                           | INTRON                                            | Ca_21006                            | K                     | ERF |
| Ca7_P4_34166530  | Ca7                                     | 34166530                      | GTTTTTTTTT/GTTTTTTTTT                                         | TATTCAGTGGGTGTAG<br>GGGC | AATCAAGAGCCCTTCC<br>CTGT | 59.8                             | 608                                           | INTRON                                            | Ca_21006                            | K                     | ERF |
| Ca7_P4_34187367  | Ca7                                     | 34187367                      | GTTTTTTTTT/GTTTTTTTTT                                         | AGGTCTGGATTCTGG<br>TTTG  | ACATCCGTGCAAGGAA<br>AAAG | 60.0                             | 646                                           | INTRON                                            | Ca_21004                            | S                     | --  |
| Ca7_P4_34187425  | Ca7                                     | 34187425                      | GAA/GAAA                                                      | AGGTCTGGATTCTGG<br>TTTG  | ACATCCGTGCAAGGAA<br>AAAG | 60.0                             | 646                                           | INTRON                                            | Ca_21004                            | S                     | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |       |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs   |
| Ca7_P4_34222603  | Ca7                                     | 34222603                      | TGGGGG/TGGGGGG                                                | TTGTTTCTCCCCAGTTT<br>TGG | GCAGTTTTGGTCCCC<br>TATT  | 59.9                             | 276                                           | INTRON                                            | Ca_20999                            | L                     | --    |
| Ca7_P4_34222973  | Ca7                                     | 34222973                      | AC/AAAATATC                                                   | GCAAACTGGGGAGAA<br>ACAA  | TCGCTTACTGGCTTCC<br>ATCT | 60.1                             | 792                                           | INTRON                                            | Ca_20999                            | L                     | --    |
| Ca7_P4_34229591  | Ca7                                     | 34229591                      | AGCTGGCTGGCTGGCTGGCTGGCT<br>GG/AGCTGGCTGGCTGGCTGG             | GCATTGGAAGCGAATG<br>GTAT | ACAGCCTGCTTTGGAA<br>CCTA | 59.9                             | 715                                           | INTRON                                            | Ca_20998                            | --                    | --    |
| Ca7_P4_34290113  | Ca7                                     | 34290113                      | T/TAG                                                         | TTTTGAACAGAACCA<br>GGGC  | GAAGAGAAAAGCCGT<br>GTTG  | 60.1                             | 362                                           | INTRON                                            | Ca_20989                            | K                     | NAC   |
| Ca7_P4_34298583  | Ca7                                     | 34298583                      | CTT/CT                                                        | CATGCTGTCACCTTTG<br>AGGA | TTGTTTGCTCTGTAGCA<br>CCG | 59.8                             | 590                                           | INTRON                                            | Ca_20988                            | --                    | NAC   |
| Ca7_P4_34300479  | Ca7                                     | 34300479                      | CAAA/CAAAA                                                    | GATGTGGCTGTTTATG<br>CCCT | CCAGCTTGCATAATTG<br>CAGA | 60.0                             | 694                                           | INTRON                                            | Ca_20988                            | --                    | NAC   |
| Ca7_P4_34350373  | Ca7                                     | 34350373                      | TAAA/TAA                                                      | AAAGAAGCGACGAATC<br>TCCA | CATGCAGGTAAATTGTT<br>GCC | 60.0                             | 599                                           | INTRON                                            | Ca_20986                            | C                     | --    |
| Ca7_P4_34351175  | Ca7                                     | 34351175                      | CT/C                                                          | TTTCGATGTCAAAATGC<br>AGG | CCACGGTTGAATGAAA<br>GGAT | 59.7                             | 493                                           | INTRON                                            | Ca_20986                            | C                     | --    |
| Ca7_P4_34351241  | Ca7                                     | 34351241                      | TAAAA/TAAA                                                    | TTTCGATGTCAAAATGC<br>AGG | CCACGGTTGAATGAAA<br>GGAT | 59.7                             | 493                                           | INTRON                                            | Ca_20986                            | C                     | --    |
| Ca7_P4_34376447  | Ca7                                     | 34376447                      | GTTTTTTTT/GTTTTTTT                                            | GGCTGCCGTGATTCTA<br>TGAT | GGTTGGTCAATTCCT<br>CCCT  | 60.1                             | 729                                           | INTRON                                            | Ca_20982                            | OUT                   | YABBY |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                               |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca7_P4_34379564  | Ca7                                     | 34379564                      | ATACTTACTTA/ATACTTA                                                           | CGGCCATTGCAATTA<br>GAAT   | CTTCGAAGCAACTCAC<br>CCTC  | 59.9                             | 604                                           | INTRON                                            | Ca_20982                            | OUT                   | YABBY       |
| Ca7_P4_34396059  | Ca7                                     | 34396059                      | TATCTTATAAAA/TATCTTATAAAATC<br>TTATAAAA                                       | GTGCCAGAGGAGGTG<br>GTAGA  | TGACATTTGGGTCAGC<br>ATGT  | 60.3                             | 944                                           | INTRON                                            | Ca_20981                            | QR                    | B3          |
| Ca7_P4_34766565  | Ca7                                     | 34766565                      | ATAATAATAATTTTAATAATAATTTTA<br>ATAATAAT/ATAATAATAATTTTAATA<br>ATAAT           | CATCCCTAAGATGCGA<br>CCAT  | AGGTTGTCCAAAGACC<br>AACG  | 59.9                             | 376                                           | INTRON                                            | Ca_17612                            | --                    | --          |
| Ca7_P4_35048654  | Ca7                                     | 35048654                      | TTATATAT/TTATATATAT                                                           | AGGTGGGCAACTTTGA<br>TGAC  | GCATCTGGCTAGGAAC<br>TTGG  | 60.0                             | 673                                           | INTRON                                            | Ca_17632                            | R                     | --          |
| Ca7_P4_3507405   | Ca7                                     | 3507405                       | AG/AGG                                                                        | AACGCGTCTCTCAAGC<br>AAAT  | TTCAGCTGCTCTGTTA<br>GCCA  | 60.0                             | 238                                           | INTRON                                            | Ca_03117                            | Z                     | MYB_related |
| Ca7_P4_35090292  | Ca7                                     | 35090292                      | GAAAAAGAAAAAGAAAAAGAAAA<br>AAGAAAAA/GAAAAAGAAAAAGAA<br>AAAAGAAAAAGAAAAAGAAAAA | TTTGCTGCATAAAACCA<br>CCA  | CTTGTGTGCTTTGCTT<br>CCA   | 60.1                             | 211                                           | INTRON                                            | Ca_17636                            | --                    | ARF         |
| Ca7_P4_3512361   | Ca7                                     | 3512361                       | AG/A                                                                          | AATTCGCATGCATATTC<br>AACA | GCAGAGATTTGATTCTG<br>AGGC | 59.0                             | 677                                           | INTRON                                            | Ca_03117                            | Z                     | MYB_related |
| Ca7_P4_3520876   | Ca7                                     | 3520876                       | AT/ATT                                                                        | GTGTTGAAAATCCGC<br>CTTA   | GGACGACGTGGATAGC<br>CTTA  | 59.9                             | 593                                           | INTRON                                            | Ca_03116                            | I                     | --          |
| Ca7_P4_3523024   | Ca7                                     | 3523024                       | GAAA/GAA                                                                      | ACTCACGAGGCCTCTT<br>CTCA  | CAGAAGGTCTTCCCAT<br>CCAA  | 60.1                             | 707                                           | INTRON                                            | Ca_03116                            | I                     | --          |
| Ca7_P4_35236069  | Ca7                                     | 35236069                      | T/TG                                                                          | GGATCAAAGCCACTCG<br>TCTC  | ATCAGGAGCCATCTCC<br>AATG  | 59.8                             | 180                                           | INTRON                                            | Ca_17642                            | --                    | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_35279048  | Ca7                                     | 35279048                      | CAGA/CA                                                       | CACGCCTTTGTACCT<br>GGTT  | TTGGAAGGACGTTGT<br>GTCA  | 60.0                             | 401                                           | INTRON                                            | Ca_17646                            | R                     | --   |
| Ca7_P4_35289603  | Ca7                                     | 35289603                      | T/TC                                                          | CGACGTCGTAACGGAT<br>TTTT | GAAGGCAGTTTGGGGA<br>CATA | 60.0                             | 841                                           | INTRON                                            | Ca_17646                            | R                     | --   |
| Ca7_P4_35290056  | Ca7                                     | 35290056                      | TT/TTATTTTCAT                                                 | TATGTCCCCAACTGC<br>CTTC  | ACGTTCTCGGCTATT<br>ATCG  | 59.9                             | 223                                           | INTRON                                            | Ca_17646                            | R                     | --   |
| Ca7_P4_35290233  | Ca7                                     | 35290233                      | TC/TCC                                                        | TATGTCCCCAACTGC<br>CTTC  | CCCAATTTTGCAATTT<br>CTGT | 59.9                             | 442                                           | INTRON                                            | Ca_17646                            | R                     | --   |
| Ca7_P4_35329400  | Ca7                                     | 35329400                      | GA/GATATA                                                     | ACATCCCTGGGGATTT<br>TCTC | CTGTTTTCGCTCTGGA<br>ATT  | 60.1                             | 883                                           | INTRON                                            | Ca_17647                            | BK                    | FAR1 |
| Ca7_P4_35330638  | Ca7                                     | 35330638                      | GA/GAA                                                        | TGCAAATACCCATCA<br>CCGA  | TCAGCCCTCTGGAAT<br>ATGG  | 59.8                             | 607                                           | INTRON                                            | Ca_17647                            | BK                    | FAR1 |
| Ca7_P4_35331304  | Ca7                                     | 35331304                      | CAAAA/CAA                                                     | GAATTTGCTTCGGAAA<br>ATCG | GCTTCCCTCAGATCAG<br>CAAC | 59.7                             | 238                                           | INTRON                                            | Ca_17647                            | BK                    | FAR1 |
| Ca7_P4_35331728  | Ca7                                     | 35331728                      | A/AG                                                          | GTTGCTGATCTGAGGG<br>AAGC | ATCTACATTGCAGGGG<br>TCCA | 60.0                             | 727                                           | INTRON                                            | Ca_17647                            | BK                    | FAR1 |
| Ca7_P4_35339612  | Ca7                                     | 35339612                      | TAAAAAAAAAAAAA/TAAAAAAAAA                                     | CAATTACCGCCTGAG<br>TCTT  | GGCTATCTCAATCGCT<br>GAGG | 60.3                             | 491                                           | INTRON                                            | Ca_17648                            | --                    | TCP  |
| Ca7_P4_35345365  | Ca7                                     | 35345365                      | A/AC                                                          | ACAAATGCACCACCTG<br>TGAA | TCTGCCATGTTTCAGC<br>CATA | 60.0                             | 504                                           | INTRON                                            | Ca_17649                            | M                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_35345432  | Ca7                                     | 35345432                      | T/TC                                                          | ACAAATGCACCACCTG<br>TGAA | AGTGTGTCAAATTTCC<br>GCC    | 60.0                             | 583                                           | INTRON                                            | Ca_17649                            | M                     | --  |
| Ca7_P4_35371175  | Ca7                                     | 35371175                      | TAGAG/TAG                                                     | AGGGCTGGCTAAACTT<br>TGGT | GGCCAAATCAGACCTT<br>CAAA   | 60.1                             | 508                                           | INTRON                                            | Ca_17651                            | --                    | --  |
| Ca7_P4_35375732  | Ca7                                     | 35375732                      | CAAAAAAAAA/CAAAAAAAAA                                         | TATTGAGGACACCACA<br>GGCA | TTGGAGAAATGGAGGT<br>TTGC   | 60.1                             | 379                                           | INTRON                                            | Ca_17651                            | --                    | --  |
| Ca7_P4_35593979  | Ca7                                     | 35593979                      | TC/TCC                                                        | ACTGCACAGCTTTTGA<br>GGGT | CTACAAGCGGCACTTC<br>ATCA   | 59.9                             | 262                                           | INTRON                                            | Ca_17767                            | --                    | --  |
| Ca7_P4_3570685   | Ca7                                     | 3570685                       | AATATAT/AATAT                                                 | CATGAGATTTTGGCAT<br>CGTG | CAAGGATTTCCCTTC<br>ACAA    | 60.1                             | 605                                           | INTRON                                            | Ca_03112                            | U                     | MYB |
| Ca7_P4_3571647   | Ca7                                     | 3571647                       | C/CAG                                                         | TGACAAATTAGCAATG<br>CCCA | CCACCACCGATAAATAT<br>TGTGA | 60.1                             | 779                                           | INTRON                                            | Ca_03112                            | U                     | MYB |
| Ca7_P4_3571890   | Ca7                                     | 3571890                       | ATTTTTTTT/ATTTTTTTT                                           | GAGACAATGTCCTCGC<br>CAAT | GTAGACCGGGGCAAGT<br>GTAA   | 60.1                             | 866                                           | INTRON                                            | Ca_03112                            | U                     | MYB |
| Ca7_P4_3580383   | Ca7                                     | 3580383                       | ATTT/ATTTT                                                    | TGTCAACAAAACCCA<br>AGCA  | TTTGACTGCTGGCTTG<br>ACTG   | 60.1                             | 339                                           | INTRON                                            | Ca_03112                            | U                     | MYB |
| Ca7_P4_3580567   | Ca7                                     | 3580567                       | GT/GTTGACTT                                                   | TGTCAACAAAACCCA<br>AGCA  | GCTGCCACATTGAAT<br>AGGT    | 60.1                             | 709                                           | INTRON                                            | Ca_03112                            | U                     | MYB |
| Ca7_P4_35879684  | Ca7                                     | 35879684                      | TAAAAAAAA/TAAAAAAAA                                           | TGCTTCCTCATAGAAC<br>GCCT | GAAACGTCCCTAAAT<br>GGGT    | 60.0                             | 484                                           | INTRON                                            | Ca_17792                            | R                     | ERF |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')   | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                     |                           |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca7_P4_3593178   | Ca7                                     | 3593178                       | ATTT/ATT                                                            | ACCCTCACCTCCTCT<br>TGAT   | GCTGGTGCCTATGGGT<br>TTTA  | 59.9                             | 608                                           | INTRON                                            | Ca_03110                            | L                     | --       |
| Ca7_P4_35933158  | Ca7                                     | 35933158                      | T/TG                                                                | TGAGACCCCGTCACAC<br>AATA  | TTTGATTCTTTTTTCGG<br>TCG  | 60.0                             | 526                                           | INTRON                                            | Ca_17798                            | T                     | M-type   |
| Ca7_P4_3629960   | Ca7                                     | 3629960                       | TTTATTA/TTTA                                                        | ATTGCCATGTGGGTCA<br>GAGT  | TGGCAACATAATGTCC<br>ATGC  | 60.4                             | 390                                           | INTRON                                            | Ca_03106                            | E                     | --       |
| Ca7_P4_3631952   | Ca7                                     | 3631952                       | TTTT/TTTTTATTT                                                      | GATAACGGCATGGAGA<br>AGGA  | TAACAACGTCCACCTG<br>CAAA  | 60.0                             | 512                                           | INTRON                                            | Ca_03106                            | E                     | --       |
| Ca7_P4_3654337   | Ca7                                     | 3654337                       | GTGGGAATCTTT/GTGGGAATCTT<br>TTCATGGGAATCTTTT                        | AAAGCAAACCTCAGCAA<br>CGGT | TATCAGAGCCTTCCATT<br>GGG  | 59.9                             | 427                                           | INTRON                                            | Ca_03103                            | U                     | LBD      |
| Ca7_P4_3654524   | Ca7                                     | 3654524                       | AACTA/AA                                                            | CCCAATGGAAGGCTCT<br>GATA  | TCCCAAGATAAATGGC<br>CAAA  | 60.0                             | 602                                           | INTRON                                            | Ca_03103                            | U                     | LBD      |
| Ca7_P4_36680795  | Ca7                                     | 36680795                      | A/ATATGT                                                            | TATTCAGATCCCTTGC<br>CCAG  | GCAAAACTTGACAGCAA<br>CAAA | 60.0                             | 959                                           | INTRON                                            | Ca_13755                            | --                    | Trihelix |
| Ca7_P4_3682108   | Ca7                                     | 3682108                       | TCGATTC/T                                                           | CCATTTGCAGATTCA<br>AGGT   | GGTGCTTTGCTACCTA<br>GCCTT | 59.9                             | 629                                           | INTRON                                            | Ca_03101                            | --                    | --       |
| Ca7_P4_3754420   | Ca7                                     | 3754420                       | GTCTCTCTCTCTCTCTCTCTCTC<br>TCT/GTCTCTCTCTCTCTCTCTCT<br>CTCTCTCTCTCT | AAATCGACGGCCACAG<br>ATAC  | CACAATGTCCATGCTC<br>CAAC  | 60.0                             | 703                                           | INTRON                                            | Ca_03092                            | BK                    | --       |
| Ca7_P4_38806740  | Ca7                                     | 38806740                      | GAAAAAA/GAAAAAAA                                                    | TGAGTGCCATTTTTCAT<br>CCA  | CATGGGAGAAGATTTC<br>AGGC  | 60.0                             | 932                                           | INTRON                                            | Ca_16429                            | QR                    | B3       |





| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca7_P4_5388602   | Ca7                                     | 5388602                       | CTATATA/CTATA                                                 | CAACCTGTGACTCCCA<br>ACCT | GGAGTTTGAATTCGT<br>TTGG  | 60.0                             | 398                                           | INTRON                                            | Ca_06831                            | R                     | --          |
| Ca7_P4_5398119   | Ca7                                     | 5398119                       | GTTT/GTT                                                      | CATGGATTGCATTGT<br>TCG   | TTGAATCAGCTCAGCC<br>AGTG | 59.9                             | 752                                           | INTRON                                            | Ca_06830                            | R                     | --          |
| Ca7_P4_5398164   | Ca7                                     | 5398164                       | CA/CAA                                                        | CATGGATTGCATTGT<br>TCG   | TTGAATCAGCTCAGCC<br>AGTG | 59.9                             | 752                                           | INTRON                                            | Ca_06830                            | R                     | --          |
| Ca7_P4_5400562   | Ca7                                     | 5400562                       | A/AC                                                          | CAACCAGATTCAGGGA<br>GGAA | AAGATCATAGTGGTTG<br>GCGG | 60.0                             | 718                                           | INTRON                                            | Ca_06830                            | R                     | --          |
| Ca7_P4_5415131   | Ca7                                     | 5415131                       | GTT/GTTT                                                      | ATCATCTTGGCATTGC<br>CTTT | AGCCTCAGAACCTTCA<br>CCAA | 59.5                             | 449                                           | INTRON                                            | Ca_06827                            | T                     | WRKY        |
| Ca7_P4_5424613   | Ca7                                     | 5424613                       | TAAAAAAAA/TAAAAAAAAA                                          | ACCTAAAGATCGGGAG<br>GTGG | GCGAGTTTACGTTGAC<br>CCAT | 60.3                             | 593                                           | INTRON                                            | Ca_06826                            | K                     | MYB_related |
| Ca7_P4_5467811   | Ca7                                     | 5467811                       | AA/AATCGAAATTCCA                                              | AACTCGGTGAGCCTCT<br>CAAA | ATACGTTTTTCCAAGGT<br>GCG | 60.0                             | 253                                           | INTRON                                            | Ca_06820                            | --                    | --          |
| Ca7_P4_5473218   | Ca7                                     | 5473218                       | AC/ACC                                                        | GGTGCAATTGGGACAC<br>TCAT | CTGCAACGTGCAAACA<br>GAAT | 60.8                             | 391                                           | INTRON                                            | Ca_06819                            | P                     | --          |
| Ca7_P4_5488147   | Ca7                                     | 5488147                       | TATTAATTAATT/TATTAATTAATTAA<br>TT                             | AACCTCCTTTTCCGTC<br>CCT  | CATTCCACAGCCTCCA<br>TTTT | 60.0                             | 781                                           | INTRON                                            | Ca_06817                            | CIQ                   | --          |
| Ca7_P4_5531129   | Ca7                                     | 5531129                       | CAAAAAAAAA/CAAAAAAAAA                                         | AATCAAATCACTCTCG<br>GCG  | CAATGGGTCTTCATT<br>GCT   | 60.2                             | 656                                           | INTRON                                            | Ca_06812                            | G                     | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca7_P4_5569644   | Ca7                                     | 5569644                       | GTGCCTATGCC/GTGCC                                             | GTCTGGAGCTTCTCCC<br>TGTG | AAGGTTTGAAGGGAA<br>CGGT  | 60.0                             | 468                                           | INTRON                                            | Ca_06806                            | --                    | --          |
| Ca7_P4_5570021   | Ca7                                     | 5570021                       | TG/T                                                          | CTAACACGTGCCTATG<br>CCCT | CAACACCGTCAGAAAG<br>CTCA | 60.2                             | 797                                           | INTRON                                            | Ca_06806                            | --                    | --          |
| Ca7_P4_5686600   | Ca7                                     | 5686600                       | CAAAAAAAAA/CAAAAAAAAA                                         | TTCCAGTCTCAGTGTG<br>ACGC | GATCAACGGGCACAGT<br>GTTA | 60.0                             | 957                                           | INTRON                                            | Ca_06788                            | Q                     | --          |
| Ca7_P4_5686646   | Ca7                                     | 5686646                       | T/TC                                                          | ATTATAACACCGGCTC<br>GCAC | GGTCCAGGATTCCAGA<br>TCAA | 60.0                             | 657                                           | INTRON                                            | Ca_06788                            | Q                     | --          |
| Ca7_P4_5686702   | Ca7                                     | 5686702                       | AGGG/AGG                                                      | ATTATAACACCGGCTC<br>GCAC | AATACCGGGCTTCACA<br>TCAG | 60.0                             | 728                                           | INTRON                                            | Ca_06788                            | Q                     | --          |
| Ca7_P4_5719975   | Ca7                                     | 5719975                       | ATGCTATTGCTATTGCTAT/ATGCTA<br>TTGCTATTGCTATTGCTAT             | TTGGAAACACACAGAC<br>CCAA | AAACCAAAGAGCCAGA<br>AGCA | 60.0                             | 806                                           | INTRON                                            | Ca_06785                            | R                     | FAR1        |
| Ca7_P4_5722804   | Ca7                                     | 5722804                       | A/AC                                                          | TGGGACAGTGAGTCAA<br>TCCA | TCCGATTTTGTCTCTCG<br>ACT | 60.1                             | 191                                           | INTRON                                            | Ca_06785                            | R                     | FAR1        |
| Ca7_P4_5724180   | Ca7                                     | 5724180                       | CA/C                                                          | TCITTAATTGGCTTGTG<br>GGG | AAGTGATTTAGCCAC<br>CACC  | 59.9                             | 347                                           | INTRON                                            | Ca_06785                            | R                     | FAR1        |
| Ca7_P4_5725732   | Ca7                                     | 5725732                       | GTT/G                                                         | AACAAAGGCCTCAAA<br>ACCT  | TTGCCTTCTTTGGATT<br>GCT  | 60.0                             | 794                                           | INTRON                                            | Ca_06785                            | R                     | FAR1        |
| Ca7_P4_5732084   | Ca7                                     | 5732084                       | GAAAAA/GAAAAAA                                                | GTCTGCTGACATGCCT<br>TGAA | CAATGCTTGAAAAAGC<br>AGCA | 60.0                             | 759                                           | INTRON                                            | Ca_06784                            | --                    | MYB_related |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_5774898   | Ca7                                     | 5774898                       | AC/A                                                          | TGAGTACACTCACCAC<br>CCCA | TGCAGCTGCTGGGTAT<br>TATG | 60.0                             | 528                                           | INTRON                                            | Ca_06781                            | R                     | --   |
| Ca7_P4_5775273   | Ca7                                     | 5775273                       | CAAAAA/CAAAAAA                                                | GGTCAATGGCTGAAGG<br>GATA | TCCACCAACACTGAAT<br>CCAA | 59.9                             | 901                                           | INTRON                                            | Ca_06781                            | R                     | --   |
| Ca7_P4_5778946   | Ca7                                     | 5778946                       | CTTT/CT                                                       | GCTGAAGCCAGTTTCT<br>GGAC | CACACCAACCAAGCA<br>ACAC  | 60.0                             | 458                                           | INTRON                                            | Ca_06780                            | F                     | --   |
| Ca7_P4_5779009   | Ca7                                     | 5779009                       | ATTTTTTTT/ATTTTTTTTT                                          | GCTGAAGCCAGTTTCT<br>GGAC | CACACCAACCAAGCA<br>ACAC  | 60.0                             | 458                                           | INTRON                                            | Ca_06780                            | F                     | --   |
| Ca7_P4_5832989   | Ca7                                     | 5832989                       | ATAAGT/ATAAGTAAGT                                             | TAGTGGCAAATTTGAA<br>GGGG | TATGCCCAAGTAATGC<br>CACA | 59.9                             | 337                                           | INTRON                                            | Ca_06776                            | --                    | --   |
| Ca7_P4_5835855   | Ca7                                     | 5835855                       | GTTT/GTTTTTT                                                  | AGGGAGCTGGGTTTGA<br>AGAT | ACAACAACATGGCAA<br>CCAA  | 60.1                             | 831                                           | INTRON                                            | Ca_06776                            | --                    | --   |
| Ca7_P4_5854578   | Ca7                                     | 5854578                       | GAGTAGT/GAGTAGTAGT                                            | TGTTGTTTGCAGCCTT<br>TCTG | CAACCTTTGCAACCAC<br>AATG | 60.0                             | 301                                           | INTRON                                            | Ca_06772                            | K                     | --   |
| Ca7_P4_5907905   | Ca7                                     | 5907905                       | GTTCAGATATACTTC/GTTCAGATAT<br>ACTTCAGATATACTTC                | GGGGTGCAACTTTCAA<br>GGTA | CAGAACTGTTGCACCT<br>TCCA | 60.0                             | 354                                           | INTRON                                            | Ca_06768                            | --                    | --   |
| Ca7_P4_5924805   | Ca7                                     | 5924805                       | TATAATAATAATAATA/TATAATAAT<br>AATAATAATAA                     | TGGACTGACCAACCAA<br>ACAA | TTTTTAACGGAGATGC<br>CTCG | 60.0                             | 848                                           | INTRON                                            | Ca_06765                            | S                     | --   |
| Ca7_P4_5931727   | Ca7                                     | 5931727                       | TAAAAAAAAAAAAAAAAA/TAAAAAAAAA<br>AA                           | AGGAAAGTGAAGGAGA<br>CGCA | TTCATCCTTTGGAAGAT<br>GGC | 60.0                             | 795                                           | INTRON                                            | Ca_06764                            | P                     | GRAS |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca7_P4_5947080   | Ca7                                     | 5947080                       | CCA/CCACA                                                     | AGGCTAACGTTGCTTT<br>TCCA | GCTTCCTCTGAGTGCA<br>CCTT | 59.9                             | 572                                           | INTRON                                            | Ca_06762                            | L                     | --  |
| Ca7_P4_5950738   | Ca7                                     | 5950738                       | T/TC                                                          | TGCAGCTTCAAGGTTT<br>GTTG | AGGGCGCTTATCTGAT<br>TGAA | 60.0                             | 774                                           | INTRON                                            | Ca_06762                            | L                     | --  |
| Ca7_P4_5951052   | Ca7                                     | 5951052                       | GTTTT/GTTT                                                    | TTTGCTTAGTCCTGG<br>ATGC  | CGAAACTTCGAAACCG<br>GTAA | 60.2                             | 986                                           | INTRON                                            | Ca_06762                            | L                     | --  |
| Ca7_P4_5955426   | Ca7                                     | 5955426                       | C/A/C                                                         | TTCCAATCACTTTGG<br>CTTC  | ATTGTGGCACTAGTGG<br>AGGG | 60.1                             | 947                                           | INTRON                                            | Ca_06761                            | A                     | AP2 |
| Ca7_P4_5979920   | Ca7                                     | 5979920                       | TG/TGG                                                        | ATGAAATGCACCAAAA<br>AGCC | TGGTGAGAATGTGGAA<br>GCTG | 59.9                             | 614                                           | INTRON                                            | Ca_06760                            | --                    | --  |
| Ca7_P4_5982890   | Ca7                                     | 5982890                       | AGG/AG                                                        | AGCTTTTGTCCAACCT<br>CTGA | AGCGGCTTGCACTACA<br>AATC | 60.0                             | 450                                           | INTRON                                            | Ca_06760                            | --                    | --  |
| Ca7_P4_5989176   | Ca7                                     | 5989176                       | GATACA/GA                                                     | TGCTCTAACTGAAGG<br>GGGA  | GTTTCGTGGACAAGAC<br>GGAT | 59.8                             | 311                                           | INTRON                                            | Ca_06760                            | --                    | --  |
| Ca7_P4_5992633   | Ca7                                     | 5992633                       | GC/G                                                          | AACGCAATCCATGACA<br>AACA | GTATGCTCTGTTTCCC<br>CCAA | 60.0                             | 497                                           | INTRON                                            | Ca_06760                            | --                    | --  |
| Ca7_P4_5994230   | Ca7                                     | 5994230                       | CAAAAAA/CAAAAAA                                               | TTCTGCGCTCATCTA<br>ATCG  | GTTGGTTTGGATGGAA<br>ATGG | 60.2                             | 179                                           | INTRON                                            | Ca_06760                            | --                    | --  |
| Ca7_P4_6013865   | Ca7                                     | 6013865                       | TAAAAAAA/TAAAAAAA                                             | GCGGGATTGTCACTT<br>AACC  | TTTGCTTCTCCTCCTT<br>GAA  | 59.4                             | 961                                           | INTRON                                            | Ca_06758                            | R                     | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)            | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                          |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca7_P4_6014043   | Ca7                                     | 6014043                       | T/TTA                                                                    | GCATTTAGTTGAAACG<br>TGGGA  | CGGCTATGACGTTGGA<br>ATTT  | 60.0                             | 596                                           | INTRON                                            | Ca_06758                            | R                     | --   |
| Ca7_P4_6024790   | Ca7                                     | 6024790                       | GAAAAAA/GAAAAAAA                                                         | TCTCGATAGAAAACGT<br>GGAAA  | TTTCGACCCCTCTCTTT<br>TAGG | 57.5                             | 918                                           | INTRON                                            | Ca_06757                            | R                     | --   |
| Ca7_P4_6025144   | Ca7                                     | 6025144                       | GAAAAA/GAAAA                                                             | GAACGCAAGAGCTAAA<br>AGAAAA | AGGGCAGAGCAATACA<br>ATGG  | 59.3                             | 597                                           | INTRON                                            | Ca_06757                            | R                     | --   |
| Ca7_P4_6037108   | Ca7                                     | 6037108                       | ATTTTT/ATTTT                                                             | ACACGTTGACACCACT<br>GCAT   | GGTCTCTCTACAAGC<br>GTCC   | 60.1                             | 569                                           | INTRON                                            | Ca_06755                            | A                     | --   |
| Ca7_P4_6038795   | Ca7                                     | 6038795                       | TAAAAA/TAAAAA                                                            | ATAGTATGGCCGCAAA<br>CCAG   | AAGCATGTTTCTCGGT<br>GTCC  | 60.0                             | 763                                           | INTRON                                            | Ca_06755                            | A                     | --   |
| Ca7_P4_6071004   | Ca7                                     | 6071004                       | CGAAGAACATTTAGAGGAAGAACA/<br>CGAAGAACATTTAGAGGAAGAACAT<br>TTAGAGGAAGAACA | TCAAAGCGATCACACC<br>ATGT   | TTGCCCTATATTTTGCC<br>TCG  | 60.1                             | 724                                           | INTRON                                            | Ca_06752                            | T                     | bZIP |
| Ca7_P4_6089215   | Ca7                                     | 6089215                       | TAA/TA                                                                   | CAAGAAACCTCCAACC<br>CAAA   | TGGCTTCTCTTGCTGA<br>TCCT  | 59.9                             | 430                                           | INTRON                                            | Ca_06750                            | O                     | --   |
| Ca7_P4_6089357   | Ca7                                     | 6089357                       | AATATGATAT/AATAT                                                         | CAAGAAACCTCCAACC<br>CAAA   | TGGCTTCTCTTGCTGA<br>TCCT  | 59.9                             | 430                                           | INTRON                                            | Ca_06750                            | O                     | --   |
| Ca7_P4_6089455   | Ca7                                     | 6089455                       | GAT/GAAAAATAACTAAT                                                       | CAAGAAACCTCCAACC<br>CAAA   | TGGCTTCTCTTGCTGA<br>TCCT  | 59.9                             | 430                                           | INTRON                                            | Ca_06750                            | O                     | --   |
| Ca7_P4_6100952   | Ca7                                     | 6100952                       | CTTTTTTTTT/CTTTTTTTT                                                     | TATTGCATGTTTGACG<br>GCAT   | CGGACTCCCCCTTTTT<br>ATTC  | 60.0                             | 558                                           | INTRON                                            | Ca_06748                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)       | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                     |                          |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca7_P4_6116383   | Ca7                                     | 6116383                       | GAAAAAAAAA/GAAAAAAAAA                                               | TGGAAAACTTTTGATG<br>CCA  | CATGTGTGTCCAAGAG<br>GGTG   | 59.1                             | 352                                           | INTRON                                            | Ca_06745                            | T                     | MYB_related |
| Ca7_P4_6710088   | Ca7                                     | 6710088                       | AAGAGAGAGAGAGAGAGAGAGA<br>GAGA/AAGAGAGAGAGAGAGAGAG<br>AGAGAGAGAGAGA | GCCATCCGATCAAAAC<br>AAGT | CAAAGGCAAAATTCGT<br>GGT    | 59.9                             | 839                                           | INTRON                                            | Ca_06690                            | R                     | --          |
| Ca7_P4_7929425   | Ca7                                     | 7929425                       | ATTTTTTT/ATTTTTTTT                                                  | AACCATTGCGACCCAA<br>TATC | TAACCCCATGATTTC<br>CAA     | 59.7                             | 824                                           | INTRON                                            | Ca_13226                            | --                    | --          |
| Ca7_P4_8166903   | Ca7                                     | 8166903                       | CAAAAAAAAA/CAAAAAAAAAA                                              | ACTCTAGGCAAAACGG<br>CAGA | AAACGCACCTTGTTTC<br>CAAC   | 60.0                             | 645                                           | INTRON                                            | Ca_13198                            | --                    | ERF         |
| Ca7_P4_8167116   | Ca7                                     | 8167116                       | TAAAAAAAA/TAAAAAAAA                                                 | ACTCTAGGCAAAACGG<br>CAGA | AAACGCACCTTGTTTC<br>CAAC   | 60.0                             | 645                                           | INTRON                                            | Ca_13198                            | --                    | ERF         |
| Ca7_P4_9823411   | Ca7                                     | 9823411                       | AATATATATATATATATAT/AATAT<br>ATATATATATATATATATAT                   | GTTCAAACCTCGTTGC<br>CTCT | TGGCAACTATCCATAAT<br>GAAGC | 59.3                             | 763                                           | INTRON                                            | Ca_12747                            | G                     | --          |
| Ca8_P4_10381692  | Ca8                                     | 10381692                      | AGG/AGGG                                                            | CGTTTCCTCTGCCTCT<br>TGAC | TTGTGAAAAACGAGCA<br>CGAC   | 60.0                             | 677                                           | INTRON                                            | Ca_18429                            | R                     | NAC         |
| Ca8_P4_1080030   | Ca8                                     | 1080030                       | TAAAAAAAAAAAA/TAAAAAAAAAA                                           | ACATGATTGCAAAAA<br>GCCC  | AAGGTATCCAACACA<br>GCGG    | 59.9                             | 457                                           | INTRON                                            | Ca_15076                            | CR                    | NAC         |
| Ca8_P4_11066480  | Ca8                                     | 11066480                      | AATATATATA/AATATATATATA                                             | TTTGGCATGGAACAAC<br>ATTC | ATTATTGCGCCAAAAAT<br>TCG   | 59.4                             | 785                                           | INTRON                                            | Ca_16843                            | R                     | B3          |
| Ca8_P4_11066722  | Ca8                                     | 11066722                      | ATT/AT                                                              | ATGGTTCTCCTTTCTG<br>GCCT | ATTATTGCGCCAAAAAT<br>TCG   | 60.1                             | 249                                           | INTRON                                            | Ca_16843                            | R                     | B3          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca8_P4_11191354  | Ca8                                     | 11191354                      | CGGG/CGG                                                      | GTGTCCTGAGTTAAGG<br>CCCA  | CTTTATGTCGTGTGGC<br>ATGG | 60.1                             | 889                                           | INTRON                                            | Ca_16839                            | R                     | MYB  |
| Ca8_P4_11359890  | Ca8                                     | 11359890                      | TC/T                                                          | CTCGAAAATTAGGCGA<br>GCAG  | CACGTGCATGACCCTA<br>AATG | 60.1                             | 605                                           | INTRON                                            | Ca_16822                            | G                     | NAC  |
| Ca8_P4_11546931  | Ca8                                     | 11546931                      | T/TCG                                                         | GCCATGTTCAGTCTTG<br>GTCA  | ACTCCACCATTGCTTG<br>CTTT | 59.7                             | 247                                           | INTRON                                            | Ca_16811                            | --                    | --   |
| Ca8_P4_12016131  | Ca8                                     | 12016131                      | ACCCC/ACCCCC                                                  | CAACTCTCGTCGCAAC<br>TCAA  | ATGCAACTTGGGAATT<br>GGAG | 60.2                             | 362                                           | INTRON                                            | Ca_23846                            | T                     | --   |
| Ca8_P4_14120816  | Ca8                                     | 14120816                      | ATAA/ATAATTAA                                                 | TTCTAGGGCCATTTC<br>TCCT   | TTTGCTTGGCCTCAG<br>CTTT  | 60.0                             | 455                                           | INTRON                                            | Ca_13048                            | --                    | GRAS |
| Ca8_P4_14121334  | Ca8                                     | 14121334                      | ATAATATTAATATTAATTAATA/AT<br>AATATTAATATTAATATTAATATTAAT<br>A | AAGCTGAGGCCAAGAC<br>AAAA  | TCGTGAGGAATCAAAG<br>ACCA | 60.0                             | 280                                           | INTRON                                            | Ca_13048                            | --                    | GRAS |
| Ca8_P4_14127063  | Ca8                                     | 14127063                      | A/AC                                                          | TCCAACTGAAACACAG<br>CACAG | TGGCCTTCTCTGGAGA<br>TTTG | 59.9                             | 154                                           | INTRON                                            | Ca_13047                            | T                     | B3   |
| Ca8_P4_14142739  | Ca8                                     | 14142739                      | CTTTT/CTT                                                     | TGACTGCGAGTCGAAC<br>CATA  | TAGGAGTGCCTGTTGT<br>GCTG | 60.4                             | 523                                           | INTRON                                            | Ca_13045                            | --                    | --   |
| Ca8_P4_14252510  | Ca8                                     | 14252510                      | C/CG                                                          | AATCTATATGCACCGC<br>CGAC  | CGCAACATTTGCATAAC<br>TGC | 60.0                             | 547                                           | INTRON                                            | Ca_13038                            | --                    | --   |
| Ca8_P4_14334094  | Ca8                                     | 14334094                      | CAAAAAA/CAAAAAA                                               | GCAAAGGTACTCCTGC<br>TCCA  | ACAACACCTTTGGTTC<br>CAGC | 60.4                             | 725                                           | INTRON                                            | Ca_13031                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca8_P4_14334449  | Ca8                                     | 14334449                      | AC/A                                                          | CAATAGCCGTGTTGAA<br>ATGC  | ACAACACCTTTGGTTC<br>CAGC | 59.2                             | 468                                           | INTRON                                            | Ca_13031                            | --                    | --          |
| Ca8_P4_14344611  | Ca8                                     | 14344611                      | TAAAAA/TAAAAA                                                 | TTGAACAAGTGTCTAA<br>GGGCA | GTTGAGCTGGGAGTTG<br>GAAA | 58.4                             | 538                                           | INTRON                                            | Ca_13030                            | T                     | bHLH        |
| Ca8_P4_14345244  | Ca8                                     | 14345244                      | GAAAATGAAAATGAAA/GAAAATGA<br>AAAATGAAAATGAAAATGAAA            | TTTCCAACCTCCAGCT<br>CAAC  | GCAAGGTCGTGGAGAA<br>ACAT | 60.2                             | 726                                           | INTRON                                            | Ca_13030                            | T                     | bHLH        |
| Ca8_P4_14578122  | Ca8                                     | 14578122                      | GTAATAA/GTAATAATAA                                            | TCGCTCGATTCTTCG<br>TCTT   | TTTGCTGAAAGGTTT<br>CTGG  | 60.1                             | 481                                           | INTRON                                            | Ca_13009                            | Z                     | MYB_related |
| Ca8_P4_14583961  | Ca8                                     | 14583961                      | AT/ATATT                                                      | GTTGAAATACGCCGT<br>CAAT   | TGGATCTGCGAACAAA<br>CTCA | 60.1                             | 778                                           | INTRON                                            | Ca_13009                            | Z                     | MYB_related |
| Ca8_P4_14632313  | Ca8                                     | 14632313                      | CTTTTT/CTTTT                                                  | TGTGTTCTGGCCAAT<br>ACAA   | AGCTGTAAAAGAGGGA<br>GGGC | 60.0                             | 412                                           | INTRON                                            | Ca_13004                            | --                    | --          |
| Ca8_P4_14636009  | Ca8                                     | 14636009                      | GATATATATATATATATATATATA<br>T/GATATATATATATATATATAT           | TTTGCAGGAAGCAAAC<br>ACTG  | GGATAATCCGGGATGC<br>CTAT | 60.0                             | 587                                           | INTRON                                            | Ca_13004                            | --                    | --          |
| Ca8_P4_14705254  | Ca8                                     | 14705254                      | AATTTTATTTTAT/AATTTTAT                                        | TAGAGGGACCAAACT<br>GCAA   | CCAGGCGTAATTTTGG<br>AAAC | 58.4                             | 366                                           | INTRON                                            | Ca_12998                            | R                     | SBP         |
| Ca8_P4_14711252  | Ca8                                     | 14711252                      | AATAACATAACATAACAT/AATAACA<br>TAACAT                          | CTTGGCGAGGAAAGAA<br>CAAG  | ATGTGAAACAAACCGC<br>ATGA | 60.0                             | 508                                           | INTRON                                            | Ca_12997                            | T                     | --          |
| Ca8_P4_14712571  | Ca8                                     | 14712571                      | ATTTTTT/ATTTTT                                                | GAAGGAACTCTCAAG<br>GGGG   | GCAAGAAGCCGAACAG<br>AATC | 60.0                             | 349                                           | INTRON                                            | Ca_12997                            | T                     | --          |



| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')      | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|------------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                  |                                         |                               |                                                               |                              |                             |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| Ca8_P4_14722366  | Ca8                                     | 14722366                      | GCAAACAAAC/GCAAAC                                             | TCCTCGCAATGAAATG<br>TCTG     | ATTCGGAAACAAATGG<br>TGGA    | 59.8                             | 668                                           | INTRON                                            | Ca_12995                            | O                     | NAC |
| Ca8_P4_14723674  | Ca8                                     | 14723674                      | CTCAAATA/CTCAAATAAACCAATTC<br>AAATA                           | CAACGAGACCTAGCCC<br>AGAA     | CAAAAGAGGCGTACCG<br>TGAT    | 60.4                             | 405                                           | INTRON                                            | Ca_12995                            | O                     | NAC |
| Ca8_P4_14727145  | Ca8                                     | 14727145                      | TA/TAA                                                        | CATTGTGAAGTGTGAG<br>TGGGA    | TTGGTTAAGGTGGTTA<br>TGATTGG | 59.6                             | 690                                           | INTRON                                            | Ca_12995                            | O                     | NAC |
| Ca8_P4_14727306  | Ca8                                     | 14727306                      | TAA/T                                                         | TTGAACTCTTAATTTCA<br>TCGAACA | TTGGTTAAGGTGGTTA<br>TGATTGG | 58.0                             | 192                                           | INTRON                                            | Ca_12995                            | O                     | NAC |
| Ca8_P4_14733700  | Ca8                                     | 14733700                      | ATTTTTTTTT/ATTTTTTTTT                                         | TCTGAACGAAGTTGGA<br>GCAA     | GGTATGTTTGTGTTGAA<br>GGGG   | 59.6                             | 787                                           | INTRON                                            | Ca_12995                            | O                     | NAC |
| Ca8_P4_14735110  | Ca8                                     | 14735110                      | T/TAGAACAA                                                    | CAGGGACAACTTGGTC<br>AAGAA    | AAATGGTGTGGGGGT<br>GTAA     | 60.1                             | 704                                           | INTRON                                            | Ca_12995                            | O                     | NAC |
| Ca8_P4_14741320  | Ca8                                     | 14741320                      | AG/A                                                          | CGATGAAATCAAACAA<br>AACTCG   | AGAGCCATCATCCTTT<br>CCA     | 59.6                             | 186                                           | INTRON                                            | Ca_12995                            | O                     | NAC |
| Ca8_P4_14742015  | Ca8                                     | 14742015                      | AATATATATATATA/AATATATATATA<br>TATATATATA                     | TTGGTGGTTGATCATA<br>CGAGAG   | GCCAAGAAATAGCCAC<br>TTGC    | 60.0                             | 645                                           | INTRON                                            | Ca_12995                            | O                     | NAC |
| Ca8_P4_14742163  | Ca8                                     | 14742163                      | T/TGA                                                         | TGGTGGTTGATCATA<br>GAGAG     | GCCAAGAAATAGCCAC<br>TTGC    | 58.6                             | 644                                           | INTRON                                            | Ca_12995                            | O                     | NAC |
| Ca8_P4_14746760  | Ca8                                     | 14746760                      | ATTCA/ATTCATTATTTTCA                                          | TGGATCTCATCCTCAT<br>CCCT     | TTGAAGTGCTTTTGGT<br>GCTG    | 59.4                             | 573                                           | INTRON                                            | Ca_12994                            | --                    | --  |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                 | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                                               |                           |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca8_P4_14750887  | Ca8                                     | 14750887                      | GTTTTTTT/GTTTTTTT                                                             | ACTCAAAAACCGTGGA<br>CTCG  | GGCACTTGGTTGGTCT<br>TCAT | 60.1                             | 781                                           | INTRON                                            | Ca_12994                            | --                    | --   |
| Ca8_P4_14751069  | Ca8                                     | 14751069                      | AAATTTCTTAAATAATTTCTTAAAA<br>TAAT/AAATTTCTTAAATAAT                            | ACTCAAAAACCGTGGA<br>CTCG  | GGCACTTGGTTGGTCT<br>TCAT | 60.1                             | 781                                           | INTRON                                            | Ca_12994                            | --                    | --   |
| Ca8_P4_14751128  | Ca8                                     | 14751128                      | TC/T                                                                          | TGATGCGTTGATAGTG<br>TTGG  | GGCACTTGGTTGGTCT<br>TCAT | 58.1                             | 619                                           | INTRON                                            | Ca_12994                            | --                    | --   |
| Ca8_P4_14806329  | Ca8                                     | 14806329                      | AGT/A                                                                         | GAGGGGAGGAGAGTA<br>GGGAA  | TATTGCTATTGTTGCAG<br>CCG | 59.6                             | 579                                           | INTRON                                            | Ca_12988                            | F                     | --   |
| Ca8_P4_14821532  | Ca8                                     | 14821532                      | T/TC                                                                          | GCATTGATTTCAACATT<br>CCC  | CATAGTCGGGTCGACC<br>TTGT | 60.1                             | 457                                           | INTRON                                            | Ca_12987                            | D                     | bHLH |
| Ca8_P4_14932583  | Ca8                                     | 14932583                      | GAAAAAAAAA/GAAAAAAAAA                                                         | CACCATTCTCCTTCAAC<br>CAAA | AACCACGCGACTCATA<br>CACA | 60.0                             | 716                                           | INTRON                                            | Ca_12980                            | P                     | MIKC |
| Ca8_P4_15110296  | Ca8                                     | 15110296                      | GTTGGTTAGTAACCTGGT/GTTGGT<br>TAGTAACCTGGTTAGTAACCTGGT                         | CCTGTTTTGGATGTTG<br>GGAC  | CCATCAACAAATCCAC<br>AGC  | 60.2                             | 762                                           | INTRON                                            | Ca_12966                            | Q                     | --   |
| Ca8_P4_1563813   | Ca8                                     | 1563813                       | ACC/AC                                                                        | AACTTTGGGAATTTTG<br>GGG   | AATTTACCTGCCCAAAA<br>GGG | 60.0                             | 987                                           | INTRON                                            | Ca_15013                            | T                     | FAR1 |
| Ca8_P4_15694311  | Ca8                                     | 15694311                      | GTATATATATATATATATATATATAT<br>ATATATATA/GTATATATATATATATA<br>TATATATATATATATA | CCGTCTCTTTCACATG<br>GGTT  | AAAGGCTCGGGTCAGT<br>CATA | 60.0                             | 438                                           | INTRON                                            | Ca_17876                            | A                     | --   |
| Ca8_P4_15696307  | Ca8                                     | 15696307                      | GTTTTTTTTTTTT/GTTTTTTTTTTTT<br>TTTTTT                                         | ATATCCCTCCGCACT<br>CTCT   | CATCAAAGTCACCTCC<br>AGCA | 60.1                             | 456                                           | INTRON                                            | Ca_17876                            | A                     | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                         | Forward primers (5'-3')   | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------|---------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                  |                                         |                               |                                                                                       |                           |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| Ca8_P4_15731151  | Ca8                                     | 15731151                      | ATTTTTTTTTT/ATTTTTTTTTT                                                               | TCATTTTGGCTAAAGG<br>CCAC  | AAGGGGAGGCCTTAA<br>ATGA  | 60.1                             | 788                                           | INTRON                                            | Ca_17871                            | Q                     | --       |
| Ca8_P4_15876633  | Ca8                                     | 15876633                      | TAAAAAAAAA/TAAAAAAAAA                                                                 | AATGGAAATACAGCGC<br>AACC  | ACACGACGAAGGTTTG<br>GTTC | 60.0                             | 487                                           | INTRON                                            | Ca_17857                            | T                     | CAMTA    |
| Ca8_P4_16038991  | Ca8                                     | 16038991                      | TAAAAAAAAA/TAAAAAAAAA                                                                 | GCAGGTAGACCTAGCC<br>AATCC | ACAACCTCGAATCCAA<br>CCG  | 60.1                             | 375                                           | INTRON                                            | Ca_15515                            | --                    | NAC      |
| Ca8_P4_16355707  | Ca8                                     | 16355707                      | TTATATATATATA/TTATATATATATA<br>TA                                                     | TCCCACTTTGCAACAG<br>TTCTT | AAAAATGAAACCCATT<br>GACA | 59.8                             | 540                                           | INTRON                                            | Ca_15558                            | I                     | --       |
| Ca8_P4_16360078  | Ca8                                     | 16360078                      | T/TA                                                                                  | GAAAAATGAAGGAGGT<br>GGCA  | GGAAAGAATGTTACGC<br>CTGC | 60.1                             | 159                                           | INTRON                                            | Ca_15558                            | I                     | --       |
| Ca8_P4_2869406   | Ca8                                     | 2869406                       | TG/T                                                                                  | CAACTGGATAACCAGC<br>TCCC  | CGGCCAAATTGATCAG<br>GTAT | 59.6                             | 565                                           | INTRON                                            | Ca_02297                            | U                     | --       |
| Ca8_P4_3074935   | Ca8                                     | 3074935                       | CATATATATATATATATATATATATA/<br>CATATATATATATATATATATATATA<br>TATA                     | ATCATGAACACACGGG<br>TCCT  | GATGAGGGCAAATAAG<br>CTGG | 60.2                             | 688                                           | INTRON                                            | Ca_02271                            | U                     | --       |
| Ca8_P4_4236396   | Ca8                                     | 4236396                       | TATTCAATTCAATTCAATTCAATTCA<br>ATTCAAT/TATTCAATTCAATTCAATT<br>CAATTCAATTCAATTCAATTCAAT | GGAAGATCGGAGCAAG<br>AGTG  | GTGCTGCAACAGACGA<br>CAAT | 60.0                             | 471                                           | INTRON                                            | Ca_02144                            | J                     | --       |
| Ca8_P4_4912312   | Ca8                                     | 4912312                       | AAC/A                                                                                 | TTTTTGTCACAATGGG<br>GGTT  | CAATAATGTGACACGG<br>CAGG | 60.1                             | 372                                           | INTRON                                            | Ca_02065                            | K                     | --       |
| Ca8_P4_5089328   | Ca8                                     | 5089328                       | C/CGAGAGTGGTCA                                                                        | GCATGATGCATGTTGA<br>GCTT  | AACAACAGCCCCAATG<br>TAGC | 59.8                             | 318                                           | INTRON                                            | Ca_02047                            | --                    | Trihelix |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                 | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------|-----------------------------------------|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                  |                                         |                               |                                                                                                                               |                           |                            |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca8_P4_5269338   | Ca8                                     | 5269338                       | CG/CCTCATG                                                                                                                    | ATCCAGAATGGAGCAAC<br>CTGG | CCACGAGATTCCTGG<br>TAAA    | 60.1                             | 478                                           | INTRON                                            | Ca_02025                            | R                     | --          |
| Ca8_P4_6121485   | Ca8                                     | 6121485                       | TCC/TC                                                                                                                        | ATTGTCAAGCTTGGTC<br>AGGG  | CGAGCCAACTTAGATA<br>GGCG   | 60.1                             | 317                                           | INTRON                                            | Ca_01934                            | O                     | NAC         |
| Ca8_P4_6492029   | Ca8                                     | 6492029                       | A/ATCAACC                                                                                                                     | TCTGTTTTGCCCAACC<br>TTTC  | ATCTCAACGATCCAAC<br>GGTC   | 60.1                             | 455                                           | INTRON                                            | Ca_10739                            | D                     | --          |
| Ca8_P4_6849647   | Ca8                                     | 6849647                       | ATGTGT/ATGTGTGT                                                                                                               | CTTCCTCGGTGGGACA<br>TCTA  | ATTCTGACGCGTCTTG<br>CTTT   | 60.1                             | 756                                           | INTRON                                            | Ca_10703                            | O                     | --          |
| Ca8_P4_6976159   | Ca8                                     | 6976159                       | GTAATAATAATAATAATAATAAT<br>AATAAT/GTAATAATAATAATAAT<br>AATAATAATAATAATAATAAT                                                  | GCGAAAAAGACAACGA<br>AAGC  | TCATCGGATTGGTCCT<br>CTTC   | 60.0                             | 255                                           | INTRON                                            | Ca_10695                            | I                     | --          |
| Ca8_P4_7777478   | Ca8                                     | 7777478                       | C/CATA                                                                                                                        | TCCAGTGGCACCATAA<br>CAAA  | TGAATCCCCGTGACGT<br>TTAT   | 60.0                             | 588                                           | INTRON                                            | Ca_10607                            | Z                     | MYB_related |
| Ca8_P4_7777713   | Ca8                                     | 7777713                       | CACATAACATA/CACATA                                                                                                            | TCCAGTGGCACCATAA<br>CAAA  | CTCCCAAGAACCCTTC<br>TTCC   | 60.0                             | 744                                           | INTRON                                            | Ca_10607                            | Z                     | MYB_related |
| Ca8_P4_7860255   | Ca8                                     | 7860255                       | CAATAATAATAATAATAATAATA<br>ATAATAATAATAATAAAAAAAT<br>AATAATA/CAATAATAATAATAAT<br>AATAATAATAATAATAATAATA<br>TAATAAAAAATAATAATA | AGCGGATGCCTCTCAT<br>TCTA  | ATCTGCTTATTCGGCC<br>CTTT   | 59.9                             | 544                                           | INTRON                                            | Ca_10599                            | MO                    | --          |
| Ca8_P4_8694777   | Ca8                                     | 8694777                       | GAA/GA                                                                                                                        | AATTGGCAGGGAAGA<br>AGAT   | TAAGGCAAAATGGTGCC<br>TACC  | 59.9                             | 715                                           | INTRON                                            | Ca_11501                            | V                     | NAC         |
| Ca8_P4_8884297   | Ca8                                     | 8884297                       | ATTTTTTTTTTT/ATTTTTTTT                                                                                                        | TGCTTAAGGCCCTTGT<br>GAAT  | TCCAACCTTCAACAATC<br>TACCA | 59.7                             | 767                                           | INTRON                                            | Ca_11519                            | --                    | --          |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca8_P4_8884679   | Ca8                                     | 8884679                       | GTTTA/GTTTATTTTA                                              | ATTGTAGCATCATTGC<br>CACT | TCTGTCTCGTGCTTCC<br>ACAC | 57.3                             | 428                                           | INTRON                                            | Ca_11519                            | --                    | --   |
| Ca8_P4_8899206   | Ca8                                     | 8899206                       | AT/A                                                          | GTGGATGACAAAACCT<br>CGTG | TTCTCATATGCCCTCC<br>AAC  | 59.0                             | 633                                           | INTRON                                            | Ca_11521                            | G                     | --   |
| Ca8_P4_8901973   | Ca8                                     | 8901973                       | TCTCTCTCTCAC/TC                                               | TTGCAATGGTTCAAGC<br>TACG | TCATTATCACCTACGG<br>CCC  | 59.9                             | 393                                           | INTRON                                            | Ca_11521                            | G                     | --   |
| Ca8_P4_8905164   | Ca8                                     | 8905164                       | AC/A                                                          | TGGTCCAGGAGGAGTC<br>AAAC | GGTCCCTGTAGGCCCA<br>TTAT | 60.1                             | 288                                           | INTRON                                            | Ca_11521                            | G                     | --   |
| Ca8_P4_8920440   | Ca8                                     | 8920440                       | TAAAAAAAA/TAAAAAAAA                                           | TGTTCATGTAAGCCATT<br>GGG | TCCAAAACCCATTTAC<br>CTC  | 59.4                             | 540                                           | INTRON                                            | Ca_11522                            | --                    | --   |
| Ca8_P4_8936631   | Ca8                                     | 8936631                       | TAGA/TA                                                       | TTAGGCACCATCCCTA<br>CGTC | CCAAAGGTTGTGAAGG<br>GAGA | 60.0                             | 862                                           | INTRON                                            | Ca_11524                            | --                    | --   |
| Ca8_P4_9013369   | Ca8                                     | 9013369                       | CATT/CATTATT                                                  | ACGTACCCCAACTGAA<br>CTGC | GCTACAAGGATGATGT<br>TGGA | 60.0                             | 147                                           | INTRON                                            | Ca_11527                            | --                    | --   |
| Ca8_P4_9098007   | Ca8                                     | 9098007                       | TTAT/TT                                                       | AACCGTTAAATCCGCA<br>ACTG | CCAAGGAAACAGCTCA<br>AAGC | 60.0                             | 794                                           | INTRON                                            | Ca_11533                            | --                    | C2H2 |
| Ca8_P4_9114161   | Ca8                                     | 9114161                       | AT/A                                                          | AAGGCAACCATGGA<br>AAAG   | TGCCCCATATACGTTT<br>CAAT | 60.0                             | 674                                           | INTRON                                            | Ca_11534                            | --                    | --   |
| Ca8_P4_9122512   | Ca8                                     | 9122512                       | T/TAACA                                                       | TAGCATGTGGGCCTAA<br>AAGG | GCCGGCAGCAAAATAT<br>AGAA | 60.1                             | 409                                           | INTRON                                            | Ca_11535                            | --                    | --   |

| INDEL marker IDs | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                  |                                         |                               |                                                               |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| Ca8_P4_9122801   | Ca8                                     | 9122801                       | CATATA/CATA                                                   | GGCAATTTGACAACCC<br>TTGA | TACTTTTCGTGTGCCCA<br>ACA | 60.9                             | 602                                           | INTRON                                            | Ca_11535                            | --                    | --   |
| Ca8_P4_9151870   | Ca8                                     | 9151870                       | CTATAT/CTATATAT                                               | CTGAGCAATGCATCTG<br>GTGT | ACCGTTGTTTGATTTCG<br>ACC | 59.9                             | 646                                           | INTRON                                            | Ca_11539                            | O                     | --   |
| Ca8_P4_9152449   | Ca8                                     | 9152449                       | A/AT                                                          | CAGCCTGTTCAAAAT<br>GCAA  | GCATTTGAGGATGCTG<br>GATT | 59.8                             | 257                                           | INTRON                                            | Ca_11539                            | O                     | --   |
| Ca8_P4_9154690   | Ca8                                     | 9154690                       | GTTT/GTT                                                      | AGCCTGGGCAACTTTC<br>TTTT | CCAGTAGGAAGCAAGC<br>CAAG | 60.2                             | 132                                           | INTRON                                            | Ca_11539                            | O                     | --   |
| Ca8_P4_9155660   | Ca8                                     | 9155660                       | AT/ATT                                                        | GGCGCAGTTCTTCCTA<br>TGAG | CCAACGGTTACATCAA<br>GGCT | 60.0                             | 610                                           | INTRON                                            | Ca_11539                            | O                     | --   |
| Ca8_P4_9157900   | Ca8                                     | 9157900                       | TAAAAAA/TAAAAA                                                | TAAATGGTGGGAAAGT<br>GGGA | CATTCCAATGCTGCTTC<br>TCA | 60.2                             | 487                                           | INTRON                                            | Ca_11539                            | O                     | --   |
| Ca8_P4_9170028   | Ca8                                     | 9170028                       | A/AC                                                          | TGTGTGGTCCAACAAG<br>GAGA | CTGTTGCGTTGAAGCA<br>GGTA | 60.1                             | 454                                           | INTRON                                            | Ca_11540                            | E                     | bZIP |
| Ca8_P4_9274060   | Ca8                                     | 9274060                       | AA/AATA                                                       | AACAACAGAGCCTGCG<br>AACT | TCCATGTTTCCGTTTT<br>CAT  | 60.1                             | 486                                           | INTRON                                            | Ca_11549                            | --                    | NAC  |
| Ca8_P4_9382621   | Ca8                                     | 9382621                       | CA/CATATAAATTGAA                                              | GTTCAAACCTGACGA<br>AGGA  | GCTCATGCTGTCATGG<br>CTAA | 60.1                             | 843                                           | INTRON                                            | Ca_11559                            | J                     | --   |
| Ca8_P4_9387474   | Ca8                                     | 9387474                       | GCC/GC                                                        | AGTTTCCACCAGCCAC<br>AAAC | TGTGGGGGAGAAGCTT<br>ATTG | 60.0                             | 193                                           | INTRON                                            | Ca_11559                            | J                     | --   |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)   | Forward primers (5'-3')  | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------|--------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                        |                                         |                               |                                                                 |                          |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| Ca8_P4_9950946         | Ca8                                     | 9950946                       | CTT/CTTGTCGATT                                                  | ACCATGGCTTATTGGT<br>CAGC | TGGCATAATGTCAGAC<br>GCAT   | 60.0                             | 310                                           | INTRON                                            | Ca_18394                            | --                    | --          |
| Ca8_P4_9960024         | Ca8                                     | 9960024                       | CATAATAATAATAAT/CATAATAATAA<br>TAATAATAATAAT                    | CCATTGGGATGTTTGC<br>TTTT | GCTCATGTGGTGGTGT<br>TTTG   | 59.8                             | 280                                           | INTRON                                            | Ca_18395                            | --                    | --          |
| scaffold1006_P4_126197 | scaffold1006                            | 126197                        | CAGCCAAA/CA                                                     | TTATCCACATCAGCC<br>AAAA  | AAATTGTTGAAAGAGG<br>AGGGG  | 60.0                             | 295                                           | INTRON                                            | Ca_18011                            | --                    | MYB_related |
| scaffold1006_P4_338954 | scaffold1006                            | 338954                        | GTGACTT/GT                                                      | GAAGCCCCAATTCAAC<br>AAAA | CCCAAAAACTCATGGC<br>CTAA   | 59.9                             | 312                                           | INTRON                                            | Ca_18027                            | --                    | BES1        |
| scaffold1006_P4_513011 | scaffold1006                            | 513011                        | CAATAATAATAATAATAATAATA<br>ATA/CAATAATAATAATAATAATA<br>ATA      | ACTGCAAAAGGGGAG<br>AAAT  | GAAGTTGGAGAATTCA<br>AATCCG | 59.9                             | 673                                           | INTRON                                            | Ca_18036                            | M                     | HB-other    |
| scaffold10227_P4_6464  | scaffold10227                           | 6464                          | AATATATATATATATATATATATAT<br>ATATATATA/AATATATATATATAT<br>ATATA | GGGAACGTGAAGAACT<br>CAGC | TGCAACAACCAACC<br>ACTT     | 59.9                             | 518                                           | INTRON                                            | Ca_28086                            | --                    | bHLH        |
| scaffold1047_P4_206533 | scaffold1047                            | 206533                        | TTATATATATATATATAT/TTATATAT<br>ATATATATATAT                     | TCCGGGTATAATGCCT<br>TTGA | GGAGTGGAGGCACAGA<br>GAAG   | 60.3                             | 677                                           | INTRON                                            | Ca_17192                            | --                    | WRKY        |
| scaffold1047_P4_313122 | scaffold1047                            | 313122                        | GAAAAAAAA/GAAAAAAAAA                                            | AAAATTCCACACGTCC<br>GAAG | TCAAAAGATCGCAGTT<br>GTGTG  | 60.0                             | 354                                           | INTRON                                            | Ca_17199                            | I                     | --          |
| scaffold1047_P4_63171  | scaffold1047                            | 63171                         | CTT/CTTAATTAGTCTTT                                              | CTGATGACGGGGAGTT<br>GTTT | TGACATGTTGTCTGCC<br>CAAT   | 60.0                             | 703                                           | INTRON                                            | Ca_17177                            | Z                     | Dof         |
| scaffold1050_P4_149500 | scaffold1050                            | 149500                        | ACGC/AC                                                         | TTCGTTCTCCCATGAC<br>ACAC | GGAGGTGCACCAACTC<br>CTTA   | 59.5                             | 676                                           | INTRON                                            | Ca_25917                            | I                     | --          |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')     | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|-----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                        |                                         |                               |                                                               |                            |                             |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| scaffold1055_P4_183552 | scaffold1055                            | 183552                        | ATTTTTTTTTTT/ATTTTTTTTTT                                      | GCCAAAGCGCTGTAAG<br>AGAC   | ATGTGAATCCCACCAG<br>GAAA    | 60.0                             | 600                                           | INTRON                                            | Ca_25312                            | --                    | --      |
| scaffold1135_P4_14111  | scaffold1135                            | 14111                         | TTAAATAAATAAATAA/TTAAATAAAT<br>AAATAAATAA                     | TCTGGCACATGAACTT<br>CAGC   | CACTCGACAATTGGGA<br>GGTT    | 60.0                             | 532                                           | INTRON                                            | Ca_26843                            | --                    | SAP     |
| scaffold1202_P4_179415 | scaffold1202                            | 179415                        | TG/TGCCG                                                      | AATAGGTAGCACGGTG<br>TGCC   | TCACATGGAACCTTCC<br>CCTC    | 60.0                             | 431                                           | INTRON                                            | Ca_24666                            | --                    | --      |
| scaffold1202_P4_179607 | scaffold1202                            | 179607                        | AG/AGG                                                        | AATAGGTAGCACGGTG<br>TGCC   | TCCCTTGCCTACATTGT<br>TCC    | 60.0                             | 814                                           | INTRON                                            | Ca_24666                            | --                    | --      |
| scaffold1202_P4_183467 | scaffold1202                            | 183467                        | GAAAAAA/GAAAAAA                                               | ACTCGAAAAATGTGCC<br>CTTA   | TTGCGTTCAAAGACTC<br>GATG    | 59.6                             | 665                                           | INTRON                                            | Ca_24666                            | --                    | --      |
| scaffold1215_P4_41563  | scaffold1215                            | 41563                         | GATATATATATATATATATATA/GA<br>TATATATATATATATATATA             | CCCTTCATTTCTTCG<br>CATA    | GAAGCAGGCTTCGATG<br>GATA    | 60.0                             | 415                                           | INTRON                                            | Ca_28164                            | --                    | G2-like |
| scaffold127_P4_270423  | scaffold127                             | 270423                        | AATTTTCATTTTCATTT/AATTTTCAT<br>TT                             | GCCACATATCTTGTT<br>GCCT    | TTCAAGCACATACTGCA<br>CCAG   | 60.0                             | 687                                           | INTRON                                            | Ca_26800                            | --                    | --      |
| scaffold128_P4_820746  | scaffold128                             | 820746                        | A/AGATGCTT                                                    | GTTTTGACCAGCTCTC<br>CTGC   | CTCAGTCGAACCTACG<br>AGGC    | 60.0                             | 666                                           | INTRON                                            | Ca_21452                            | D                     | --      |
| scaffold128_P4_853519  | scaffold128                             | 853519                        | CCATACATA/CCATACATACATA                                       | AACACATCCGGGATCC<br>ATTA   | AATGACGACGACGATG<br>ATGA    | 60.0                             | 551                                           | INTRON                                            | Ca_21452                            | D                     | --      |
| scaffold1281_P4_192341 | scaffold1281                            | 192341                        | TTATATATATATATATATATATATA<br>TATA/TTATATATATATATATATAT<br>A   | CGAAGAATCACTTTAAA<br>CCCCA | TCCTTGGTCCATGTATA<br>TAAGCC | 60.3                             | 916                                           | INTRON                                            | Ca_21513                            | --                    | bHLH    |



| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                                    | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                        |                                         |                               |                                                                                                                                  |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| scaffold1309_P4_49935  | scaffold1309                            | 49935                         | CATATATATATATATA/CATATATATA<br>TATATATATA                                                                                        | TGGGTGCTATTGCAAT<br>TCAA   | TTTGTCTCGACACTGT<br>TGC   | 60.1                             | 245                                           | INTRON                                            | Ca_26762                            | --                    | Trihelix |
| scaffold1324_P4_577131 | scaffold1324                            | 577131                        | TAAAAAAAAA/TAAAAAAAAA                                                                                                            | CACAAATGCTAACCG<br>CAAA    | TTTGACACACTTGCTCC<br>AGG  | 59.7                             | 230                                           | INTRON                                            | Ca_19780                            | --                    | --       |
| scaffold1331_P4_54719  | scaffold1331                            | 54719                         | TTATATATATATATATAT/TTATAT<br>ATATATATATATATAT                                                                                    | CCGTACCGTTTCTGGG<br>ATAA   | CGCGCAGATTGTCAA<br>TAGA   | 59.8                             | 740                                           | INTRON                                            | Ca_26942                            | --                    | --       |
| scaffold134_P4_47232   | scaffold134                             | 47232                         | TAA/TA                                                                                                                           | CTGCCATGCATACAAC<br>AACC   | ACGCGTGCATGAGTTC<br>AAT   | 60.0                             | 176                                           | INTRON                                            | Ca_22578                            | O                     | C2H2     |
| scaffold1351_P4_199024 | scaffold1351                            | 199024                        | TATAATAATAATAATAATAATAA<br>TAATAATAATGATAATAATAATA<br>ATAATAAT/TATAATAATAATAAT<br>AATAATAATAATAATAATGATAA<br>TAATAATAATAATAATAAT | ACCTCCCACTGGGTG<br>TTTT    | GCTAATAGGGGGTCGT<br>TTCC  | 60.6                             | 713                                           | INTRON                                            | Ca_21997                            | R                     | --       |
| scaffold1418_P4_21418  | scaffold1418                            | 21418                         | AG/A                                                                                                                             | GCCATAATTGCTTCTG<br>CAGTTT | TCGCGGTGTGGTAAGT<br>CATA  | 60.6                             | 235                                           | INTRON                                            | Ca_25261                            | QR                    | B3       |
| scaffold1418_P4_38513  | scaffold1418                            | 38513                         | CTTTTATTTTTATTT/CTTTTATTT<br>TTATTTTTTATTT                                                                                       | CTTTCCTAAAGCCCA<br>ATCC    | TTGCTCCCTTTACTCAT<br>CTGC | 59.9                             | 811                                           | INTRON                                            | Ca_25262                            | S                     | --       |
| scaffold1450_P4_10288  | scaffold1450                            | 10288                         | AATATATATATATATATATATAT<br>/AATATATATATATATATATAT                                                                                | CGTTGCACCAAGATGA<br>AAAA   | GAGACCGGCGTGAAAA<br>ATTA  | 59.7                             | 463                                           | INTRON                                            | Ca_28008                            | --                    | --       |
| scaffold1504_P4_161420 | scaffold1504                            | 161420                        | AT/ATT                                                                                                                           | TCAATGCGGTCTCTGA<br>AGTG   | GCCCAACAGCAAGCTA<br>TTTC  | 60.0                             | 349                                           | INTRON                                            | Ca_24092                            | --                    | Trihelix |
| scaffold1511_P4_145021 | scaffold1511                            | 145021                        | CTTTTTTTTT/CTTTTTTTT                                                                                                             | AACTTGCTGCTGTGGG<br>AGTT   | TTTGATTCCGCGAAAA<br>TTC   | 59.9                             | 744                                           | INTRON                                            | Ca_25147                            | R                     | --       |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3') | Reverse primers (5'-3') | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-------------------------|-------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                        |                                         |                               |                                                               |                         |                         |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| scaffold1511_P4_71214  | scaffold1511                            | 71214                         | GAAAAA/GAAAAA                                                 | TAAGCGGAGTTCCCATC       | CAAGGAAGGTCATTGCAACA    | 60.0                             | 742                                           | INTRON                                            | Ca_25144                            | --                    | MYB_related |
| scaffold157_P4_314324  | scaffold157                             | 314324                        | ATT/ATTTT                                                     | TGAGGTTCCCTTCTGATTGC    | GACACATGGCAAAGCTTCCT    | 60.2                             | 521                                           | INTRON                                            | Ca_21077                            | --                    | MYB_related |
| scaffold157_P4_352152  | scaffold157                             | 352152                        | CTTTTTT/CTTTTTTTTT                                            | CGATGAGGAAGAATGACGGT    | TGCGTTCCATTTCATATCA     | 60.1                             | 986                                           | INTRON                                            | Ca_21079                            | --                    | SBP         |
| scaffold157_P4_354709  | scaffold157                             | 354709                        | TA/TACAA                                                      | GTTAACGTGCTCCCGTGTTT    | ACTGTTTCCCGACCTCAACA    | 60.0                             | 377                                           | INTRON                                            | Ca_21079                            | --                    | SBP         |
| scaffold157_P4_355593  | scaffold157                             | 355593                        | GACACACA/GACACA                                               | TGCTTCTGATGACAGGCAAC    | GTGATGTTGATGCGGAACAC    | 60.0                             | 643                                           | INTRON                                            | Ca_21079                            | --                    | SBP         |
| scaffold1580_P4_254441 | scaffold1580                            | 254441                        | A/ATAATAATAT                                                  | ACCTTCCTCTCCTTCAAA      | TTGCTCCTCCCATTTATTG     | 60.0                             | 440                                           | INTRON                                            | Ca_20799                            | B                     | --          |
| scaffold167_P4_288909  | scaffold167                             | 288909                        | A/AGT                                                         | TCATCCTCCCCAATTTCAAC    | CATTGTTTCATGCATTTGGC    | 59.7                             | 705                                           | INTRON                                            | Ca_24156                            | C                     | --          |
| scaffold1710_P4_43434  | scaffold1710                            | 43434                         | AT/ATT                                                        | TCGCTTTTTGTGTTGAGCAG    | ATGGCTCTCTCCCGGTAAT     | 60.2                             | 813                                           | INTRON                                            | Ca_25722                            | --                    | --          |
| scaffold1722_P4_65936  | scaffold1722                            | 65936                         | A/AT                                                          | CGTAGCGATAAACCTGGGA     | CGGGCCAGAATACTTACAGC    | 60.1                             | 802                                           | INTRON                                            | Ca_26630                            | G                     | --          |
| scaffold174_P4_189673  | scaffold174                             | 189673                        | GTTTTTTTTT/GTTTTTTTTT                                         | AACCCCATAGCAGCATGAC     | AAAGAAAAATGCGATCGGTG    | 60.0                             | 615                                           | INTRON                                            | Ca_21713                            | R                     | C2H2        |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                            |                            |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold174_P4_434745  | scaffold174                             | 434745                        | CAA/CAAA                                                      | TTTGGCCATTCCAAGTT<br>TCC   | TTGATCTCGTGAAGTTT<br>GCG   | 59.9                             | 350                                           | INTRON                                            | Ca_21723                            | A                     | C3H |
| scaffold174_P4_447089  | scaffold174                             | 447089                        | AT/ATCGCCT                                                    | GGGAAACAGCCTTGAT<br>TGAA   | ATCGAATTCTGCCCTT<br>GATG   | 60.1                             | 760                                           | INTRON                                            | Ca_21723                            | A                     | C3H |
| scaffold174_P4_450819  | scaffold174                             | 450819                        | AT/A                                                          | AAGATCACCGTGCAAA<br>AAGG   | GCCTCCACGACCACTA<br>CAAT   | 60.1                             | 433                                           | INTRON                                            | Ca_21723                            | A                     | C3H |
| scaffold186_P4_178754  | scaffold186                             | 178754                        | TATTGTAA/TA                                                   | AGCGATGCATGTCTCA<br>AGTG   | GCCCTTCTTCTTTTCCT<br>GGT   | 60.0                             | 501                                           | INTRON                                            | Ca_24795                            | --                    | --  |
| scaffold1866_P4_41886  | scaffold1866                            | 41886                         | CTTTTTTTTT/CTTTTTTTTT                                         | TGGAGTGGGGTACCTA<br>GTGG   | GGGACAGAAAGAAAGG<br>GGAG   | 59.8                             | 758                                           | INTRON                                            | Ca_26041                            | R                     | --  |
| scaffold1866_P4_44313  | scaffold1866                            | 44313                         | TA/TAATAATAA                                                  | ACGCTGATTGAAGTTT<br>GGCT   | TCTCATGTTCTCCAGT<br>TGCT   | 59.9                             | 429                                           | INTRON                                            | Ca_26041                            | R                     | --  |
| scaffold1866_P4_62792  | scaffold1866                            | 62792                         | AAATAAA/AAATAAATAGAATAAA                                      | TTGCTCCTACGTATCT<br>CCCG   | TTAAGTTGGTTTGGGC<br>TTGG   | 60.2                             | 855                                           | INTRON                                            | Ca_26041                            | R                     | --  |
| scaffold1943_P4_243638 | scaffold1943                            | 243638                        | TACACACA/TACACACACA                                           | TGGTGGCATAACTAAG<br>TGCTCA | AAAGGAACCAAGTTTT<br>GGACAG | 59.7                             | 181                                           | INTRON                                            | Ca_21926                            | R                     | --  |
| scaffold1981_P4_344185 | scaffold1981                            | 344185                        | TC/T                                                          | TTGGCACATGTTTGAC<br>ACCT   | AGACCTTGGCATTGGA<br>AGTG   | 60.0                             | 470                                           | INTRON                                            | Ca_21268                            | --                    | --  |
| scaffold1981_P4_382455 | scaffold1981                            | 382455                        | TTGTAGAA/T                                                    | TTTCAAGTGGCTATGC<br>CAGA   | ACAACCCTCCAAGCTG<br>GTTA   | 59.4                             | 410                                           | INTRON                                            | Ca_21269                            | L                     | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                        |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| scaffold1981_P4_393601 | scaffold1981                            | 393601                        | GAAAAAAAAA/GAAAAAAAAA                                         | ACCTCATCTGGAATGG<br>TTGC | CGGTGTCCAAGTTGTG<br>ATTG  | 59.9                             | 739                                           | INTRON                                            | Ca_21270                            | A                     | --   |
| scaffold1981_P4_393663 | scaffold1981                            | 393663                        | CATAT/CAT                                                     | TCTAAGCCTTCCAGGT<br>GTGG | CGGTGTCCAAGTTGTG<br>ATTG  | 60.2                             | 560                                           | INTRON                                            | Ca_21270                            | A                     | --   |
| scaffold1981_P4_394144 | scaffold1981                            | 394144                        | CTTTTT/CTTTT                                                  | CAATCACAACTTGAC<br>ACCG  | AGGCATGGAGGCTGCT<br>ATAA  | 60.0                             | 492                                           | INTRON                                            | Ca_21270                            | A                     | --   |
| scaffold1981_P4_395440 | scaffold1981                            | 395440                        | TCC/TC                                                        | AACCCACACCAAATTC<br>CAAA | GGGTGGTGGTGAAGT<br>ATTG   | 60.1                             | 445                                           | INTRON                                            | Ca_21270                            | A                     | --   |
| scaffold202_P4_61873   | scaffold202                             | 61873                         | GTAAATGAAATAAAATGA/GTAAAT<br>TGAAATAAAATGAAATAAAATGA          | CAGCCCTTGAATTCGA<br>TCAT | GCTGTTTGGCTCAACC<br>ATT   | 60.0                             | 331                                           | INTRON                                            | Ca_27125                            | --                    | --   |
| scaffold202_P4_93885   | scaffold202                             | 93885                         | C/CT                                                          | GTGCAGTGAAAGGGTT<br>CCAT | AATTTGATATCGTGGC<br>GGAG  | 60.0                             | 881                                           | INTRON                                            | Ca_27126                            | U                     | --   |
| scaffold202_P4_96872   | scaffold202                             | 96872                         | T/TC                                                          | AAATTGGTGGCCAAAT<br>GTGT | ACCAATAACACCAGCC<br>GAAC  | 60.1                             | 730                                           | INTRON                                            | Ca_27126                            | U                     | --   |
| scaffold202_P4_97456   | scaffold202                             | 97456                         | CTTTTTTTT/CTTTTTTTTT                                          | GTTCGGCTGGTGTTAT<br>TGGT | GTTGCCTGCTGTTTTTC<br>CAT  | 59.9                             | 447                                           | INTRON                                            | Ca_27126                            | U                     | --   |
| scaffold208_P4_375288  | scaffold208                             | 375288                        | CAAA/CAA                                                      | TTTAGTTTCGCGTTCCT<br>CGT | TGCGTTAGTGGTAGCA<br>GAACA | 59.9                             | 386                                           | INTRON                                            | Ca_25684                            | K                     | MIKC |
| scaffold2170_P4_12258  | scaffold2170                            | 12258                         | CTTTTT/CTTTT                                                  | TGCTTTGTCAATTGCT<br>TGC  | GGAGTCCCGGAAAATT<br>TCAT  | 60.0                             | 531                                           | INTRON                                            | Ca_26929                            | O                     | --   |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |     |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----|
|                        |                                         |                               |                                                               |                          |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs |
| scaffold2170_P4_14347  | scaffold2170                            | 14347                         | AC/ACC                                                        | GCTCATTCTTGTCCTC<br>AAAA | GCCTCTGCTAATTGGT<br>CTCG  | 60.1                             | 583                                           | INTRON                                            | Ca_26929                            | O                     | --  |
| scaffold2170_P4_5002   | scaffold2170                            | 5002                          | AACCTTACCTTACCTTACCT/AACCT<br>TACCTTACCT                      | GCAAATCAAGGTTGCA<br>GTCA | ACACTCTAATGGGGAC<br>AGCG  | 59.8                             | 222                                           | INTRON                                            | Ca_26928                            | YU                    | --  |
| scaffold2170_P4_5357   | scaffold2170                            | 5357                          | C/CTATTGGG                                                    | CGCTGTCCCCATTAGA<br>GTGT | GTTTGCCAATTAGGGC<br>ACAT  | 60.1                             | 387                                           | INTRON                                            | Ca_26928                            | YU                    | --  |
| scaffold2170_P4_6851   | scaffold2170                            | 6851                          | AC/A                                                          | TTTGTGCTTCACTACC<br>GCTG | TTGGCAAATTTTCCCA<br>GAG   | 60.1                             | 547                                           | INTRON                                            | Ca_26928                            | YU                    | --  |
| scaffold2192_P4_87516  | scaffold2192                            | 87516                         | AACACACACA/AACACACA                                           | TTGAACACCTTCAATG<br>GCAA | ACTTGATGTCGTGCT<br>GAGA   | 60.1                             | 826                                           | INTRON                                            | Ca_26813                            | R                     | --  |
| scaffold2192_P4_93608  | scaffold2192                            | 93608                         | AAGAGAGAGAGAGAGAGAGAGA/AA<br>GAGAGAGAGAGAGAGAGA               | TCATCAAAAGCCACGA<br>ATGA | TTTGGTTGAGGGACTT<br>GGAA  | 60.2                             | 713                                           | INTRON                                            | Ca_26813                            | R                     | --  |
| scaffold224_P4_170558  | scaffold224                             | 170558                        | TATT/TATTTTAATT                                               | GTGACTTACCAGCCAA<br>CCGT | ACAGGAAGGCAATCAA<br>ATGG  | 60.0                             | 399                                           | INTRON                                            | Ca_26343                            | --                    | --  |
| scaffold227_P4_135497  | scaffold227                             | 135497                        | TCC/TCCC                                                      | CTTGATGTGGTAGCC<br>GTTT  | GGTCTTGTGGTGGCTT<br>TTGT  | 60.0                             | 651                                           | INTRON                                            | Ca_25190                            | --                    | --  |
| scaffold227_P4_140947  | scaffold227                             | 140947                        | TTA/TTAAAAGTA                                                 | ACCCTTTTGTCCACAC<br>GAG  | TACGGATGTTGACGCA<br>ATGT  | 60.0                             | 511                                           | INTRON                                            | Ca_25190                            | --                    | --  |
| scaffold2356_P4_138194 | scaffold2356                            | 138194                        | TT/TTCT                                                       | CCTTGAAGTGTGTCT<br>GGCA  | CCAACAACATCAAATTC<br>ATCG | 59.9                             | 687                                           | INTRON                                            | Ca_24344                            | Q                     | --  |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                     | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |      |
|------------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|------|
|                        |                                         |                               |                                                                                   |                           |                              |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| scaffold2356_P4_138866 | scaffold2356                            | 138866                        | TG/TGAG                                                                           | ACCCAATTCCTTCATGT<br>CCA  | AGATCCACCAAAGGCA<br>ACAG     | 60.2                             | 213                                           | INTRON                                               | Ca_24344                            | Q                     | --   |
| scaffold2368_P4_55017  | scaffold2368                            | 55017                         | A/AG                                                                              | TTGCATCATGTACGCC<br>AAAT  | ACTTTTCAGTGGCTCGG<br>AGAA    | 60.0                             | 392                                           | INTRON                                               | Ca_26720                            | P                     | --   |
| scaffold2373_P4_64133  | scaffold2373                            | 64133                         | CAAGTCTAAGTCT/CAAGTCTAAGTC<br>TAAGTCT                                             | AAGCAGTATTGACGG<br>GGTG   | ATGCATGGATTGATTG<br>GGAT     | 60.0                             | 802                                           | INTRON                                               | Ca_27075                            | --                    | --   |
| scaffold2373_P4_69360  | scaffold2373                            | 69360                         | TTATATATATATATATATATATATATA<br>TATATATAT/TTATATATATATATATA<br>TATATATATATAT       | ATATTGGGCCCTGCTT<br>CTTC  | CAAACGGTGCTGACAC<br>ATCT     | 60.4                             | 502                                           | INTRON                                               | Ca_27075                            | --                    | --   |
| scaffold2560_P4_31602  | scaffold2560                            | 31602                         | ATT/AT                                                                            | TGTTTCGAGAGAGGGAA<br>GAGG | ACTGCGTCTTTGCTAT<br>GGCT     | 59.5                             | 414                                           | INTRON                                               | Ca_27049                            | S                     | --   |
| scaffold2575_P4_169411 | scaffold2575                            | 169411                        | ACTCT/ACTCTTTCTCTCT                                                               | GCGTCAACTCAACCTG<br>ACCT  | AAAAAGGGAAAAGCGG<br>AAAA     | 60.3                             | 350                                           | INTRON                                               | Ca_23000                            | S                     | --   |
| scaffold2722_P4_76421  | scaffold2722                            | 76421                         | CTACGTAC/CTAC                                                                     | ATGGATGCAGAAGGCA<br>ACTT  | CCACAAAAATATTGGC<br>GACC     | 59.7                             | 734                                           | INTRON                                               | Ca_27216                            | --                    | C2H2 |
| scaffold2748_P4_27802  | scaffold2748                            | 27802                         | TCA/TCACA                                                                         | TCTCGTTTAGATCGTC<br>CGCT  | TGGAATCTTCTCCAAT<br>GCC      | 60.0                             | 551                                           | INTRON                                               | Ca_28188                            | --                    | --   |
| scaffold2763_P4_195921 | scaffold2763                            | 195921                        | TTATATATATATATATATATATA/TTA<br>TATATATATATATATATA                                 | CAAGATGGAGGCTCTT<br>TGGA  | TAAAGGACCAAGTCGG<br>GAAA     | 60.3                             | 460                                           | INTRON                                               | Ca_24404                            | R                     | --   |
| scaffold284_P4_117212  | scaffold284                             | 117212                        | TTATATATATATATATATATATATA<br>TATATATATAT/TTATATATATATATA<br>TATATATATATATATATATAT | TGGTGCACTGGAATCT<br>TATCA | TCCACAAAGCATTTGTC<br>TATTTTT | 59.1                             | 633                                           | INTRON                                               | Ca_20588                            | Q                     | NAC  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                       |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| scaffold287_P4_22647  | scaffold287                             | 22647                         | AA/AATTA                                                      | TTTAAACAGATGTCCG<br>CCC    | GGAACAATGTAGGCAA<br>GGGA  | 59.9                             | 708                                           | INTRON                                            | Ca_25380                            | --                    | --       |
| scaffold290_P4_177449 | scaffold290                             | 177449                        | TAAAAAAAAAAAA/TAAAAAAAAAAAA                                   | TTGCCTACCAAATAATG<br>CGA   | ATGACGATTGCTTCGA<br>TGTG  | 59.2                             | 744                                           | INTRON                                            | Ca_19830                            | F                     | --       |
| scaffold290_P4_206705 | scaffold290                             | 206705                        | GATAT/GATCAATTAATAT                                           | TCCCTCTTTTCAAGTCA<br>ACTCA | TCGCTCTAGGCTAATC<br>CAACT | 59.0                             | 318                                           | INTRON                                            | Ca_19830                            | F                     | --       |
| scaffold290_P4_255269 | scaffold290                             | 255269                        | T/TGG                                                         | TGTTGCTCGTTCTATG<br>CTGC   | ACAGCTGCTGCTCTTT<br>GTGA  | 60.2                             | 296                                           | INTRON                                            | Ca_19833                            | Z                     | --       |
| scaffold2907_P4_30444 | scaffold2907                            | 30444                         | ATATATATATTATATATAT/ATATATA<br>TAT                            | TATTCAGATCCCTTGC<br>CCAG   | TGGGTGCTATTTGCAA<br>TCAA  | 60.0                             | 635                                           | INTRON                                            | Ca_27010                            | --                    | Trihelix |
| scaffold2950_P4_10165 | scaffold2950                            | 10165                         | AGG/AGGG                                                      | AGTTGTTTGGATACAC<br>CGGC   | AGTGCTGTGGCTGGAC<br>CTAT  | 59.9                             | 662                                           | INTRON                                            | Ca_27517                            | L                     | FAR1     |
| scaffold2950_P4_10696 | scaffold2950                            | 10696                         | G/GT                                                          | TGATGATATCAGGCAA<br>CGGA   | TGTCCCCACAGGTAGC<br>TTTC  | 60.0                             | 588                                           | INTRON                                            | Ca_27517                            | L                     | FAR1     |
| scaffold2950_P4_8204  | scaffold2950                            | 8204                          | T/TG                                                          | TGGTCAGAATGGGCTT<br>TACC   | TTCAGAAGGCCAGAA<br>GAAA   | 59.9                             | 506                                           | INTRON                                            | Ca_27517                            | L                     | FAR1     |
| scaffold298_P4_212123 | scaffold298                             | 212123                        | CAAAAAAAAAAAAA/CAAAAAAAAAAAAA                                 | ATAGCCTCCCTTTTGG<br>GCAT   | TGCAGCTTCTGGTGTT<br>CATC  | 59.9                             | 371                                           | INTRON                                            | Ca_27492                            | --                    | --       |
| scaffold299_P4_158960 | scaffold299                             | 158960                        | TA/TAA                                                        | TACGAACCGGTAGAAC<br>CGTC   | CGTGGTAATCGCGTAG<br>GAAT  | 60.0                             | 574                                           | INTRON                                            | Ca_25996                            | AJ                    | --       |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |           |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-----------|
|                       |                                         |                               |                                                                           |                            |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs       |
| scaffold3016_P4_87899 | scaffold3016                            | 87899                         | TTATATATATATATATATATATATA<br>TATA/TTATATATATATATATATAT<br>ATATATATATATATA | TCCTCACTCTTCGCAC<br>CTCT   | CATTGGCTTTGTTGGT<br>GATG  | 60.1                             | 674                                           | INTRON                                            | Ca_26725                            | C                     | NAC       |
| scaffold303_P4_64412  | scaffold303                             | 64412                         | AATATATATATATATATATATA/AA<br>TATATATATATATATATATATA                       | CGTGACATGGTAAGGC<br>ATTG   | GCACGCATCCCTGAAA<br>TAGT  | 60.0                             | 271                                           | INTRON                                            | Ca_26657                            | --                    | --        |
| scaffold3058_P4_16160 | scaffold3058                            | 16160                         | TGA/T                                                                     | TATTACCGTCTTCGGTT<br>CGC   | TCCTACGTATCCCCAA<br>GTGC  | 60.1                             | 319                                           | INTRON                                            | Ca_27792                            | A                     | --        |
| scaffold306_P4_477894 | scaffold306                             | 477894                        | TAAAAAAAAA/TAAAAAAAAA                                                     | CGTCATTGCTTCTTCC<br>CAT    | TGGGACTTAAAGCGT<br>CGTT   | 60.1                             | 880                                           | INTRON                                            | Ca_22723                            | C                     | NAC       |
| scaffold3134_P4_15211 | scaffold3134                            | 15211                         | TAAA/TAAAAA                                                               | CCTGGTTGAGTCTGGA<br>TAGCA  | GCATTGGCGTATCTTG<br>TTCA  | 60.3                             | 874                                           | INTRON                                            | Ca_27104                            | O                     | C2H2      |
| scaffold3155_P4_24057 | scaffold3155                            | 24057                         | GAAAAAAAA/GAAAAAA                                                         | TGCATATTTTGAACGA<br>ATGACA | TGCAACCATCGGTTAA<br>AATG  | 60.4                             | 505                                           | INTRON                                            | Ca_27114                            | R                     | NF-YB     |
| scaffold3155_P4_24408 | scaffold3155                            | 24408                         | GTAATAATAATAATAA/GTAATAA<br>TAATAATAA                                     | GGATGCGACCTTCTTC<br>TGTG   | TTGTCAAATCGGAGGA<br>AGTTG | 60.8                             | 630                                           | INTRON                                            | Ca_27114                            | R                     | NF-YB     |
| scaffold335_P4_137368 | scaffold335                             | 137368                        | TAAAAAAAAA/TAAAAAAAAA                                                     | GTATGGGTGTTTGGG<br>TTGC    | GGGCTGTTGTTCTGCA<br>AAAT  | 60.1                             | 469                                           | INTRON                                            | Ca_26029                            | --                    | NAC       |
| scaffold340_P4_257007 | scaffold340                             | 257007                        | AC/A                                                                      | GGCACATAGTTGCAAG<br>GGAT   | TTGCTCCATTGCTGAA<br>CTG   | 60.0                             | 564                                           | INTRON                                            | Ca_24961                            | --                    | S1Fa-like |
| scaffold340_P4_98841  | scaffold340                             | 98841                         | AC/A                                                                      | GAGGATCAATTGTTTG<br>CCAGA  | TCCCTACGCATAACCG<br>ACTC  | 60.1                             | 824                                           | INTRON                                            | Ca_24959                            | U                     | --        |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                                       | Forward primers (5'-3')    | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------------------|----------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                       |                                         |                               |                                                                                                                     |                            |                          |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| scaffold340_P4_99127  | scaffold340                             | 99127                         | GAAAAAAAA/GAAAAAAAAA                                                                                                | ATTCCCCGTTTGTCTAT<br>CAG   | TCCATAGCACCGGGAG<br>ATAC | 59.8                             | 564                                           | INTRON                                            | Ca_24959                            | U                     | --      |
| scaffold349_P4_263853 | scaffold349                             | 263853                        | AAATAATAATAATAATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AA/AAATAATAATAATAATAATA<br>TAATAATAATAATAATAATAATA<br>ATAATAA | AGCAAGCTTGATTGCC<br>TCAT   | GCTGAAAGTTTAGCCG<br>CATC | 60.0                             | 790                                           | INTRON                                            | Ca_24507                            | T                     | NAC     |
| scaffold366_P4_61217  | scaffold366                             | 61217                         | TCT/TCTACT                                                                                                          | TTGAGCTTGCAACTTG<br>ATCACT | CATTGGGCAAAGAAAC<br>ACCT | 60.1                             | 515                                           | INTRON                                            | Ca_26528                            | --                    | --      |
| scaffold379_P4_162943 | scaffold379                             | 162943                        | ATATTATTATTATTATTATTATTA<br>TTATT/ATATTATTATTATTATTATTA<br>TTATTATTATTATT                                           | TATGTTGGTTTTGGCA<br>AGCA   | GAGTTGCTGTTGAGG<br>AAGC  | 60.1                             | 872                                           | INTRON                                            | Ca_26157                            | U                     | --      |
| scaffold3945_P4_12983 | scaffold3945                            | 12983                         | G/GATCCTC                                                                                                           | TTCCAACCTCGATCCAG<br>CTCT  | ATACCGATTGACTGG<br>GCTG  | 60.0                             | 531                                           | INTRON                                            | Ca_26970                            | --                    | --      |
| scaffold395_P4_131314 | scaffold395                             | 131314                        | CATATATATATATATATAT/CATATAT<br>ATATAT                                                                               | CCACAAACCTTGGGCT<br>TCTA   | ATGACGGCCGTTTCTA<br>ACAC | 60.1                             | 641                                           | INTRON                                            | Ca_24514                            | K                     | G2-like |
| scaffold398_P4_179307 | scaffold398                             | 179307                        | CAA/CAAGGCTTAA                                                                                                      | TCGAAGAGGACAAAGT<br>GCCT   | CATCTTGAGTCCCGGT<br>TCAT | 60.0                             | 721                                           | INTRON                                            | Ca_22284                            | A                     | --      |
| scaffold398_P4_345675 | scaffold398                             | 345675                        | CATAAT/CAT                                                                                                          | AGAATCACCACAGGCA<br>CACA   | TGCCTCATTAGCTCAA<br>GGGT | 60.2                             | 522                                           | INTRON                                            | Ca_22294                            | K                     | C3H     |
| scaffold398_P4_346462 | scaffold398                             | 346462                        | CAAAAAA/CAAAAAA                                                                                                     | CCTTGAGCTAATGAGG<br>CACC   | TGACCGTTGTTCTGT<br>TCAT  | 59.8                             | 530                                           | INTRON                                            | Ca_22294                            | K                     | C3H     |
| scaffold40_P4_1054951 | scaffold40                              | 1054951                       | AC/ACC                                                                                                              | CGCTGGTTTAAAGCCT<br>CTGA   | TGGCTTGCTACTTGTG<br>TTGG | 60.5                             | 674                                           | INTRON                                            | Ca_19000                            | O                     | MYB     |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PfII)                                                                         | Forward primers (5'-3')   | Reverse primers (5'-3')    | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                          |                                  | Functional annotation |             |
|-----------------------|-----------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------|---------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------|----------------------------------|-----------------------|-------------|
|                       |                                         |                               |                                                                                                                                        |                           |                            |                                  |                                               | Sequence components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene accession IDs | NCBI-KOG              | TFs         |
| scaffold40_P4_846364  | scaffold40                              | 846364                        | GC/GCC                                                                                                                                 | CCTCAGCAGGATCAAA<br>CCAT  | TTACACTGCTGGGGTT<br>GTTG   | 60.1                             | 642                                           | INTRON                                         | Ca_18992                         | --                    | MYB_related |
| scaffold40_P4_846720  | scaffold40                              | 846720                        | ATT/ATTTT                                                                                                                              | CAACAACCCCAGCAGT<br>GTAA  | ACGAAACAGAAATGGG<br>CAAG   | 59.6                             | 408                                           | INTRON                                         | Ca_18992                         | --                    | MYB_related |
| scaffold408_P4_35918  | scaffold408                             | 35918                         | TTATATATATATATATATATATATA<br>TAT/TTATATATATATATATATATATA<br>TATATATATATATAT                                                            | TTGTTAGTTTGACGAG<br>GGCA  | TTTTGTTGTGGTAGGG<br>CACACA | 59.3                             | 423                                           | INTRON                                         | Ca_25271                         | --                    | Trihelix    |
| scaffold418_P4_71090  | scaffold418                             | 71090                         | ATTATTTTATTTTATT/ATTATTTATT<br>ATTTATTT                                                                                                | ACGCCAACGTCAAATC<br>CTAC  | CTGCATACATGTGCTC<br>GTCA   | 60.0                             | 276                                           | INTRON                                         | Ca_24674                         | --                    | --          |
| scaffold419_P4_158386 | scaffold419                             | 158386                        | TACTCA/TA                                                                                                                              | AAAATTGTTTCGCGTTAT<br>GCC | TCCCATTTTCCTTATCA<br>GCG   | 60.0                             | 263                                           | INTRON                                         | Ca_26399                         | U                     | --          |
| scaffold4383_P4_25907 | scaffold4383                            | 25907                         | TATAATAATAATAATAATAATAA<br>TAATAATAATAATAATAATAATA<br>ATAATAATAATAATA/TATAATAATA<br>ATAATAATAATAATAATAATAAT<br>AATAATAATAATAATAATAATAA | TGATCTCTAACGGACC<br>ACCC  | TCATGTGCTTTTACTGC<br>CCA   | 59.9                             | 781                                           | INTRON                                         | Ca_28195                         | --                    | --          |
| scaffold4387_P4_5637  | scaffold4387                            | 5637                          | TTCTT/TTCTCTCT                                                                                                                         | TCAAAAAGAGGCGAGC<br>ATTT  | GGCGATTGTGGAAGA<br>CAGT    | 60.0                             | 191                                           | INTRON                                         | Ca_27838                         | U                     | --          |
| scaffold44_P4_242545  | scaffold44                              | 242545                        | CATATATATATATATATATATATA<br>TATATATATATATATA/CATATATA<br>TATATATATATATATATATATATAT<br>ATATATATATA                                      | AATAAGTTCACGTGGC<br>CTGG  | AGAGTGCAGTCGCTCA<br>CAGA   | 60.0                             | 555                                           | INTRON                                         | Ca_25415                         | --                    | FAR1        |
| scaffold4452_P4_34079 | scaffold4452                            | 34079                         | CTATATATATATATATATATATAT<br>AT/CTATATATATATATATATATAT<br>ATATATAT                                                                      | TGAGCACGTCGAAATT<br>GAAG  | GTGACATGGAACATG<br>GTGG    | 60.0                             | 559                                           | INTRON                                         | Ca_26055                         | --                    | B3          |
| scaffold4452_P4_95348 | scaffold4452                            | 95348                         | TAAAAAAAA/TAAAAAAAAA                                                                                                                   | CCAAAAACCGAGAGAA<br>ACAA  | TCTCGATCTTACCTCTT<br>GGCA  | 60.1                             | 649                                           | INTRON                                         | Ca_26058                         | QR                    | B3          |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')        | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |             |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|-------------|
|                        |                                         |                               |                                                               |                                |                               |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs         |
| scaffold4511_P4_38356  | scaffold4511                            | 38356                         | GTTTTTTTTT/GTTTTTTTTT                                         | AATGCCACCCATAAT<br>TTCA        | CTGGGCAAGGGATCTG<br>AATA      | 60.0                             | 642                                           | INTRON                                            | Ca_28219                            | --                    | Trihelix    |
| scaffold453_P4_385361  | scaffold453                             | 385361                        | TT/TTAT                                                       | TTTGAATAGCTTAGTT<br>GATTGACTTG | TTTGGGGTTTAGGGT<br>GTCA       | 59.4                             | 602                                           | INTRON                                            | Ca_21741                            | --                    | Trihelix    |
| scaffold453_P4_496517  | scaffold453                             | 496517                        | CAAAAAAAAA/CAAAAAAAAA                                         | TTTCTCACGCTGGATC<br>CTCT       | AAAGTGATGCCGATGA<br>AAGG      | 60.0                             | 875                                           | INTRON                                            | Ca_21748                            | --                    | --          |
| scaffold453_P4_79397   | scaffold453                             | 79397                         | AG/ACTAAGATTG                                                 | TTGTTTGACCCATTGTA<br>CTTTGA    | TTGCTAGTTGCTGATG<br>TGCC      | 59.4                             | 183                                           | INTRON                                            | Ca_21728                            | --                    | MYB_related |
| scaffold453_P4_80166   | scaffold453                             | 80166                         | T/TCATG                                                       | AATTTAAACCGGCCAA<br>AACC       | TCACTCATAAATATCCT<br>CATGGACA | 60.1                             | 578                                           | INTRON                                            | Ca_21728                            | --                    | MYB_related |
| scaffold466_P4_166277  | scaffold466                             | 166277                        | ACTC/ATAATCATTACTC                                            | AAGTTTCCCGTGTG<br>AGTG         | TAACGAGGATCCATTG<br>GAGG      | 60.0                             | 800                                           | INTRON                                            | Ca_25699                            | --                    | --          |
| scaffold466_P4_169717  | scaffold466                             | 169717                        | A/ATGCAAAAGATTCTA                                             | CTTTCGTGCCCTTGAT<br>TTGT       | CGTGGCCTATCGATCC<br>TTTA      | 60.1                             | 740                                           | INTRON                                            | Ca_25699                            | --                    | --          |
| scaffold466_P4_170442  | scaffold466                             | 170442                        | CA/CACGGA                                                     | ACCCTTTTGTCCACAC<br>GAG        | AAGCTGACTTCGGTTG<br>GCTA      | 60.0                             | 270                                           | INTRON                                            | Ca_25699                            | --                    | --          |
| scaffold4777_P4_118728 | scaffold4777                            | 118728                        | CTTTTTTT/CTTTTTTTTT                                           | AACGGTTTGGTTTGAT<br>CTGC       | ACGTCGTCAAACAGAT<br>GCAC      | 60.0                             | 231                                           | INTRON                                            | Ca_26711                            | R                     | --          |
| scaffold496_P4_211993  | scaffold496                             | 211993                        | GTATATATATAT/GTATATATAT                                       | CCTTCATGAACCGCAA<br>TACA       | TCTCCGCATAAGCTTTC<br>GAT      | 59.5                             | 651                                           | INTRON                                            | Ca_27203                            | --                    | --          |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                                          | Forward primers (5'-3')       | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|-----------------------|-----------------------------------------|-------------------------------|--------------------------------------------------------------------------------------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                       |                                         |                               |                                                                                                        |                               |                           |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| scaffold674_P4_135503 | scaffold674                             | 135503                        | TCC/TC                                                                                                 | GGCCTCATGAATGTT<br>TAGGT      | TGCAACATGTGTGTAT<br>GGAGG | 59.4                             | 536                                           | INTRON                                            | Ca_20154                            | --                    | --   |
| scaffold682_P4_253027 | scaffold682                             | 253027                        | AATATATATATATAT/AATATATATAT                                                                            | TATTCAGATCCCTTGC<br>CCAG      | TGGGTGCTATTTGCAA<br>TCAA  | 60.0                             | 626                                           | INTRON                                            | Ca_23190                            | --                    | --   |
| scaffold6903_P4_4993  | scaffold6903                            | 4993                          | CA/CTTGTTTCATGGATAA                                                                                    | CATCAGCGTGAAATGT<br>GCTT      | TCCATTTTGTGTGGTG<br>TGC   | 59.9                             | 768                                           | INTRON                                            | Ca_28223                            | --                    | --   |
| scaffold6903_P4_5314  | scaffold6903                            | 5314                          | A/AT                                                                                                   | GCACACCACAACAAAA<br>TGGA      | GCATCCTCTGATTGTT<br>GGG   | 60.4                             | 458                                           | INTRON                                            | Ca_28223                            | --                    | --   |
| scaffold696_P4_52341  | scaffold696                             | 52341                         | CATATAT/CATATATAT                                                                                      | AACGGAAGTCAAAAGA<br>GGCA      | TGACTGAGGCAAGATG<br>GTTG  | 59.9                             | 692                                           | INTRON                                            | Ca_25809                            | --                    | bHLH |
| scaffold716_P4_135403 | scaffold716                             | 135403                        | AATTATTATTATTATTATTATTAT<br>TATTATTATTATTATTATTAT/AATTA<br>TTATTATTATTATTATTATTATTA<br>TTATTATTATTAT   | TGATCATATAAAACAA<br>ATGCTCACA | TGTGCAAGATTCTGTT<br>CCA   | 59.8                             | 410                                           | INTRON                                            | Ca_24965                            | --                    | bHLH |
| scaffold724_P4_101398 | scaffold724                             | 101398                        | TA/TAGA                                                                                                | ATCTTGCCCAATGTTG<br>ATGA      | TGGGATAGCGGCATTT<br>TTAC  | 58.9                             | 249                                           | INTRON                                            | Ca_25051                            | Q                     | NAC  |
| scaffold724_P4_21848  | scaffold724                             | 21848                         | TATAAAATAAAATAAAATAAA<br>TAAAAATAAAATAAA/TATAAAAT<br>AAAAATAAAATAAAATAAAATAA<br>AAATAAAATAAAATAAAATAAA | CAGAACAAACACGAGA<br>GCCA      | ATCAGAGCACATCATC<br>GCAT  | 60.0                             | 620                                           | INTRON                                            | Ca_25043                            | O                     | --   |
| scaffold731_P4_365330 | scaffold731                             | 365330                        | T/TGCTTATCTCCAACCTCG                                                                                   | CTACGAGATCACCCCA<br>AGGA      | CCTAATGTGGGTGGAT<br>TTGG  | 60.1                             | 498                                           | INTRON                                            | Ca_23818                            | --                    | --   |
| scaffold731_P4_371953 | scaffold731                             | 371953                        | T/TCACTTCCGC                                                                                           | CATCAGTTACTTCAGC<br>GCCA      | GTTTGCCTAGAAGCAG<br>CCAC  | 60.0                             | 641                                           | INTRON                                            | Ca_23820                            | --                    | --   |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                           | Forward primers (5'-3')  | Reverse primers (5'-3')  | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |        |
|-----------------------|-----------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------|--------------------------|--------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|--------|
|                       |                                         |                               |                                                                                         |                          |                          |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs    |
| scaffold731_P4_374028 | scaffold731                             | 374028                        | AA/AAGGGAGATAGTGCA                                                                      | TCCTTGGGGTGATCTC<br>GTAG | ATGGACGGTAGTTGGA<br>GTCG | 60.1                             | 222                                           | INTRON                                            | Ca_23820                            | --                    | --     |
| scaffold731_P4_390482 | scaffold731                             | 390482                        | C/CAA                                                                                   | TATCATAGGCCGTAGG<br>CCAG | TTATTGCTCCAATTCCC<br>TCG | 60.1                             | 482                                           | INTRON                                            | Ca_23820                            | --                    | --     |
| scaffold731_P4_392660 | scaffold731                             | 392660                        | TT/TTTTTGCTAATCTAAT                                                                     | GAACGACGGAACCTGT<br>GAAT | AGGAAGCCCAAGTTCC<br>AAAT | 60.0                             | 665                                           | INTRON                                            | Ca_23820                            | --                    | --     |
| scaffold7355_P4_1852  | scaffold7355                            | 1852                          | CAA/CA                                                                                  | GTGCAATATTGGATCC<br>ACCC | AGCTGCAATGAAACCT<br>GCTT | 60.0                             | 386                                           | INTRON                                            | Ca_28031                            | --                    | NF-YB  |
| scaffold757_P4_12918  | scaffold757                             | 12918                         | ATTTTTTTTT/ATTTTTTTTT                                                                   | GGGGTATGAGAGATGG<br>CTGA | CGTGCAACGAGAGTAA<br>ATGA | 60.0                             | 542                                           | INTRON                                            | Ca_27764                            | --                    | --     |
| scaffold766_P4_206125 | scaffold766                             | 206125                        | GTT/GTTT                                                                                | AAAGGAATTGAGGGGA<br>TTGG | CCTTGAGTTCGACACT<br>CGGT | 60.1                             | 227                                           | INTRON                                            | Ca_24691                            | I                     | bHLH   |
| scaffold775_P4_347207 | scaffold775                             | 347207                        | AATATATATATATATATATATATAT<br>ATATATATATAT/AATATATATATATA<br>TATATATATATATATATATATATATAT | CACTGAGTTGGTCCCC<br>TTGT | ACCAAGATCCAAAAGG<br>TCCC | 60.0                             | 533                                           | INTRON                                            | Ca_23412                            | --                    | --     |
| scaffold809_P4_99867  | scaffold809                             | 99867                         | AAAAATATAAA/AAAA                                                                        | CATGGGCAACAAGCCT<br>TTAT | TTTCTCTTTTATCCCC<br>GCT  | 60.0                             | 675                                           | INTRON                                            | Ca_26625                            | L                     | HB-PHD |
| scaffold811_P4_159571 | scaffold811                             | 159571                        | TTATATATATATATATATATATATATA<br>T/TTATATATATATATATATATATATA<br>T                         | TTGCAACATGCTATTTT<br>CCA | TGGGTGCTATTTGCAA<br>TCAA | 60.1                             | 613                                           | INTRON                                            | Ca_27462                            | --                    | --     |
| scaffold845_P4_29439  | scaffold845                             | 29439                         | TAAACAAAACAAA/TAAACAAA                                                                  | GCTTCTGACTTGTTTT<br>CGC  | ACTAAATGCATCACGG<br>GGAG | 60.0                             | 516                                           | INTRON                                            | Ca_22410                            | --                    | bHLH   |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)                         | Forward primers (5'-3')    | Reverse primers (5'-3')    | Annealing<br>temperature<br>(0C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                                |                                     | Functional annotation |          |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------------------|----------------------------|----------------------------|----------------------------------|-----------------------------------------------|------------------------------------------------------|-------------------------------------|-----------------------|----------|
|                       |                                         |                               |                                                                                       |                            |                            |                                  |                                               | Sequence<br>components<br>of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| scaffold845_P4_331317 | scaffold845                             | 331317                        | GAIAIAIA/GAIAIAIA                                                                     | CATGTGCAATTTGCTT<br>GTCC   | GATCAAGCATTGAGTT<br>GGCA   | 60.1                             | 614                                           | INTRON                                               | Ca_22427                            | --                    | --       |
| scaffold845_P4_356717 | scaffold845                             | 356717                        | TTTTATTATTTATTTATTTATTTATTT<br>TATTTATTT/TTTTATTTATTTATTTAT<br>TTATTTATTTATTTATTTATTT | GGAGGGTTAGCTTGG<br>GAGAC   | TGCATGCAGGACCAAT<br>TAAA   | 60.1                             | 532                                           | INTRON                                               | Ca_22428                            | R                     | G2-like  |
| scaffold857_P4_4229   | scaffold857                             | 4229                          | TG/T                                                                                  | TTGCAAACCTATAATC<br>CCG    | ACTTACGACAAACGCG<br>AGGT   | 59.8                             | 984                                           | INTRON                                               | Ca_27907                            | --                    | Trihelix |
| scaffold864_P4_29919  | scaffold864                             | 29919                         | TTATATATATATATATATATATATATA<br>TA/TTATATATATATATATATATATA                             | AAAAGTGCCAAGAAAA<br>TGCG   | GCCATGTGAGGGTTTT<br>TGTT   | 60.2                             | 397                                           | INTRON                                               | Ca_24203                            | --                    | FAR1     |
| scaffold873_P4_89467  | scaffold873                             | 89467                         | GAIAIAIAIA/GAIAIAIAIAIA                                                               | AAGCTGATCAAAGACG<br>TGCC   | AAAAATGGAAAGCGCA<br>TCAG   | 60.4                             | 706                                           | INTRON                                               | Ca_23476                            | R                     | --       |
| scaffold892_P4_25346  | scaffold892                             | 25346                         | G/GGT                                                                                 | CTCCATCCATTTTCGT<br>GCTT   | CGGAACCAGCTTTGAG<br>TAGC   | 60.1                             | 408                                           | INTRON                                               | Ca_27454                            | R                     | --       |
| scaffold895_P4_49790  | scaffold895                             | 49790                         | TAAATAIAIAIAATIAIAIAIAATAIA<br>AAAA/TAAATAIAIAIAATIAIAIAIA                            | GTCACGGGAGTCCAAA<br>GGTA   | TTTTTGGAACATCATCA<br>TCAGC | 60.0                             | 623                                           | INTRON                                               | Ca_24249                            | G                     | NAC      |
| scaffold9_P4_34748    | scaffold9                               | 34748                         | CACAACAA/CACAA                                                                        | GGACAAACTACCCCTC<br>CTTTTC | TCTTCCCCATAAACCA<br>ACA    | 60.2                             | 317                                           | INTRON                                               | Ca_27384                            | --                    | WOX      |
| scaffold93_P4_338023  | scaffold93                              | 338023                        | TCCCC/TCCC                                                                            | AAACTTGCAAGCCATT<br>CCAG   | TTTGAGAAATATGCTG<br>GGGC   | 60.2                             | 876                                           | INTRON                                               | Ca_23073                            | L                     | GRAS     |
| scaffold93_P4_573293  | scaffold93                              | 573293                        | AATAT/AAT                                                                             | AATTTAGCCCGATTTTG<br>CCT   | CCTAAACGGGCTAGAG<br>GTCC   | 59.9                             | 711                                           | INTRON                                               | Ca_23083                            | --                    | --       |

| INDEL marker IDs       | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII)             | Forward primers (5'-3')   | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |          |
|------------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------------------|---------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|----------|
|                        |                                         |                               |                                                                           |                           |                              |                                  |                                               | Sequence<br>components of<br><i>Kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs      |
| scaffold937_P4_124790  | scaffold937                             | 124790                        | TTGTG/TTG                                                                 | TCGCATATGGAAGTGG<br>ATCA  | AACGATTAGAATGGG<br>GAGG      | 60.0                             | 614                                           | INTRON                                            | Ca_25987                            | --                    | --       |
| scaffold959_P4_57749   | scaffold959                             | 57749                         | GAAAAAAAAA/GAAAAAAAAA                                                     | AAGGCGTGCATATCCC<br>ATAC  | TGTTTCGTCAAAATGTCC<br>CAA    | 59.8                             | 553                                           | INTRON                                            | Ca_27234                            | --                    | Trihelix |
| scaffold962_P4_36020   | scaffold962                             | 36020                         | AATATATATATATATTTATATATATAT<br>/AATATATATATATATATATATATATT<br>TATATATATAT | TGCACGTCTTGAGCAA<br>AAAC  | GTGCAGTCTCTCACGG<br>ACAA     | 60.0                             | 859                                           | INTRON                                            | Ca_26498                            | --                    | Trihelix |
| C11177592_P4_12510     | C11177592                               | 12510                         | ATTTTTTT/ATTTTTTTT                                                        | TTTGAAATTGGTTCCG<br>CAAT  | GACCCGTTAATGTACA<br>ACAACAAA | 60.3                             | 864                                           | URR                                               | Ca_27747                            | --                    | --       |
| C11181782_P4_11139     | C11181782                               | 11139                         | ATTTTTTTTTTT/ATTTTTTTTTTTTTTT<br>TT                                       | TGGTAGGGGTCGAGG<br>ACTTA  | CTGAATTTTGTTCGCCC<br>CTA     | 59.5                             | 214                                           | URR                                               | Ca_27691                            | --                    | --       |
| scaffold1120_P4_11138  | scaffold1120                            | 11138                         | C/CA                                                                      | TTCATCCAAAGAATCTG<br>GGC  | TGCAAGAGGAGTGCCT<br>TTCT     | 60.0                             | 486                                           | URR                                               | Ca_27900                            | --                    | --       |
| scaffold1196_P4_206626 | scaffold1196                            | 206626                        | ATT/ATTT                                                                  | TTCTGCCAAGTTCCCA<br>TTTC  | TAAAGGATTCCCACTG<br>TGCC     | 60.1                             | 699                                           | URR                                               | Ca_26186                            | --                    | Trihelix |
| scaffold1197_P4_458259 | scaffold1197                            | 458259                        | TATTC/T                                                                   | TGATTCAACAAAACTC<br>AAGGG | AAAATCACATGCCATA<br>ACAAGT   | 59.1                             | 693                                           | URR                                               | Ca_24075                            | U                     | MYB      |
| scaffold1452_P4_29738  | scaffold1452                            | 29738                         | ATTT/ATTTT                                                                | GAAGCCTTTTCAGCAG<br>GTTG  | TAGTGTGCCCACTC<br>CAAA       | 60.0                             | 648                                           | URR                                               | Ca_27551                            | R                     | ZF-HD    |
| scaffold1499_P4_141350 | scaffold1499                            | 141350                        | TAAAAAAAAAAAAA/TAAAAAAAAAAAAA<br>A                                        | ACAACATCAGTCCAAT<br>GCCA  | CAGCAGTGTGAAACGA<br>AGGA     | 60.0                             | 765                                           | URR                                               | Ca_26939                            | --                    | Dof      |



| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')         | Reverse primers (5'-3')        | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|---------------------------------|--------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                       |                                         |                               |                                                               |                                 |                                |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| scaffold1561_P4_70851 | scaffold1561                            | 70851                         | GTT/GTTT                                                      | AGGCTGTTGTGATGT<br>GCAG         | CATCATCAAAAAGGGG<br>GAGA       | 59.9                             | 390                                           | URR                                               | Ca_28168                            | --                    | --   |
| scaffold1641_P4_2927  | scaffold1641                            | 2927                          | AATATATATATATATATAT/AATAT<br>ATATATATATATATATAT               | TTGGCCAGTATGATTC<br>GACA        | GGGTGTTGGGTTTAGG<br>GTTT       | 60.1                             | 711                                           | URR                                               | Ca_28140                            | J                     | --   |
| scaffold1810_P4_98576 | scaffold1810                            | 98576                         | GGTTGT/GGTTGTTGT                                              | TGACGATACGAAACGA<br>TGGA        | AGCGATGCATGTCTCA<br>AGTG       | 60.1                             | 430                                           | URR                                               | Ca_26004                            | --                    | --   |
| scaffold2010_P4_6749  | scaffold2010                            | 6749                          | T/TC                                                          | TTCCCTTTCGTTGTGA<br>TCG         | GGGCACCGATGTTACA<br>TAAA       | 58.6                             | 857                                           | URR                                               | Ca_27976                            | --                    | --   |
| scaffold2010_P4_7925  | scaffold2010                            | 7925                          | ATTTTTTTTT/ATTTTTTTTTT                                        | AAAGTGCCTTCTTCTT<br>GGCA        | ATGTTTTCTTTGGGTT<br>GCG        | 60.0                             | 564                                           | URR                                               | Ca_27976                            | --                    | --   |
| scaffold202_P4_103827 | scaffold202                             | 103827                        | AGGG/AGG                                                      | TCAATAAGACGTGATA<br>AGTTAATCCA  | TTGGAGAAAGATATGA<br>TACGATAGGA | 58.3                             | 847                                           | URR                                               | Ca_27127                            | A                     | --   |
| scaffold202_P4_103994 | scaffold202                             | 103994                        | ATTTTTTTTT/ATTTTTTTTTTTT                                      | AAATTGCTTATTTAGTA<br>GTGTCAATCG | AACTCAGCAAAACCCA<br>AAACA      | 58.5                             | 409                                           | URR                                               | Ca_27127                            | A                     | --   |
| scaffold202_P4_104373 | scaffold202                             | 104373                        | TAAAAAAAAA/TAAAAAAAAA                                         | TGTTTTGGGTTTTGCT<br>GAGTT       | TGGATGGATTGGATGA<br>ATGA       | 59.6                             | 180                                           | URR                                               | Ca_27127                            | A                     | --   |
| scaffold2170_P4_38090 | scaffold2170                            | 38090                         | AATATATATATATATATATA/AATA<br>TATATATATATATATATA               | TGTGGTCTCAAATCCA<br>CCAA        | TGACGGATATTTGTCAT<br>GTGG      | 59.9                             | 720                                           | URR                                               | Ca_26931                            | QI                    | bHLH |
| scaffold2368_P4_59799 | scaffold2368                            | 59799                         | TC/TCTCC                                                      | CTCCAAATCCCAATCT<br>CCAA        | CTCACTGTCAAGGTGC<br>CGTA       | 59.9                             | 725                                           | URR                                               | Ca_26721                            | --                    | MYB  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')    | Reverse primers (5'-3')   | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                       |                                         |                               |                                                               |                            |                           |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| scaffold2433_P4_2074  | scaffold2433                            | 2074                          | AATATATAT/AATATAT                                             | ACGATACGTTGTCGGC<br>TAGG   | TTGTGTCAAGCGGGAT<br>CATA  | 60.2                             | 432                                           | URR                                               | Ca_27860                            | --                    | --   |
| scaffold2433_P4_2752  | scaffold2433                            | 2752                          | CATATA/CATA                                                   | TATGATCCCGCTTGAC<br>ACAA   | CCCAACTAGATTGCTA<br>CGCC  | 60.1                             | 655                                           | URR                                               | Ca_27860                            | --                    | --   |
| scaffold2458_P4_1738  | scaffold2458                            | 1738                          | CAAAAA/CAAAA                                                  | CGATTTCCTGCATGT<br>TTTT    | CCCGTGATAGGCAGTA<br>CGTT  | 59.9                             | 620                                           | URR                                               | Ca_28112                            | --                    | --   |
| scaffold2603_P4_50338 | scaffold2603                            | 50338                         | AATATATATATATATATATA/AATA<br>TATATATATATATATATA               | TTGGCAACAAGGTGGG<br>TAAT   | TGGTGCTCCAATTTGT<br>GAA   | 60.2                             | 594                                           | URR                                               | Ca_27950                            | --                    | --   |
| scaffold2722_P4_77542 | scaffold2722                            | 77542                         | ATTTTTTTTT/ATTTTTTTT                                          | GGAAGGAGAACGCCTA<br>AGGT   | AAAAATGGATCTCACG<br>GTGC  | 59.7                             | 946                                           | URR                                               | Ca_27216                            | --                    | C2H2 |
| scaffold3019_P4_20892 | scaffold3019                            | 20892                         | A/AATGGT                                                      | TGCATGAGTTGTTAAG<br>GCGA   | TATGC AAAACGGGACT<br>TCCT | 60.4                             | 582                                           | URR                                               | Ca_28069                            | --                    | --   |
| scaffold3258_P4_34164 | scaffold3258                            | 34164                         | TAAAAAAAAA/TAAAAAAAAA                                         | GGGTTTGCTTACCGAA<br>CTCA   | TACGG AAAATTACCCA<br>CGGA | 60.1                             | 375                                           | URR                                               | Ca_27898                            | --                    | --   |
| scaffold3258_P4_34821 | scaffold3258                            | 34821                         | TAAAAAAAAA/TAAAAAAAAA                                         | TGCAGAAATTGTCTTC<br>ATGCTT | GTGACACGTCGGAAGG<br>AAAT  | 58.9                             | 837                                           | URR                                               | Ca_27898                            | --                    | --   |
| scaffold3329_P4_3842  | scaffold3329                            | 3842                          | C/CT                                                          | TCTAAGCAGGGGCCTA<br>ATGA   | TTGGACCTGCCAAGT<br>TAAG   | 59.8                             | 427                                           | URR                                               | Ca_28259                            | --                    | --   |
| scaffold3794_P4_72529 | scaffold3794                            | 72529                         | ATTTTTTTTT/ATTTTTTTTTT                                        | GATGATTTTGGTCAAT<br>GGGG   | TACCGG AAAACATGTG<br>GATG | 60.0                             | 598                                           | URR                                               | Ca_26696                            | GMW                   | NAC  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')  | Reverse primers (5'-3')      | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |      |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|--------------------------|------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|------|
|                       |                                         |                               |                                                               |                          |                              |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs  |
| scaffold398_P4_491025 | scaffold398                             | 491025                        | ATAT/ATATTTAT                                                 | CCGATATTGAAGGGCA<br>TTGT | GGAAAATAATTGCATGA<br>TGGG    | 59.8                             | 550                                           | URR                                               | Ca_22300                            | --                    | C2H2 |
| scaffold398_P4_491040 | scaffold398                             | 491040                        | T/TTTAG                                                       | CCGATATTGAAGGGCA<br>TTGT | GGAAAATAATTGCATGA<br>TGGG    | 59.8                             | 550                                           | URR                                               | Ca_22300                            | --                    | C2H2 |
| scaffold420_P4_344571 | scaffold420                             | 344571                        | CTTTTTTTTT/CTTTTTTTTT                                         | TCCTCTATGTTGCCGT<br>TTCC | TCACTCTCCAAATGGAA<br>CCC     | 60.1                             | 192                                           | URR                                               | Ca_22212                            | G                     | NAC  |
| scaffold433_P4_169477 | scaffold433                             | 169477                        | ATTATTTATTTATTTATTTA/ATTATT<br>TATTTATTTATTTATTTA             | CTAGTGGGTACCCGCA<br>AAAA | GGTGGGCATATTACAA<br>CGCT     | 60.0                             | 576                                           | URR                                               | Ca_26821                            | --                    | --   |
| scaffold453_P4_497792 | scaffold453                             | 497792                        | CAATAATAATAATA/CAATAATAA<br>TAATAATAATA                       | GCCGTGATTTGGAAAA<br>AGAA | TGTCAGTTTTGAGCCC<br>AATG     | 60.1                             | 479                                           | URR                                               | Ca_21748                            | --                    | --   |
| scaffold453_P4_498751 | scaffold453                             | 498751                        | GATAT/GATATAT                                                 | GCCCTCAAAGATAAC<br>CCAT  | GACCATGATTTCTTACT<br>AGCCGTT | 60.2                             | 838                                           | URR                                               | Ca_21748                            | --                    | --   |
| scaffold537_P4_258578 | scaffold537                             | 258578                        | CTTTTTTAATTT/CTTTTTTATTTTTTA<br>TTT                           | GATGTTTGGATTGGGG<br>TTTG | AAGCACATATTTGTTGC<br>CCC     | 60.0                             | 288                                           | URR                                               | Ca_23292                            | R                     | --   |
| scaffold593_P4_211628 | scaffold593                             | 211628                        | TT/TTGTGAT                                                    | TACGTACGGCAGTAGC<br>CCTT | ATTTCCCGGAATCATT<br>AGG      | 59.8                             | 673                                           | URR                                               | Ca_26412                            | --                    | C2H2 |
| scaffold6878_P4_1840  | scaffold6878                            | 1840                          | TC/T                                                          | TGGACACGACGGTGAA<br>ATAA | GTTTGAAATCTGACCC<br>GGAA     | 60.0                             | 704                                           | URR                                               | Ca_27881                            | --                    | --   |
| scaffold724_P4_126741 | scaffold724                             | 126741                        | CTTTTT/CTTTT                                                  | TCGCACTTCAATATGCT<br>TCG | AAAGGCCATGCAAGAA<br>GAGA     | 60.0                             | 851                                           | URR                                               | Ca_25052                            | Q                     | NAC  |

| INDEL marker IDs      | Chromosomes/<br>unanchored<br>scaffolds | Physical<br>positions<br>(bp) | InDels ( <i>Kabuli</i> reference genome-<br>CDC Frontier/PII) | Forward primers (5'-3')     | Reverse primers (5'-3')       | Annealing<br>temperature<br>(°C) | Expected<br>amplified<br>product size<br>(bp) | Structural annotation                             |                                     | Functional annotation |         |
|-----------------------|-----------------------------------------|-------------------------------|---------------------------------------------------------------|-----------------------------|-------------------------------|----------------------------------|-----------------------------------------------|---------------------------------------------------|-------------------------------------|-----------------------|---------|
|                       |                                         |                               |                                                               |                             |                               |                                  |                                               | Sequence<br>components of<br><i>kabuli</i> genome | <i>Kabuli</i> gene<br>accession IDs | NCBI-KOG              | TFs     |
| scaffold7355_P4_6659  | scaffold7355                            | 6659                          | CTATTTTATTTTATTTT/CTATT<br>TTTATTTT                           | CACGTCTATATCCACG<br>CCCT    | TCACAATTGCAATACAT<br>GGGA     | 60.0                             | 537                                           | URR                                               | Ca_28031                            | --                    | NF-YB   |
| scaffold7650_P4_9735  | scaffold7650                            | 9735                          | T/TG                                                          | TATGGCATTGTGGTGC<br>ACTT    | GGATTAAAATTGGAATT<br>GTTCAAGA | 60.0                             | 482                                           | URR                                               | Ca_27809                            | O                     | --      |
| scaffold7650_P4_9922  | scaffold7650                            | 9922                          | CA/CATA                                                       | CCGCAATTATATCTGC<br>GACA    | AGTTCAAAAATACGCG<br>GGTG      | 59.7                             | 857                                           | URR                                               | Ca_27809                            | O                     | --      |
| scaffold766_P4_243668 | scaffold766                             | 243668                        | GTTA/GTTAATTA                                                 | CTCAACATGCATGCAA<br>AACC    | TCCCAACCCAAATAAAC<br>CAA      | 60.1                             | 537                                           | URR                                               | Ca_24693                            | --                    | --      |
| scaffold787_P4_434296 | scaffold787                             | 434296                        | TAAAAAAAAA/TAAAAAAAAA                                         | GCCACGCAGTGTTTTA<br>TTGA    | ACATCGAATCGTCCAT<br>GTCA      | 59.7                             | 645                                           | URR                                               | Ca_25848                            | R                     | NAC     |
| scaffold7923_P4_25395 | scaffold7923                            | 25395                         | ATC/A                                                         | AAAATATGCCATTTCGAT<br>CAAGA | AAATGGCTTGGTTATG<br>GCTG      | 58.6                             | 200                                           | URR                                               | Ca_27507                            | QI                    | bHLH    |
| scaffold893_P4_10161  | scaffold893                             | 10161                         | GAA/GAAA                                                      | AAGGTTTTGACTCTGC<br>CCCT    | GTGCCAGTCGATTGCC<br>TAAT      | 60.1                             | 304                                           | URR                                               | Ca_27923                            | --                    | B3      |
| scaffold982_P4_14935  | scaffold982                             | 14935                         | CT/CTAAACTCTCGTAACAGT                                         | GTCCATAGTCTTGCCG<br>GTGT    | GCGATGAGTTGGATGG<br>AAGT      | 60.0                             | 632                                           | URR                                               | Ca_28025                            | --                    | G2-like |